

From: Bunner, Bridget
Sent: Tuesday, March 29, 2005 11:15 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:

1. the nucleic acid sequence encoding the protein of SEQ ID NO: 5
2. the nucleic acid sequence encoding the protein of SEQ ID NO: 4
3. the nucleic acid sequence of SEQ ID NO: 1

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

1 - 3071 NA
4 - 897 AA
5 - 888 AA

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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| Result No. | Query % | | | DB | ID | Description |
|------------|---------|-------|--------|----|--------------------|--------------------|
| | Score | Match | Length | | | |
| 1 | 3040.4 | 99.0 | 3137 | 4 | US-09-590-304-1 | Sequence 1, Appli |
| 2 | 2890.8 | 94.1 | 3111 | 4 | US-09-825-147-3 | Sequence 3, Appli |
| 3 | 2857.4 | 93.0 | 3074 | 4 | US-09-813-148-1 | Sequence 1, Appli |
| 4 | 2635.4 | 85.8 | 2772 | 4 | US-09-825-147-1 | Sequence 1, Appli |
| 5 | 518 | 16.9 | 2196 | 4 | US-09-949-016-1823 | Sequence 1823, Ap |
| 6 | 518 | 16.9 | 2335 | 3 | US-09-492-361-1 | Sequence 1, Appli |
| 7 | 517.6 | 16.9 | 2373 | 3 | US-09-177-650-88 | Sequence 88, Appli |
| 8 | 511.6 | 16.7 | 2169 | 3 | US-09-105-058C-22 | Sequence 22, Appli |
| 9 | 509.8 | 16.6 | 582 | 4 | US-09-495-050A-303 | Sequence 303, App |
| 10 | 465.4 | 15.2 | 896 | 3 | US-09-105-058C-1 | Sequence 1, Appli |
| 11 | 463.6 | 15.1 | 2814 | 3 | US-09-177-650-90 | Sequence 90, Appli |
| 12 | 460.8 | 15.0 | 2565 | 3 | US-09-105-058C-26 | Sequence 26, Appli |
| 13 | 460.8 | 15.0 | 2914 | 3 | US-09-177-650-6 | Sequence 6, Appli |
| 14 | 452 | 14.7 | 575 | 4 | US-09-495-050A-305 | Sequence 305, App |
| 15 | 425 | 13.8 | 3287 | 3 | US-09-105-058C-19 | Sequence 19, Appli |
| 16 | 423.4 | 13.8 | 3232 | 3 | US-09-177-650-1 | Sequence 1, Appli |
| 17 | 423.4 | 13.8 | 3237 | 3 | US-09-177-650-95 | Sequence 95, Appli |
| 18 | 421.4 | 13.7 | 900 | 3 | US-09-105-058C-3 | Sequence 3, Appli |
| 19 | 420.6 | 13.7 | 900 | 3 | US-09-105-058C-5 | Sequence 5, Appli |
| 20 | 363.8 | 11.8 | 930 | 3 | US-09-105-058C-17 | Sequence 17, Appli |
| 21 | 334.2 | 10.9 | 735 | 3 | US-09-105-058C-7 | Sequence 7, Appli |
| 22 | 276.4 | 9.0 | 284 | 4 | US-09-495-050A-304 | Sequence 304, App |
| 23 | 267.8 | 8.7 | 2028 | 3 | US-09-634-920-1 | Sequence 1, Appli |
| 24 | 267.8 | 8.7 | 2028 | 4 | US-09-840-125-1 | Sequence 1, Appli |
| 25 | 267.8 | 8.7 | 3181 | 3 | US-09-135-021-1 | Sequence 1, Appli |
| 26 | 267.8 | 8.7 | 3181 | 3 | US-09-135-020-1 | Sequence 1, Appli |
| 27 | 267.8 | 8.7 | 3181 | 3 | US-09-135-010A-1 | Sequence 1, Appli |

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| 361 | GCCTCAAGTTGCTCTCTTGATCTGAGTTCGTGATGATGTCGTCTTTGGTTGGAGTTC | 420 | 1441 | CCACCACCTTAAATCTGTCATTCGAGCTATCAGAAATTATGAATTTTCATGTTGGTCAAAACGG | 1500 |
| 362 | | | 1442 | | 1501 |
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| 436 | | | 1516 | | 1575 |

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Qy 2590 GCTGCTTTGANTCAGACTCTCTAAGGACTGGAAGGTCAAGGATCATCTCAGAGCAATTTGT 2649
Db 2581 GCTGCTTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGGATCATCTCAGAGCAATTTGT 2640
Qy 2650 AAGGCAGAGAAAGTACAGATGCTCTAGCTTGGCTCATGTCAAACTGAAATAGTTCTT 2709
Db 2641 AAGGCAGAGAAAGTACAGATGCTCTAGCTTGGCTCATGTCAAACTGAAATAGTTCTT 2700
Qy 2710 CATTTCTTTCCAGGCATAGCAGTTCTTTTAGCATATATATATGCAATGCAATTTTCG 2769
Db 2701 CATTTCTTTCCAGGCATAGCAGTTCTTTTAGCATATATATATGCAATGCAATTTTCG 2760
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Qy 2950 AACACAGCTAATGCTATGGGTGTATGAATATGTCAAGTTTAGTCAATTTAGAGATTTG 3009
Db 2941 AACACAGCTAATGCTATGGGTGTATGAATATGTCAAGTTTAGTCAATTTAGAGATTTG 3000
Qy 3010 ACACGTATTTTGAATATGAGGATTAACACCTTCAAAATTTCA 3053
Db 3001 ACACGTATTTTGAATATGAGGATTAACACCTTCAAAATTTCA 3044
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RESULT 2

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US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3
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Query Match 94.1%; Score 2890.8; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

Qy 1 GGCAGCGCATGAAGGATGTGAGTCCGGCGGGGACGGGTGCTGCTCAACTCGGCAGCC 60
Db 156 GGCAGCGCATGAAGGATGTGAGTCCGGCGGGGACGGGTGCTGCTGAACTCGGCAGCC 215
Qy 61 GCCAGGGCGCAGCGGCTGCTACTGCTGGGCACCCGGCGGGCCACGCTTGGTGGCGGGCGC 120
Db 216 GCCAGGGCGCAGCGGCTGCTACTGCTGGGCACCCGGCGGGCCACGCTCGTGGCGGGCGC 275
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Qy 121 GGTGGCTGAGGAGAGCGCCCGGGGCAAGCAGGGGGCCCGATGAGCTGCTGGGGAAG 180
Db 276 GGTGGCTGAGGAGAGCGCCCGGGGCAAGCAGGGGGCCCGATGAGCTGCTGGGGAAG 335
Qy 181 CCGCTCTCTTACACAGTAGCAGAGTGCCTGCGGCGCAACGTCAGAGTCAAGTCCGGCGGGTGCAG 240
Db 336 CCGCTCTCTTACACAGTAGCAGAGTGCCTGCGGCGCAACGTCAGAGTCAAGTCCGGCGGGTGCAG 395
Qy 241 AACTACCTGTATCAACGTCGTGAGAGAGACCCCGCGCTGGGCGTTCAATCTACACGCTTTTC 300
Db 396 AACTACCTGTATCAACGTCGTGAGAGAGACCCCGCGCTGGGCGTTCAATCTACACGCTTTTC 455
Qy 301 GTTTTCTCTCTGCTTTGCTTGTGCTGATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCAC 360
Db 456 GTTTTCTCTCTGCTTTGCTTGTGCTGATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCAC 515
Qy 361 AAAAAATGGGCTCAAGTTGCTCTTGATCTGAGAGTTCGATGATGTTGCTCTTTTGGT 420
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Db 576 TTGAGTTTCATCATTTGCAATCTGCTGCGGGTTGCTGTTGCTGATATAGAGGATGGCAA 635
Qy 481 GGAAGACTGAGGTTGCTCGAAGCCCTTCTGTTTATAGATACCATTTGTTTATCGCT 540
Db 636 GGAAGACTGAGGTTGCTCGAAGCCCTTCTGTTTATAGATACCATTTGTTTATCGCT 695
Qy 541 TCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATATTTTGGCACGCTGCACTCAGA 600
Db 696 TCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAAATATTTTGGCACGCTGCACTCAGA 755
Qy 601 AGTCTCCGTTTCTTACAGATCCTCCGATGCTGCGCATGAGACCGAAGGGAGGCACTTGG 660
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Qy 661 AAATTTACTGGGTTTCAAGTGGTTTATGCTCAGCAGCAAGGAATTAATCAGAGCTTGGTACATA 720
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Qy 841 GGCTATGGAGACAACCTCCCTAACTTGGCTGGAGATTTGCTTCTGCAAGGCTTTTGA 900
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Qy 1021 CTCATTGAGTGTGTTGGCGTAGTTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACC 1080
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Db 1236 TGAAGCCACACTTTGAAGCCCTTGACACCTGAGCCCTTACCAAGAAAGAAACAAGGGAA 1279
Qy 1141 GCATCAAGCAGCTCAGAAAGCTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCAAGGGC 1200
Db 1280 -----TCAGAGCTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCAAGGGC 1328
Qy 1201 CAGAGTATTAGAGCCGCAAGCCCTCAGTGTGACAGGAGGTCCCCAAGCACCGACATC 1260
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| Query Match 93.0%; Score 2857.4; DB 4; Length 3074; Best Local Similarity 99.7%; Pred. No. 0; Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0; | | | | | | | | | |
| Qy | 1 | GGCAGCGCATGAGGATGTGAGTCTGGGCGCGGGCAGGGTGCTGTGAACTCGGAGCC | 60 | | | | | | |
| Db | 206 | GGCAGCGCATGAAGGATGTGGAGTCGGCGCGGGCAGGGTGCTGTAACCTCGGAGCC | 265 | | | | | | |
| Qy | 61 | GCCAGGGGCGACGGCCTGTACTCTGTGGGCAACCGCGCGGGCAGCGTTGTTGGTGGCGGCG | 120 | | | | | | |
| Db | 266 | GCCAGGGGCGACGGCCTGTACTCTGTGGGCAACCGCGCGGGCAGCGTTGTTGGTGGCGGCG | 325 | | | | | | |
| Qy | 121 | GGTGGCTGAGGGAGAGACCGCCGGGGCAAGCAGAGGGGCGCGGATGAGCCTGCTGGGGAAG | 180 | | | | | | |
| Db | 326 | GGTGGCTGAGGGAGAGCGCCGGGGCAAGCAGAGGGGCGCGGATGAGCCTGCTGGGAAGC | 385 | | | | | | |
| Qy | 181 | CCGCTCTTTACAGAGTAGCAGAGTCGCGGGCGCAACGTCAGTAGCCGGGGTGCAG | 240 | | | | | | |
| Db | 386 | CGCTCTCTTTACAGAGTAGCAGAGTCGCGGGCGCAACGTCAGTAGCCGGGGTGCAG | 445 | | | | | | |
| Qy | 241 | AACTACCTGTACAAAGTGTGGAGAGACCCGCGGCTGGGGTTCATCTACACAGCTTTC | 300 | | | | | | |
| Db | 446 | AACTACCTGTACAAAGTGTGGAGAGACCCGCGGCTGGGGTTCATCTACACAGCTTTC | 505 | | | | | | |
| Qy | 301 | GTTTTTCTCCTGTCTTTTGGTGTGCTTGAATTTTGTCACTGTTTTCTACATCCCTGAGCAC | 360 | | | | | | |
| Db | 506 | GTTTTCTCTCTGTCTTTTGGTGTGCTTGAATTTTGTCACTGTTTTCTACCATCCCTGAGCAC | 565 | | | | | | |
| Qy | 361 | ACAAATTTGGCTCAAGTTCGCTTGTGATCTGTGAGTTCGTGATGATGCTCTTTGGT | 420 | | | | | | |
| Db | 566 | ACAAATTTGGCTCAAGTTCGCTTGTGATCTGTGAGTTCGTGATGATGCTCTTTGGT | 625 | | | | | | |
| Qy | 421 | TTGGAGTTTCATCATTCGAACTCTGCTCTGCGGGTGTCTGTTGTCGATATAGAGATGGCAA | 480 | | | | | | |
| Db | 626 | TTGGAGTTTCATCATTCGAACTCTGCTCTGCGGGTGTCTGTTGTCGATATAGAGATGGCAA | 685 | | | | | | |
| Qy | 481 | GGAGACTGAGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCT | 540 | | | | | | |
| Db | 686 | GGAGACTGAGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCT | 745 | | | | | | |
| Qy | 541 | TCAATAGCAGTTGTTCTGCAAAACTCAGGGTAAATTTTTCGCCAGCTCTGCACCTCAGA | 600 | | | | | | |
| Db | 746 | TCAATAGCAGTTGTTCTGCAAAACTCAGGGTAAATTTTTCGCCAGCTCTGCACCTCAGA | 805 | | | | | | |
| Qy | 601 | AGTCTCCGTTTCTTACAGATCCTCCGCAATGGTGGCATGGACCGAAGGGGAGGACCTTGG | 660 | | | | | | |
| Db | 806 | AGTCTCCGTTTCTTACAGATCCTCCGCAATGGTGGCATGGACCGAAGGGGAGGACCTTGG | 865 | | | | | | |
| Qy | 661 | AAATTACTGGGTTGAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTTGGTACATA | 720 | | | | | | |
| Db | 866 | AAATTACTGGGTTGAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTTGGTACATA | 925 | | | | | | |
| Qy | 721 | GGATTTTGGTTCCTTAATTTTTTCTCTTCTCTGCTATCTGTTGGAAGGATGCCAAT | 780 | | | | | | |
| Db | 926 | GGATTTTGGTTCCTTAATTTTTTCTCTTCTCTGCTATCTGTTGGAAGGATGCCAAT | 985 | | | | | | |
| Qy | 781 | AAAGAGTTTTCTACATATGAGATGCTCTCTGTTGGGGCACAATTAATTCACAACTATT | 840 | | | | | | |
| Db | 986 | AAAGAGTTTTCTACATATGAGATGCTCTCTGTTGGGGCACAATTAATTCACAACTATT | 1045 | | | | | | |
| Qy | 841 | GGCTATGGAGACAAACTCCCTTAACCTTGGCTGGGAAGATTCCTTCTGCAGGCTTTGCA | 900 | | | | | | |
| Db | 1046 | GGCTATGGAGACAAACTCCCTTAACCTTGGCTGGGAAGATTCCTTCTGCAGGCTTTGCA | 1105 | | | | | | |
| Qy | 901 | CTCCTTGGCATTTCTTTCTTTTGCACTTCTCTCGCGCATTTCTTGGCTCAGGTTTTGCAATTA | 960 | | | | | | |
| Db | 1106 | CTCCTTGGCATTTCTTTCTTTTGCACTTCTCTCGCGCATTTCTTGGCTCAGGTTTTGCAATTA | 1165 | | | | | | |
| Qy | 961 | AAAGTACAGAAACACACCGGCAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAAC | 1020 | | | | | | |
| Db | 1166 | AAAGTACAGAAACACACCGGCAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAAC | 1225 | | | | | | |

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|----|------|--|------|
| Qy | 1021 | CTCATTCAGTGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTCAATTCGAACC | 1080 |
| Db | 1226 | CTCATTCAGTGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTCAATTCGAACC | 1285 |
| Qy | 1081 | TGGAAGCCACACTTGAAGGCTTCACACCTGCGAGCCTTACCAAGAAAGAACAGGGGAA | 1140 |
| Db | 1286 | TGGAAGCCACACTTGAAGGCTTCACACCTGCGAGCCTTACCAAGAAAGAACAGGGGAA | 1345 |
| Qy | 1141 | GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCCGAGGGC | 1200 |
| Db | 1346 | GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCCGAGGGC | 1405 |
| Qy | 1201 | CAGAGTATTAAGACCCAGAACCTCAGTAGGTGACAGAGGTCCTCCAGCACGACATC | 1260 |
| Db | 1406 | CAGAGTATTAAGACCCAGAACCTCAGTAGGTGACAGAGGTCCTCCAGCACGACATC | 1465 |
| Qy | 1261 | ACAGCCAGGCGAGTCCACCACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGC | 1320 |
| Db | 1466 | ACAGCCAGGCGAGTCCACCACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGC | 1525 |
| Qy | 1321 | TTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCCAAAACCAAGTATGATGCTGACACA | 1380 |
| Db | 1526 | TTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCCAAAACCAAGTATGATGCTGACACA | 1585 |
| Qy | 1381 | GCCCTTGGCACTGATGATGATATATGATGAAAAGATGCCAGTGTGATGATCAGTGAA | 1440 |
| Db | 1586 | GCCCTTGGCACTGATGATGATATATGATGAAAAGATGCCAGTGTGATGATCAGTGAA | 1645 |
| Qy | 1441 | GACCTACCCACCACTTAAACCTGCTATTCGAGCTATCAGAAATTTGAAATTTTCATGTT | 1500 |
| Db | 1646 | GACCTACCCACCACTTAAACCTGCTATTCGAGCTATCAGAAATTTGAAATTTTCATGTT | 1705 |
| Qy | 1501 | GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGTAAGAGATGTCATTTGAAACA | 1560 |
| Db | 1706 | GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGTAAGAGATGTCATTTGAAACA | 1765 |
| Qy | 1561 | TATTCGCTGGTCTATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAACACGCTTTCAT | 1620 |
| Db | 1766 | TATTCGCTGGTCTATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAACACGCTTTCAT | 1825 |
| Qy | 1621 | CAAAATCTTGAAAGGGCAAAATCACATCAGATGAAGAGAGCCGAGAGAAATTAACAGCA | 1680 |
| Db | 1826 | CAAAATCTTGAAAGGGCAAAATCACATCAGATGAAGAGAGCCGAGAGAAATTAACAGCA | 1885 |
| Qy | 1681 | GAAATGAGACCAAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAG | 1740 |
| Db | 1886 | GAAATGAGACCAAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAG | 1945 |
| Qy | 1741 | GTACAGTCCATAGAAATCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG | 1800 |
| Db | 1946 | GTACAGTCCATAGAAATCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG | 2005 |
| Qy | 1801 | AAAGGCTCTGCTCAGCCCTCGCTTTGCTTTCATTCAGATTCACACCTTTTGAATGTCAA | 1860 |
| Db | 2006 | AAAGGCTCTGCTCAGCCCTCGCTTTGCTTTCATTCAGATTCACACCTTTTGAATGTCAA | 2065 |
| Qy | 1861 | CAGACATCTGACTATCAAGGCTGCTGGATAGCAAGAGATCTTTCGGGTTCGCGCAAAAAC | 1920 |
| Db | 2066 | CAGACATCTGACTATCAAGGCTGCTGGATAGCAAGAGATCTTTCGGGTTCGCGCAAAAAC | 2125 |
| Qy | 1921 | AGTGGCTCTTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTGCGATTCATTCCTG | 1980 |
| Db | 2126 | AGTGGCTCTTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTGCGATTCATTCCTG | 2185 |
| Qy | 1981 | ACGCCAAATGAGTTTCAGTGCAGCTTTCATCGCGCTTAGCCCTACTATGACAGTCAA | 2040 |
| Db | 2186 | ACGCCAAATGAGTTTCAGTGCAGCTTTCATCGCGCTTAGCCCTACTATGACAGTCAA | 2245 |
| Qy | 2041 | GCAACACAGGTGCGAATTAAGTCAAAGCGATGGCTCAGCAGTGGCGGACCAACCACTTT | 2100 |
| Db | 2246 | GCAACACAGGTGCGAATTAAGTCAAAGCGATGGCTCAGCAGTGGCGGACCAACCACTTT | 2305 |
| Qy | 2101 | GCAAAACCAATTAATACGGCACCCCAAGCAGCAGCCCAACCACTTTACAGATCCACCT | 2160 |

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Db 2306 GCAACCAATAATACGACCAACCAAGCCAGCAGCCCAACAACATTTACAGATCCCACT 2365
Qy 2161 CCTCTCCAGCCATCAAGCATCTCCAGGCCAGAAATCTGCAACCCCTAACCCCTGCAGGC 2220
Db 2366 CCTCTCCAGCCATCAAGCATCTCCAGGCCAGAAATCTGCAACCCCTAACCCCTGCAGGC 2425
Qy 2221 TTACAGGAAGCATTTCTGAGCTCACCACCTGCTTGTGCTTCCCAAGGAATAATGTTTCAG 2280
Db 2426 TTACAGGAAGCATTTCTGAGCTCACCACCTGCTTGTGCTTCCCAAGGAATAATGTTTCAG 2485
Qy 2281 GTTGACAGTCAAAATCTCACCAGAGCGTTCTATGAGGAAAGCTTTGACATCGGAGGA 2340
Db 2486 GTTGACAGTCAAAATCTCACCAGAGCGTTCTATGAGGAAAGCTTTGACATCGGAGGA 2545
Qy 2341 GAAACTCTGTTGTTCTGCTGCCATGTCGCGAGGAGCTTTGGGCAAAATCTTTGCTGTG 2400
Db 2546 GAAACTCTGTTGTTCTGCTGCCATGTCGCGAGGAGCTTTGGGCAAAATCTTTGCTGTG 2605
Qy 2401 CAAACCTGATCAGGTGCAACGAGGAACTGAATACAACTTTCAGGAGTGAGTCAAGT 2460
Db 2606 CAAACCTGATCAGGTGCAACGAGGAACTGAATACAACTTTCAGGAGTGAGTCAAGT 2665
Qy 2461 GGCTCCAGAGCAGCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTAACT 2520
Db 2666 GGCTCCAGAGCAGCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTAACT 2725
Qy 2521 GATGAAGAGTGGTCCGAGAGAGACAGACACATTTTGTATGCGGACCCAGCCT 2580
Db 2726 GATGAAGAGTGGTCCGAGAGAGACAGACACATTTTGTATGCGGACCCAGCCT 2785
Qy 2581 GCCAGGAGCTGCTTGTGATCAGACTCTGAAGACTGGAAGTCAAGATCAATCTCAG 2640
Db 2786 GCCAGGAGCTGCTTGTGATCAGACTCTGAAGACTGGAAGTCAAGATCAATCTCAG 2845
Qy 2641 AGCATTTGTAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700
Db 2846 AGCATTTGTAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2905
Qy 2701 TAAGTCTTCATTTCTTCAGGATAGCAGTCTTTAGCCATACATATCATTTGCATGA 2760
Db 2906 TAAGTCTTCATTTCTTCAGGATAGCAGTCTTTAGCCATACATATCATTTGCATGA 2965
Qy 2761 ACTATTTCCGAAGCCCTCTAAAAGTTGAAATTCGAAGATCGGGAAGACATGAAGG 2820
Db 2966 ACTATTTCCGAAGCCCTCTAAAAGTTGAAATTCGAAGATCGGGAAGACATGAAGG 3025
Qy 2821 CAGTTTATAAGCCGTTACCTTTTAAATTCGATGAAATGCAATGTTTAGG 2869
Db 3026 CAGTTTATAAGCCGTTACCTTTTAAATTCGATGAAATGCAATGTTTAGG 3074
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RESULT 4

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US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-1

Query Match 85.8%; Score 2635.4; DB 4; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 1 GG CAG CGG C A T G A A G A T G T G A G T C G G C C G G G G C A G G T G C T G C T G A C T C G G C A G C C 60
Db 97 G G C A G C G G C A T G A A G G A T G T G A G T C G G C C G G G G C A G G T G C T G T G A A C T C G G C A G C C 156
Qy 61 G C C A G G G G C A C C G C T G T A C T G T G G C C A C C C G G C C A C G T T G G T G G C G G C G G C 120
Db 157 G C C A G G G G C A C C G C C T G T A C T G T G G G C A C C C G G C C A C G T T G G T G G C G G C G G C 216
Qy 121 G G T G G C C T G A G G G A G A C C G C C G G G G C A A G C A G G G G C C C G G A T G A G C C T G T G G G G A A G 180
Db 217 G G T G G C C T G A G G G A G A C C G C C G G G G C A A G C A G G G G C C C G G A T G A G C C T G T G G G G A A G 276
Qy 181 C C G C T C T T A C A C G A G T A C C A G A C T G C C G G G C A A C G T C A A G T A C C G G C G G T G C A G 240
Db 277 C C G C T C T T A C A C G A G T A C C A G A C T G C C G G G C A A C G T C A A G T A C C G G C G G T G C A G 336
Qy 241 A A C T A C C T G T A C A C G T G T G G A G A C C C C G G G G T T G C A T C T A C C A C G C T T T C 300
Db 337 A A C T A C C T G T A C A C G T G T G G A G A C C C C G G G C T T G G C G T T C A T C T A C C A C G C T T T C 396
Qy 301 G T T T T T C C T T G T T G T T G T T G A T T T T G T C A G T T T T T T T T T T T T T T T T T T T T T T T T T 360
Db 397 G T T T T T C C T T G T T G T T G T T G A T T T T T G T C A G T T T T T T T T T T T T T T T T T T T T T T T T 456
Qy 361 A C A A A T T G C C C T C A A G T T G C C T T G A T C C T G A G T T C G T G A T G A T G T G C T T T T G G T 420
Db 457 A C A A A T T G C C C T C A A G T T G C C T T G A T C C T G A G T T C G T G A T G A T G T G C T T T T G G T 516
Qy 421 T T G A G T T C A T C A T T C A A T C T G G T C T G C G G G T T G C T T G T T G T C G A T A T A G A G A T G C A A 480
Db 517 T T G A G T T C A T C A T T C A A T C T G G T C T G C G G G T T G C T T G T T G T C G A T A T A G A G A T G C A A 576
Qy 481 G G A A G A C T A G A G T T G C T C G A A A G C C C T T C T G T G T T A T A G A T A C C A T T G T C T T A T C G C T 540
Db 577 G G A A G A C T A G A G T T G C T C G A A A G C C C T T C T G T G T T A T A G A T A C C A T T G T C T T A T C G C T 636
Qy 541 T C A A T A G C A G T T G T T C T G C A A A A A C T C A G G T A A T A T T T T T G C C A C G T C T G C A C T C A G A 600
Db 637 T C A A T A G C A G T T G T T C T G C A A A A A C T C A G G T A A T A T T T T T G C C A C G T C T G C A C T C A G A 696
Qy 601 A G T C C C G T T T C C T A C A G A T C C T C C G C A T G G T G C G A T G G A C C G A A G G G A G G C A C T T G G 660
Db 697 A G T C C C G T T T C C T A C A G A T C C T C C G C A T G G T G C G A T G G A C C G A A G G G A G G C A C T T G G 756
Qy 661 A A A T T A C T G G G T T C A G T G G T T A T G C T C A C A G C A A G A A T T A A T C A C A G C T T G T A C A T A 720
Db 757 A A A T T A C T G G G T T C A G T G G T T A T G C T C A C A G C A A G A A T T A A T C A C A G C T T G T A C A T A 816
Qy 721 G G A T T T T G G T T C T T A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 780
Db 817 G G A T T T T G G T T C T T A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 876
Qy 781 A A A G A G T T T T C A T A T A G C A G A T G C T C T C T G T G G G G C A C A A T T A C A T T G A C A C A C T A T T 840
Db 877 A A A G A G T T T T C A T A T A G C A G A T G C T C T C T G T G G G G C A C A A T T A C A T T G A C A C A C T A T T 936
Qy 841 G G C T A T G G A C A A A A C T C C C C T A A C T T G G C T G G A A G A T T G C T T C T G C A G G C T T T G C A 900
Db 937 G G C T A T G G A C A A A A C T C C C C T A A C T T G G C T G G A A G A T T G C T T C T G C A G G C T T T G C A 996
Qy 901 C T C C T T G G C A T T T C T T T T T T T G C A C T T C C T C C C G G C A T T C T T G G C T C A G G T T T T G C A T T A 960
Db 997 C T C C T T G G C A T T T C T T T T T T T G C A C T T C C T C C C G G C A T T C T T G G C T C A G G T T T T G C A T T A 1056
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| | | | |
|----|------|---|------|
| Qy | 961 | AAAGTACAGAAACAAACACCGCCGAAACACTTTGAGAAAAAGAGAAACCCAGCTGCCAAC | 1020 |
| Db | 1057 | AAAGTACAAGAAACAAACACCGCCGAAACACTTTGAGAAAAAGAGAAACCCAGCTGCCAAC | 1116 |
| Qy | 1021 | CTCATTCAAGTGTGTTTCGGCTAGTTCAGCGACGTGATGAGAAATCTGTTTCCATTGCAACC | 1080 |
| Db | 1117 | CTCATTCAAGTGTGTTTCGGCTAGTTCAGCGACGTGATGAGAAATCTGTTTCCATTGCAACC | 1176 |
| Qy | 1081 | TGGAAGCCACACTTTGAAGGCGCTTGCCACACCTGCAGCCCTACCAAGAAAGAACAAAGGGAA | 1140 |
| Db | 1177 | TGGAAGCCACACTTTGAAGGCGCTTGCCACACCTGCAGCCCTACCAA----- | 1220 |
| Qy | 1141 | GCATCAAGCAGTCAGAAAGCTTAAGTTTTAAGAGGCGAGTGCAGCATGGCTAGCCCCAGGGC | 1200 |
| Db | 1221 | -----TCAGAAGCTAAGTTTTAAGGAGCGAGTGGCGCATGGCTAGCCCCAGGGC | 1269 |
| Qy | 1201 | CAGAGTATTAAAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCAAGACCGACATC | 1260 |
| Db | 1270 | CAGAGTATTAAAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCAAGACCGACATC | 1329 |
| Qy | 1261 | ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAAAGCTGAGACTTCAACGACCGAACCCGC | 1320 |
| Db | 1330 | ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAAAGCTGAGACTTCAACGACCGAACCCGC | 1389 |
| Qy | 1321 | TTCCGGCCCTCGCTCGCCCTCAAAGTTCTCAGCCAAAACACAGTGATAGATGCTGCACACA | 1380 |
| Db | 1390 | TTCCGGCCCTCGCTCGCCCTCAAAGTTCTCAGCCAAAACACAGTGATAGATGCTGCACACA | 1449 |
| Qy | 1381 | GCCCTTGGCACTGATGATGATATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGAA | 1440 |
| Db | 1450 | GCCCTTGGCACTGATGATGATATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGAA | 1509 |
| Qy | 1441 | GACCTCACCCACACACTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTTTCATGTT | 1500 |
| Db | 1510 | GACCTCACCCACACACTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTTTCATGTT | 1569 |
| Qy | 1501 | GCAAAACGGAAGTTTAAAGAAACRRTTACGTCCATATGATGTAAAGATGTCATTGAAACAA | 1560 |
| Db | 1570 | GCAAAACGGAAGTTTAAAGAAACATTAAGTCCATATGATGTAAAGATGTCATTGAAACAA | 1629 |
| Qy | 1561 | TATTCTGCTGGTCACTGHCACATGTTGTGTAGAAATTAAGAGCCTTCAACACAGTGTGAT | 1620 |
| Db | 1630 | TATTCTGCTGGTCACTGHCACATGTTGTGTAGAAATTAAGAGCCTTCAACACAGTGTGAT | 1689 |
| Qy | 1621 | CAAAATCTTGGAAAGGCGAAATCACATCAGATAAGAGAGCGCGAGAGAAATAACAGCA | 1680 |
| Db | 1690 | CAAAATCTTGGAAAGGCGAAATCACATCAGATAAGAGAGCGCGAGAGAAATAACAGCA | 1749 |
| Qy | 1681 | GAACATGAGACCAAGACGATCTCAGTATGCTCGGTTCGGTGGTCAAGTGTGAAAAACAG | 1740 |
| Db | 1750 | GAACATGAGACCAAGACGATCTCAGTATGCTCGGTTCGGTGGTCAAGTGTGAAAAACAG | 1809 |
| Qy | 1741 | GTACAGTCCATAGAAATCAAGCTGGAATGCGCTACTAGACATCTATCAACAGGTCCCTCGG | 1800 |
| Db | 1810 | GTACAGTCCATAGAAATCAAGCTGGAATGCGCTACTAGACATCTATCAACAGGTCCCTCGG | 1869 |
| Qy | 1801 | AAAGGCTTCGCCCTCAGCCCTCGCTTTGGCTTCATTCAGTTCGCCACTTTTGAATGTGAA | 1860 |
| Db | 1870 | AAAGGCTTCGCCCTCAGCCCTCGCTTTGGCTTCATTCAGATTCGCCACTTTTGAATGTGAA | 1929 |
| Qy | 1861 | CAGACATCTGACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCGACAAAAC | 1920 |
| Db | 1930 | CAGACATCTGACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCGACAAAAC | 1989 |
| Qy | 1921 | AGTGGCTGCTTATCCAGATCAACTAGTGCACAACATCTCGAGAGCGCTGCAAGTTCATTCTG | 1980 |
| Db | 1990 | AGTGGCTGCTTATCCAGATCAACTAGTGCACAACATCTCGAGAGCGCTGCAAGTTCATTCTG | 2049 |
| Qy | 1981 | ACGCCAAATGAGTTCAAGTGCAGACTTTCTACGCGCTTAGCCCTACTATGCAAGCTCAA | 2040 |
| Db | 2050 | ACGCCAAATGAGTTCAAGTGCAGACTTTCTACGCGCTTAGCCCTACTATGCAAGCTCAA | 2109 |

| | | | |
|----|------|--|------|
| QY | 2041 | GCAACACAGGTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTT | 2100 |
| DB | 2110 | GCAACACAGGTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTT | 2169 |
| QY | 2101 | GCAAAACCAATTAATACGGCACCCCAAGCCAGCAGCCCCCAACAACTTTTACAGATCCCAACCT | 2160 |
| DB | 2170 | GCAAAACCAATTAATACGGCACCCCAAGCCAGCAGCCCCCAACAACTTTTACAGATCCCAACCT | 2229 |
| QY | 2161 | CCTCTCCAGGCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTTGAGGC | 2220 |
| DB | 2230 | CCTCTCCAGGCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAACCTTGAGGC | 2289 |
| QY | 2221 | TTACAGGAAAGCATTTCTGACGTCACCAACCTGCTTGTTCCTTCAAGGAAAAATGTTTCAG | 2280 |
| DB | 2290 | TTACAGGAAAGCATTTCTGACGTCACCAACCTGCTTGTTCCTTCAAGGAAAAATGTTTCAG | 2349 |
| QY | 2281 | GTTCACAGTCAAACTCTCAACCAAGGACCGTTTCTATGAGGAAAAAGCTTTGACATGGGAGGA | 2340 |
| DB | 2350 | GTTCACAGTCAAACTCTCAACCAAGGACCGTTTCTATGAGGAAAAAGCTTTGACATGGGAGGA | 2409 |
| QY | 2341 | GAAACTCTGTTGCTGTCTGCTCCCATGGTGCAGGAGACTTGGGCAAACTCTTTGCTGTG | 2400 |
| DB | 2410 | GAAACTCTGTTGCTGTCTGCTCCCATGGTGCAGGAGACTTGGGCAAACTCTTTGCTGTG | 2469 |
| QY | 2401 | CAAAACCTGATCAGGTGCAGCCGAGGAACCTGAATATACAACTTTTCAGGGAGTGAGTCAAGT | 2460 |
| DB | 2470 | CAAAACCTGATCAGGTGCAGCCGAGGAACCTGAATATACAACTTTTCAGGGAGTGAGTCAAGT | 2529 |
| QY | 2461 | GGCTCCAGAGGCAGCCAAAGATTTTATCCCAAAATGGAGGGAATCCAAAATGTTTATAACT | 2520 |
| DB | 2530 | GGCTCCAGAGGCAGCCAAAGATTTTATCCCAAAATGGAGGGAATCCAAAATGTTTATAACT | 2589 |
| QY | 2521 | GATGAAGAGGTGGGTCCCGAAGACAGACAGACAGACACTTTTTCATGCCGACCGCAGCCCT | 2580 |
| DB | 2590 | GATGAAGAGGTGGGTCCCGAAGACAGACAGACAGACACTTTTTCATGCCGACCGCAGCCCT | 2649 |
| QY | 2581 | GCCAGGGAAGCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTTCAG | 2640 |
| DB | 2650 | GCCAGGGAAGCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTTCAG | 2709 |
| QY | 2641 | AGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTGCAAACTGAAA | 2700 |
| DB | 2710 | AGCATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTGCAAACTGAAA | 2769 |
| QY | 2701 | TAA | 2703 |
| DB | 2770 | TAA | 2772 |

RESULT 5

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RES001 3
US-09-949-016-1823
; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1823

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(2335)
NAME/KEY: CDS
LOCATION: (83)..(2170)
US-09-492-361-1

Query Match 16.9%; Score 518; DB 4; Length 2335;
Best Local Similarity 60.1%; Pred. No. 5.3e-145;
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

226 TACGGGGGTCGAGAACTACCTGACAACTGCTGGAGAGACCCCGCGCTGGCGTTC 285
Db TACCGCGCCCTGCGAAGCTGGGTCTACAAAGTCTGGAGCGCGCCCGCGCTGGCGTTC 379
286 ATCTACCAACGCTTTCCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 345
Db GTCTACCAACGCTTTCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
346 ACCATCCCTGAGCACAACAAATGGCTTCAAGTTGCTTCTGCTGCTGCTGCTGCTG 405
Db ACTATCCAGGAGCACCAGGAATGGCTTCAAGTTGCTTCTGCTGCTGCTGCTGCTG 499
406 ATTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTG 465
Db ATCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTG 559
466 TATAGAGATCGCAAGGAAGACTGAGGTTTCTCGAAGCCCTTCTGCTGCTTATAGATAC 525
Db TACCGAGATCGCAAGGTCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 619
526 ATTGCTTCTTATGCTTCAATAGCAGTTGTTTCTGCAAAATCTCAGGGTAAATTTTGG 585
Db ATCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 679
586 ACCTGCTGACCTAGAGTCTCGTTTCTCAGATCTCCGATCTCGGATGCTGCGATGAC 645
Db ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
646 AGGGGAGCACTTGAATTAATCTGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 705
Db CGCGGGCACTGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
706 ACAGCTTGGTACATAGGATTTTGGTCTTATTTTCTGCTTCTGCTTCTGCTTCTG 765
Db ACCGCTTGGTACATAGGATTTTGGTCTTATTTTCTGCTTCTGCTTCTGCTTCTG 859
766 GAAAGGATGCAATAGAGTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTG 825
Db GAGAGGATGCAATAGAGTTTCTACATATGAGATGCTCTGCTGCTGCTGCTGCTG 919
826 ACATTGACCACTATTGGCTATGAGACAAACTCCCTAATCTGCTGCTGCTGCTGCT 885
Db ACATTGACCACTATTGGCTATGAGACAAACTCCCTAATCTGCTGCTGCTGCTGCT 979
886 TCTGAGCTTGGCACTCTTGGCACTTCTTCTTCTGCACTTCTGCTGCTGCTGCTG 945
Db GCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1039
946 TCAGGTTTGGATTAAGAGTACAGAACACACCGCAGAAACACTTTGAGAAAGAGG 1005
Db TCAGGTTTGGATTAAGAGTACAGAACACACCGCAGAAACACTTTGAGAAAGAGG 1099
1006 AACCCAGCTGCCAATCTCATTGCTGCTTGGGCTGCTTACGAGCTGATGAGAAATCT 1065
Db ATGCGGAGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1159
1066 GTTTTCCATGCACTTGAAGCCACACTTGAAGGCTTTCGACACCTGTCAGC----- 1116
Db GCCTTACCTGACAGCCACCTGCTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1219
1117 CCTACCAAGAAAGAACAGGGGAGATCAAGAGCTGACAGAGCTA----- 1161

RESULT 7

US-09-177-650-88

; Sequence 88, Application US/09177650

; Patent No. 6413719

; GENERAL INFORMATION:

; APPLICANT: Leppert, Mark F.

; APPLICANT: Singh, Nanda

; APPLICANT: Charlier, Carole

; TITLE OF INVENTION: KNO2 AND KNO3 - POTASSIUM CHANNEL GENES WHICH ARE

| ; | TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC) |
|---|--|
| : | TITLE OF INVENTION: AND OTHER EPILEPSIES |

| Query Match | 16.9%; | Score 517.6; | DB 3; | Length 2273; |
|-----------------------|--------------|--|-----------------|-------------------|
| Best local Similarity | 57.7%; | Pred. No. 6.8e-145; | | |
| Matches 1031; | Conservative | 2; | Mismatches 683; | Indels 72; Gaps 4 |
| Qy | 73 | GGCCTGCTACTGCTGGGCACCGCGCGGCCACGCTTGCTGGCGCGCGGTGGCGCTGAGG | 132 | |
| Db | 67 | GGCTTCGTGGGCTGGACCCCGCGGCGCCGANTCCACACGGACGGCNCTACTCATC | 126 | |
| Qy | 133 | GAGAGCCCGCGGGCAAGACAGGGGGCCCGAGTGAAGCTGTGGGGAAGCCGCTCTCTTAC | 192 | |
| Db | 127 | GCGGGCTCCGAGGCCCCCAAGCGCGGCANCTNTTTGACAAAGCGCGACGGCGGCGCG | 186 | |
| Qy | 193 | ACGAGTAGCACAGAGCTCCGCGGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTGTAC | 252 | |
| Db | 187 | GGANCCGGGAAGCCCCNNAANCGCAACGCCCTTCTACCGCAAGCTGCAGAAATTCCTCTAC | 246 | |
| Qy | 253 | AACGTGCTGGAGAGACCCCGCGGTGGGCGTTCATCTACCAAGCTTCGTTTTCTCTCT | 312 | |
| Db | 247 | AACGTGCTAGAGCGGCCCGCGGTGGCGTTCATCTACCAAGCTTACGTCTCTCTCTG | 306 | |
| Qy | 313 | GTCTTTGGTTCCTTGAATTTTGTCAAGTGTTTTCTACCATCCCTGAGCACACAAAATGGCC | 372 | |
| Db | 307 | GTTTTCTCTCGCTTGCTTCTCTGTGTTCCTTCCACCATCAAGGAGTACGAGAAGAGCTCT | 366 | |
| Qy | 373 | TCAGTTGCTCTTGAATCTCGAGGTTCTGATGATTTGCTCTTTGGTTGGAGTTCATC | 432 | |
| Db | 367 | GAGGGGCGCTCTACATCTTGAAATCTGTACTATCGTGGTATTCGGTGTGGAGTACTT | 426 | |
| Qy | 433 | ATTCCGAATCTGGTCTCGCGGTTGCTTGTGCATATAGAGGATGCAAGGAAGACTGAGG | 492 | |
| Db | 427 | GTGAGGATCTGGGCTGCAGGCTGCTGTTGCCGATTCAGGCTCGAGGGCAGGCTCAAG | 486 | |
| Qy | 493 | TTTGCTCGAAGCCCTCTGTGTTATAGATACCATGTTCTTATCGCTTCAATACAGT | 552 | |
| Db | 487 | TTTGCCAGGAACCGTCTGTGTGATTCATTCATGCTGTGCTGATTCGCTCCATTCCTGTG | 546 | |
| Qy | 553 | GTTCCTCGAATACTCAGGGTAATATTTTCCACGCTCTGCATCAGAGCTCCGTTTC | 612 | |
| Db | 547 | CTGGCTGTGGTTCGAGGCAATGCTTTGCCACATCTGGCTTCGGAGCTTCGGGTTTC | 606 | |
| Qy | 613 | CTACAGATCCTCCGATGGTCGATGACACCGAAGGGAGGCACTTGGAATTTACTGGGT | 672 | |
| Db | 607 | TTGCAATCTTCGGATGATCCGATATGACCGAGGGGTGGCACCTGGAAAGCTCTGGGA | 666 | |
| Qy | 673 | TCAGTGTTTATGCTCACAGCAAGGAATTAATTCACAGCTTGGTATCATAGGATTTTGGTT | 732 | |
| Db | 667 | TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGGCTTGTGTACATTTGGCTTCTCTGC | 726 | |
| Qy | 733 | CTTATTTTTCTCTTCTCTTCTATCTCTGTGGGAAAGGATGCCAATAAAGAGTTTTCT | 792 | |
| Db | 727 | CTCATCTGGGCTCATTTCTCGTGATCTTGGCAAGAAAGGGTGAGAAATGACCACTTTGAC | 786 | |
| Qy | 793 | ACATATGCAGATGCTCTCTGGTGGGCAACAATTAATTGACAACTATTGGCTATGGAGAC | 852 | |
| Db | 787 | ACCTACGCAGATGCACTCTGGTGGGCTGTGATCAACCTGACGACCATTTGGCTACGGGAC | 846 | |

Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Query Match 16.7%; Score 511.6; DB 3; Length 2169;
Best Local Similarity 58.2%; Pred. No. 4.3e-143;
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;

Qy 73 GGCCTGCTACTGCTGGGCAACCGCGCGCCACGCTTGGTGGCGGGCGGTGGGCTGAGG 132
Db |||||
Db 67 GGCCTGCTGGGCTGGACCCCGCGCGCCGACTCCACCGGCGGGCGCTACTCATC 126
Qy 133 GAGAGCGCCCGGGCAAGACGAGGGGCCCGGATGAGCTGTGGGAAACCGCTCTTTAC 192
Db |||||
Db 127 GCGGCTCCGAGGCCCCCAAGCGCGCAGCGTTTGTAGCAAGCCGCGACGGGGCGCG 186
Qy 193 ACGAGTAGCAGCTGCGCGGCAACCTCAAGTACCGCGGGTGCAGAACTACTGTAC 252
Db |||||
Db 187 GGAGCGGGGAAGCCCCGAAGCGCAACGCCCTTACCGCAAGCTGCAGAACTTCTCTAC 246
Qy 253 AACGTGCTGGAGAGACCCCGGGCTGGCGCTTCACTACCAAGCTTTCGTTTTCTCTCT 312
Db |||||
Db 247 AACGTGCTAGAGCGGCCCGGGCTGGCGCTTCACTACCAAGCTTTCGTTTTCTCT 306
Qy 313 GCTTTGCTGCTGATTTGTCAGTGTTCATCCATCCCTGAGACACAAAAATGGCC 372
Db |||||
Db 307 GTCCTTCTGCTGTGCTTCTGTGTTTCCACCATCAAGGAGTACGAGAAAGCTCT 366
Qy 373 TCAGTTCCCTCTGATCCTGAGTTCGTGATGATGTCGTTTGGTTTGGAGTTCTATC 432
Db |||||
Db 367 GAGGGGGCCCTTACATCTTGGAAATCGTACTATCGTGGTATTGGGTGTGAGTACTTT 426
Qy 433 ATTGCAATCTGCTGCGGGTGTGTTGTGATATAGAGATGCAAGGAAGACTGAGG 492
Db |||||
Db 427 GTGAGATCTGGGCTGAGGCTGCTGTTCGCGGTATCGAGCTGGAGGGCGAGCTCAAG 486
Qy 493 TTTGCTCGAAGCCCTCTGTGTTATAGATACCAATGTTCTTATGCTTCAATAGCAGTT 552
Db |||||
Db 487 TTTGCCAGGAAGCCGTTCTGTGTGATGATATCATGTGTGCTGATTCCTCCATGCTGTG 546
Qy 553 GTTTCTGCAAAACCTCAGGTAATATTTTCCAGCTCTGCACACAGAGTCTCGTTTC 612
Db |||||
Db 547 CTGGCTGTGTTCCAGGGCAATGCTTTTGCACATCTGGCGCTTCGGAGCTTCGGGTT 606
Qy 613 CTACAGATCCTCGCATGCTGCGCATGGACCGAAGGGAGGCACTTGGAAATTAATCTGGGT 672
Db |||||
Db 607 TTGCAAAATCTTGGGATGATCGTATGACCGGAGGGTGGCACTGGAAGCTCTTGGGA 666
Qy 673 TCAGTGGTTTATGCTCAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTGGTT 732
Db |||||
Db 667 TCGGTAGTCTACGCTCAGCAAGAGAGCTGGTGTGCTGCTGTAATTTGGCTTCTCTGC 726
Qy 733 CTTATTTTCTGCTCTTCTGCTCTATCTGGTGGAAAGGATGCCAATAAGAGTTTCT 792
Db |||||

Db 727 CTATCTCTGGCCTCATTTCTGGTGTACTTGGCAGAAAGGGTGAGATGACCACTTTGAC 786
Qy 793 ACATATGAGATGCTCTCTGTTGGGGCACAATTAATTAATTAATTAATTAATTAATTAAT 852
Db |||||
Db 787 ACCTACGAGATGCACTCTGTTGGGTCTGATCACCTCTGACACCAATTTGGCTACGGGAC 846
Qy 853 AAAACTCCCTAATCTGCTGGGGAAGATTGCTTTCTGAGGCTTTGCACTCTTGGCAAT 912
Db |||||
Db 847 AAGTACCCTCAGACTCTGAAACGGGAGGCTGCTGCGAGCACTTTTACCTCATTTGGTCT 906
Qy 913 TCTTTCTTGGCACTCTGCTGGGCAATCTTGGCTCAGGTTTGCATTAATAAGTACAAGAA 972
Db |||||
Db 907 TCGTTCTTGGCTCTTCTGCTGGCAATTTTGGATCCGGCTTTGCTGAAAGTCCAAGAG 966
Qy 973 CAACACCCCGCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACCCTCATTCAGT 1032
Db |||||
Db 967 CAGCATCGGCAAAACACTTTGAGAAACGGGCAACCCCTGCGGAGGCTCTGATCCAGTCT 1026
Qy 1033 GTTTGGGCTAGTTAGCAGCTGATGAGAAAT----- 1063
Db |||||
Db 1027 GCCTGGAGATTCTATGCTACTTAACCTCTCAGCACCGACCTGCACTCCACGTGGCAGTAC 1086
Qy 1064 -----CTGTTTCCATTGCAACCTGGAAGCCACACTTCAAGGCTTTGAC 1107
Db |||||
Db 1087 TACGAGCGGACAGTCACTGCTCCCATGTACAGACTATCCCACTCTGAAACAGCTGGAG 1146
Qy 1108 ACCTGCAAGCCCTACCAAGA-----AAGAAACAAGGGGAA 1140
Db |||||
Db 1147 CTGCTGAGGAATCTCAAGAGCAAAATCTGGACTCACCTTTCAGGAAGAGCCACAGCCAG 1206
Qy 1141 GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGGAG-----TGCGCATGGCTAGCCCCAGG 1197
Db |||||
Db 1207 CCATCACCAGTCAAGAGTCAAGTTTGAAGATCGTGTCTTCTCAGCCCCCGAGGCAATG 1266
Qy 1198 GGCCAGAGTATTAAGAGCCGACAAAGCCTCAGTAGTGACAGAGGTGCTCCCAAGCAACCGAC 1257
Db |||||
Db 1267 GCTCCAGGAAGAGGGTCTCCAGGCCAGAGGCTCGGCGGTCCCCAGCTGGAT 1326
Qy 1258 ATCAAGCCGAGGCGAGTCCACCAAAAGTGAGAGAGCTGAGCTTCAACGACCGAAACC 1317
Db |||||
Db 1327 CAGAGTCTTGATGACAGCCCGAGCAAGGTGCCAAGAGCTGGAGCTTTGGTGACCGCAGC 1386
Qy 1318 CGCTTCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCCAAACAGTATGATAGTCTGAC 1377
Db |||||
Db 1387 CGCACGCCAGGCTTTCCGCATCAAGGGTCTGCATCCCGGCAAGATTCAGAAAGCAAGC 1446
Qy 1378 ACAGCCCTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
Db |||||
Db 1447 C---TCCCTGGGAGGACATGATAGAGCAACAGAGCTGTAAGTCTGAGTCTGAGT 1503
Qy 1438 GAAGACCTCACCCACCACTTAAAACTGTCTATTCGAGCTATCAGAAATTAATTAATTAAT 1497
Db |||||
Db 1504 GAAGATCTTACCCCTGGCCTCAAAAGTTAGCATCAGAGCTGTGTGTTTATGCGGTTCTTG 1563
Qy 1498 GTTCCAAAACGGAAGTTTAAGGAAACRTTACGTCCATATGATGTAAGAGATGTCATTA 1557
Db |||||
Db 1564 GTATCTAAGCGAAAAGTTCAAGAGAGAGTTCGCGCCCATATGATGATGATGATGATGAT 1623
Qy 1558 CAATATCTGCTGCTGATCTGACATGTTGTGTGATGATGATGATGATGATGATGATGATG 1617
Db |||||
Db 1624 CAGTACTCGGCTGACACACTTGGATATGTTGTCGCGCATCAAGAGCTGAGTCCAGAGTG 1683
Qy 1618 GATCAAAATTTTGGAAAGGSCAAATCAATCAGATAGAAAGAGCCGAGAGAAATAACA 1677
Db |||||
Db 1684 GACCAGATTGGGGCGGGGCCCAACAATAACGGATAAGGA---TCGCACCAAGGCCCA 1740
Qy 1678 GCAGAAATGAGACCAAGAGCATCTCAGTATGCTCGTCCGGTGGTCAAGGTTGAAAAA 1737
Db |||||
Db 1741 GCGGAAACGGAGCTGCCCGAGACCCAGCATGATGGGACGGCTTGGGAAGGTGGAGAAA 1800
Qy 1738 CAGGTACAGTCCATAGAAATCAAGCTGACCTGCTACTAGACATCTATCAACAG 1791
Db |||||
Db 1801 CAGGTCTTGTCCATGGAAAGAGAGCTGACCTTCTTGGTGGACATCTATACAG 1854

RESULT 9

US-09-495-050A-303
; Sequence 303, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guesler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495.050A
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 303
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CTT
US-09-495-050A-303

Query Match 16.6%; Score 509.8; DB 4; Length 582;
Best Local Similarity 99.4%; Pred. No. 5.4e-143;
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 1630 GGAAGGGGCAATACATACATAGATAGAGAGCGAGAGAAATAACAGACAGACATGAG 1689
Db 1 GGAAGGGGCAATACATACATAGATAGAGAGCGAGAGAAATAACAGACAGACATGAG 60

Qy 1690 ACCACAGACATCTCAGTATGCTCGGTGGGTGCTCAAGTTGAAAAACAGGTACAGTCC 1749
Db 61 ACCACAGACATCTCAGTATGCTCGGTGGGTGCTCAAGTTGAAAAACAGGTACAGTCC 120

Qy 1750 ATAGAAATCCAGCTGGAGTGGCTACTAGACATCTATCAACAGGTCCCTTCGGAAGGCTCT 1809
Db 121 ATAGAAATCCAGCTGGAGTGGCTACTAGACATCTATCAACAGGTCCCTTCGGAAGGCTCT 180

Qy 1810 GCCTCAGCCCTCGCTTTGGCTTCATTCAGTTCGCCACCTTTTGAATGTGAACAGACATCT 1869
Db 181 GCCTCAGCCCTCGCTTTGGCTTCATTCAGTTCGCCACCTTTTGAATGTGAACAGACATCT 240

Qy 1870 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGCCAACAACAGTGGCTGC 1929
Db 241 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGCCAACAACAGTGGCTGC 300

Qy 1930 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGCCCTGCAATCTCTGACGCCAAAT 1989
Db 301 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGCCCTGCAATCTCTGACGCCAAAT 360

Qy 1990 GAGTTCAAGTCCAGACTTTCTACGCTGTAGCCCTACTATGCAAGTCAAGTCAACACAG 2049
Db 361 GAGTTCAAGTCCAGACTTTCTACGCTGTAGCCCTACTATGCAAGTCAAGTCAACACAG 420

Qy 2050 GTGCCAATTAGTCAAGCGATGGTTCAGAGTGGGAGCCACCAACACATTTGCAAAACAA 2109
Db 421 GTGCCAATTAGTCAAGCGATGGTTCAGAGTGGGAGCCACCAACACATTTGCAAAACAA 480

Qy 2110 ATAAATACGGACCAACAGCCAGCCCAACAACTTTTACAGATC 2154
Db 481 ATAAATACGGACCAACAGCCAGCCCAACAACTTTTACAGATC 524

RESULT 10

US-09-105-058C-1
; Sequence 1, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:

; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubaer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105.058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 896
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D
; OTHER INFORMATION: y=c or t; f=a or g; m=a or c; k=g or t; s=g or c;
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a
US-09-105-058C-1

Query Match 15.2%; Score 465.4; DB 3; Length 896;
Best Local Similarity 53.7%; Pred. No. 1.9e-129;
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;

Qy 199 AGCCAGAGCTGCCGGCCCAACGTCAGTACCGGGGTGCAGAACTACCTGTACAACGTG 258
Db 13 RGSNRSCMSYSAAAGMGMAACGCCWSTACCGSMRSMTCARAMTTTSMCTACACGYS 72

Qy 259 CTGGAGAGACCCCGCGGTGCGGTTCATCATCACGCTTTCGTTTTCCTTCCTTCTTT 318
Db 73 CTRGAGMGRCSCGGGCTGGCGGYTSMYTTACACGCTWSGTGTTCTCTHTDGTYYTS 132

Qy 319 GGTTCGTGATTTTGTTCAGTGTTCCTACCATCCTCGACGACACAAAATTTGGCCTCAAGT 378
Db 133 KSSTGCTTBRKTKGCTGHS-YKCCACMWTCAAGAGTAYGAGAMKRYTCBGRGRS 191

Qy 379 TGCTCTTGATCTCTGGAGTTCTGATGATTCGTCCTTTGTTGGAGTTTCATCATTCGA 438
Db 192 KSSCTYWSMTWTGGARAYMKRYATYKTSRTVTYGGHGYBGAGTYKYKTCGWR 251

Qy 439 ATCTGCTCGGGTTCCTGCTGTCGATATAGAGATGGCAAGGAACTGAGGTTTGTCT 498
Db 252 ATCTGGCYCGWGGMTYTSYTGCCGRTACMRWGGCTGSMGGGSMGRTCSAAGTTTGCC 311

Qy 499 CGAAAGCCCTTCGTGTTATAGATACCATTTGTTCTTCAATAGCAGTTGTTCT 558
Db 312 MGGAACCVTSTGRTGTGTGAYATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371

Qy 559 GCAAAAATCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCTCGTTTCTCTACAG 618
Db 372 GYBGHMMCCARGCAAYGVYTKGVACVTCY---CTBGRAGCYTGGSTTCTVTRCAR 428

Qy 619 ATCTCCGCTGCTGCGCATGGACGAAAGGGAGGCACTTGGAAATTAAGTGGTTCAGTG 678
Db 429 ATYTRCGSATGTTSCGATGGACCGMGRRGGHGGACCTGGAAAGCTBYTGGGTCGTYV 488

Qy 679 GTTTATCTCACAGAGGAATTAATCACAGCTTGGTACATAGGATTTTGGTTCTTATT 738
Db 489 RTCTRYGCTACAGCAAGGARTSRTSACKGCTGGTACATYGGYTTCTTBSHCTCATC 548

Qy 739 TTTTCGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798
Db 549 CTKKCYTCRTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608

Qy 799 GCAGATGCTCTCTGGTGGGCAATTTACATTCAGCACTATTCGCTATGAGACAAACT 858
Db 609 GCRGATGCTCTGCTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668

Db 1707 TGACWTCTCATTCGACATGATCCCTCCCTWAAGGCTGCCATCCGAGCTGTCAGAAAT 1766
Qy 1485 TATGAATTTTCATGTTCCAAAACGGAATTTAAGGAAACATTAGCTCATATGATGTAAA 1544
Db 1767 TCTACAGTTCCGCTATATATAAAAAAAGTTCAAGGAGACGTTGAGGCTTTATGATGTAA 1826
Qy 1545 AGATGTCATTGAAACAATTTCTGCTGTCATCTGGACATGTTGTGTAAGAAATTAAGAGCCT 1604
Db 1827 AGATGTCATTGAGCAGTATTTGGCGGAGACATCTTGACATGCTTTCCAGGATAAAGTACCT 1886
Qy 1605 TCAACACAGCTGTTGATCAAAATTTCT 1628
Db 1887 ACAGACAAGAATAGATATGATTTT 1910

RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105.058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

Query Match 15.0%; Score 460.8; DB 3; Length 2565;
Best Local Similarity 57.9%; Pred. No. 1.1e-127;
Matches 953; Conservative 0; Mismatches 627; Indels 66; Gaps 5;

Qy 22 GAGTCGGCCGGGACAGGTCTCTGNACTCGCAGCCGCGGCGGAGCGGCTGCTA 81
Db 43 GCGGCGGCGGCGGCGGCGGAGGCGGAAAGTGGGGCTGGCGCCCGCGAGCTGGAGCAA 102
Qy 82 CTGCTGGGCAACCGCGGCGCACGCTTGGTGGCGGCGGCTGGCCCTGAGGGAGAGCGCG 141
Db 103 GTACCTTGGCGCTCGGGGCGGAGCGGCGGAGCGGACCTGCTGCTGGAGGGCGGC 162
Qy 142 CGGGGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCGGCTCTCTTACACAGTAGC 201
Db 163 GCGCGGCAAGCAGGGGCGGAGGAGCGGCGGAGCGGCGGCTCTGGGCGGCGGCGGCGG 222
Qy 202 CAGAGCTGCC-----GGCGCAAGCTCAAGTACCGGCGGCGGCGGAGCACTCTGTAC 252
Db 223 CTGAGCGCGCGCGAGTCAAGAGAAACAACCGCAAGTACCGGCGGCGGCGGCGGCGGCGG 282
Qy 253 AACGTGCTGGAGAGACCGCGGCGGCTGCGGCTCTATACACGCTTTTCGTTTTCTCCTT 312
Db 283 GACGCGCTGGAGAGACCGCGGCGGCTGGCGCTGCTTTACACGCGTGTGCTGCTGATT 342
Qy 313 GTCTTTGCTGCTGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
Db 343 GTCTTGGGGTGTGATTCTGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402
Qy 373 TCAAGTTCCTCTGATCTCGAGTTCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
Db 403 GGAGACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 462

Qy 433 ATTGGAATCTGGTCTGCGGGTGTCTTGTCTGATATAGAGGATGGCAAGAAAGACTGAGG 492
Db 463 TTGAGGATCTGGGCTGCTGGAATGTTGCTGCCGATACAAAGGCTGGCGGGCCGACTGAAG 522
Qy 493 TTTGCTCGAAAGCCCTTCTGTTTATGATATACCATTTGTTTCTTATCGCTTCAATAGCAGTT 552
Db 523 TTTGCGAGGAAGCCCTTCTGCTATGTTGGACATCTTTTGTGCTGATTCCTCTGTGCCAGTG 582
Qy 553 GTTTCCTGCAAAACTCAGGCTAATATTTTGGCCAGCTCTGCACTCAGAAAGTCTCCGCTTC 612
Db 583 GTTTCCTGCGGAAACCAAGGCAATGTTCTGGCCACT---CCCTGCAAGCTGCGCTTC 639
Qy 613 CTACAGATCTCTCGCATGTTGGCATGGAACCGAAGGGGAGGCACTTTGGAATTTACTGGGT 672
Db 640 CTGACATCTCTCGCATGTTGGCATGGAACCGAAGGGTGGCACTCTGGAAGCTTCTGGGC 699
Qy 673 TCAGTGGTTTATGCTCAGACGAAGGAATTAATCAGACGTTGGTACATAGGATTTTGGTT 732
Db 700 TCAGCCATCTGTGCCCAACAGCAAACTCATCAGCGCTGGTACATCGGTTTCTGACA 759
Qy 733 CTATTTTCTGTTCTTCTGCTATCTGTTGGAAGGATGCC----- 777
Db 760 CTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 819
Qy 778 -----AATAAGAGTTTCTTCTATATGCAATGCAATGCTCTCTGTTGGGCGACA 822
Db 820 CAAAGGAGGAGATGAAGAGGAGTTTGAGACCTATGCAATGCCCTGTGTTGGGCGCTG 879
Qy 823 ATTACATTTGACAACTATTGCTATGAGCAAACTCCCTACTTGGCTGGGAAGATTG 882
Db 880 ATCACACTGGCCACCTTGGCTATGAGCAACAGACACCAAAACGTTGGAGGCGGCTG 939
Qy 883 CTCTCTGAGGCTTTCACCTCTTGGCATTTCTTCTTCTGCACTCTCTGCGGCACTTCTT 942
Db 940 ATTGCGGCACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 999
Qy 943 GGCTCAGGTTTTCATATAAGTACAAAGCAACACCGCGGAGAAACACTTTTGAAGAAAGA 1002
Db 1000 GGGTCGGGCTGGCCCTCAAGGTGCAAGGAGCAACACCGTCAGAAAGCACTTTTGAAGAAAG 1059
Qy 1003 AGGAACCCAGCTGCCAACCCTCATTCAGTGTGTTTGGCGTAGTTACGAGCTGATGAGAA 1062
Db 1060 AGGAACCCAGCTGCCAACCCTCATTCAGTGTGTTTGGCGTAGTTACGAGCTGATGAGAA 1119
Qy 1063 TCTGTTTCCATTGCAACCTGGAAAGCCACACTTGAAGGCTTGCACACCTGACGCGCTTACC 1122
Db 1120 AGGATTGACCTGTGGCGACATGAGATTTTATGAATCAGTCTCTTCTTCTTCTTCTTCTTCT 1179
Qy 1123 AAGAAAGAAACAGGGGAGGATCAAGCAGTCAAGTAAAGTTTAAAGGAGCGAGTGGC 1182
Db 1180 AAGAAAGAAACAGCTGGAGGAGCATCCAGCCAAAGCTGGGTCTCTTGGATCGGGTTCGC 1239
Qy 1183 ATGGCTAGCCCGAGGGGCCAGAGTATTAAAGAGCCGCAAGCCCTCAGTAGGTGACAGGAG 1242
Db 1240 CTTTCTAATCTCTGTGTAGCAATCTAA-----AGAAAGCTATTT 1281
Qy 1243 TCCTCAAGCAACCGAGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCG 1302
Db 1282 ACCCTCTGAATGTAGATGCCATAGAAGAAAGTCTTCTTAAAGAAACCAAGACCTGTTGGC 1341
Qy 1303 TTCAACGACGAAACCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCGCTTCCGCG 1362
Db 1342 TTAACAAATAAAGAGCGTTTCCGCAACGCTTCCGCAATGAAGGCT-----ACGCTTTC 1395
Qy 1363 GTGATAGATCTGACACAGCGCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGAT 1422
Db 1396 TGGCAGAGTTCTGAGATGCGGAGCAGGTGAACCCATGGCGGAGACAGAGGCTATGGG 1455
Qy 1423 TGTGATGATCAGTGGAGACCTCAACCCACCACTTAAACCTGTCTATTCAGTATCAGATCAGA 1482
Db 1456 AATGACTTCCCATCGAAGACATGATCCCAACCTGAAAGCCGCGCATCCGAGCGGCTCAGA 1515

| | | | |
|----|------|--|------|
| Qy | 1483 | ATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGA | 1542 |
| Db | 1516 | ATTCTACAAATTCGCTCTATAAAAAAAATTCAGGAGACTTTGAGGCCCTTACGATGTG | 1575 |
| Qy | 1543 | AAAGATGTCATTGAAACAATATTCTGCTGGTCACTCGACACATGTTGTAGAAATTAAGAAGC | 1602 |
| Db | 1576 | AAGGATGTGATTGAGCAGTATTTCTCGCGGGCATCTCGACATGCTTTCCAGAGTAAAGTAC | 1635 |
| Qy | 1603 | CTTCAACACGTTGTTGATCAAAATTC | 1628 |
| Db | 1636 | CTTCAGACGAGAAATAGATATGATATTT | 1661 |

RESULT 13

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US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCN02 AND KCN03 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
US-09-177-650-6

```

| | | | |
|----|------|---|------|
| QY | 82 | CTGCTGGGCACCCGCGCGGCCACGCTTTGGTGGCGCGCGCGTGGCTGTAGGGAGAGCGCGC | 141 |
| DB | 175 | GTCACTTTGGCGTCTGGGGCCGGAGCGGACAAAGACGGGACCTGTCTGTCTGGAGGCGCGC | 234 |
| QY | 142 | CGGGCAAGCAGAGGGGGCCGGATGAGCGCTCTCTGGGGAAGCGCTCTCTTACACGAGTAGC | 201 |
| DB | 235 | GGCCGCGACGAGGGGCGAGGAGGACCCCGCAGGGCATCGGGCTCTTGCCCAAGACCCCG | 294 |
| QY | 202 | CAGAGCTGCC-----GGCGCAAGCTCAAGTACCGCGGGTGCAGACTACCTGTGTAC | 252 |
| DB | 295 | CTGAGCGCCCGAGTCAAGAGAGAAACAACGCCAAGTACCGGCGCATCCAAACTTTTGATCTAC | 354 |
| QY | 253 | AACGTGCTGAGAGACCCCGCGCTGGCGGTTCATCTACCAACGCTTTGGTTTTCTTCCTT | 312 |
| DB | 355 | GACGCCCTGAGAGACCGCGGGGCTGGCGCTCTCTTACACGCGTGTGGTGTCTCTGATT | 414 |
| QY | 313 | GTCTTTGGTTGCTTGATTTTGTCAAGTGTTTTTCACCATCCCTGAGCAGACAAAAATTTGGCC | 372 |
| DB | 415 | GTCTTGGGGTGTGATTCTGGCTGCTGACACATTTCAAGGAGTATGAGACTGTCTCG | 474 |
| QY | 373 | TCAAGTTGCCCTTTGTACTCTGAGTTCGTGATGATTGTCTCTTTGTTGGAGTTTCATC | 432 |
| DB | 475 | GGAGACTGGCTCTGTGTACTTGAGACATTTGCTATTTCATCTTTGGAGCCGAGTTGCT | 534 |
| QY | 433 | ATTGCAATCTGGTCTGGGGTTGCTGTGTGCATATAGAGGATGGCAAGAAAGACTGAGG | 492 |
| DB | 535 | TTGAGGATCTGGGCTGCTGATGTGCTGCCGATACAAAGGCTTGGGGGCCGACTGAAG | 594 |
| QY | 493 | TTTGTCTGAAAGCCCTCTGTGTATAGATACCATTTGTTCTTATCGTTCCTCAATAGCAGTT | 552 |
| DB | 595 | TTTGCCAGGAAGCCCTGTGCAATGTTGGACATCTTTGTGCTGATGCGCTCTGTGCCAGTG | 654 |
| QY | 553 | GTTTCTGCAAAAATCAGGGTAATATTTTGGCACGCTGCACTCAGAAAGTCTCCGTTTC | 612 |
| DB | 655 | GTTGCTGTGGAAACCAAGCAATGTTCTGGCACCT---CCCTGCGAAGCTTCGCGCTTC | 711 |
| QY | 613 | CTACAGATCCTCCGCATGTGCGCATGGACCGGAAGGGAGGCATTTGGAAATTACTGGGT | 672 |
| DB | 712 | CTGCAGATCTCGGCATGCTGCGGATGGACCGGAGAGGTGGCACCTGGAAGCTTCCTGGGC | 771 |
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| DB | 772 | TCAGGCCATCTGTCCCAACAGAAAGCACTCATACGCGCTGGTATCATCGGTTTCTCTGACA | 831 |
| QY | 733 | CTTATTTTTTCGTTCTTCCTGTCTATCTGGTGGAAAAAGATGCC----- | 777 |
| DB | 832 | CTCATCTTTTCTCATATTTCTTGCTACCTGGTTGAGAAAGCATGCCAGAGGTGGATGCA | 891 |
| QY | 778 | -----AATAAGAGTTTTCATATATGCAGATGCTCTCTGGTGGGGCAC | 822 |
| DB | 892 | CAAGGAGAGGAGATGAAAGAGGAGTTTGAGACCTATGCAGATGCCCTGTGTTGGGGCCTG | 951 |
| QY | 823 | ATTACATTGACAATATTGGCTATGAGAGACAAACCTCCCTTAATCTTGGCTGGGAAGATTG | 882 |
| DB | 952 | ATCACACTGCCACCAATTGGCTATGAGACAAGACACCCAAAAAGTGGGAAGGCCGCTCTG | 1011 |
| QY | 883 | CTTCTGTCGAGCTTTGCACCTCTGGCATTTCTTTTGTGCACTTCTCTCGCGGCATTCTT | 942 |
| DB | 1012 | ATTGCGGCCACCTTTTCTTAAITGGCGTCTCTCTTTTGGCCCTTCAGCGGGCATCTCTG | 1071 |
| QY | 943 | GGCTCAGGTTTTGCAATTAAGATACAGAACACACCGCCAGAAAAACATTTGAGAAAAAGA | 1002 |
| DB | 1072 | GGGTCCGGGCTGGCCCTCAAGGTGCAGAGGCAACAAGTACAGAGCACTTTGAGAAAGG | 1131 |
| QY | 1003 | AGGAACCCAGCTGCACACTTCATCTAGTGTGTTTGGGTAGTTTACGAGCTGATGAGAA | 1062 |
| DB | 1132 | AGGAAGCCAGCTGCTGAGTCTCATTCAGGCTGCTGGAGGTATTATGCTACCAACCCCAAC | 1191 |
| QY | 1063 | TCGTGTTTCATTCGAACCTGGAGCCACACTTGAAGGCTTTGACACACTGCGCCCTACC | 1122 |
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Db 247 GCGCGGGGAAGCCCCCAAGCGAAGCCCTTCTACCGAAGCTGCAGAAATTTCTCTAC 306
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Job time : 501 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
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Searched: 4708233 seqs, 24227607955 residues

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Listing first 45 summaries

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- 12: gb_sy.*
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- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 1 | 3040.4 | 99.0 | 3137 | 6 | AR430568 Sequence |
| 2 | 3040.4 | 99.0 | 3137 | 6 | AX056817 Sequence |
| 3 | 3040.4 | 99.0 | 3137 | 9 | AF202977 Homo sapi |
| 4 | 2936.2 | 95.6 | 3718 | 6 | BD275572 Novel Hum |
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| 7 | 2857.4 | 93.0 | 3074 | 6 | AR393778 Sequence |
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| 15 | 2401.6 | 78.2 | 3108 | 10 | AF263836 Mus muscu |
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| 20 | 1240 | 40.4 | 198017 | 2 | AC151025 | AC151025 Callithri |
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| 36 | 496 | 16.2 | 2750 | 6 | AX456861 | AX456861 Sequence |
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ALIGNMENTS

RESULT 1
AR430568
LOCUS AR430568 3137 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6649371.
ACCESSION AR430568
VERSION AR430568.1 GI:40191384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3137)
AUTHORS Jentsch, T.J.
TITLE Potassium channel KCNQ5 and sequences encoding the same
JOURNAL Patent: US 6649371-A 1 18-NOV-2003;
FEATURES
Location/Qualifiers
source 1..3137
/organism="unknown"
/mol_type="genomic DNA"

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| | | Best Local Similarity | 99.9%; | Pred. No. 0; | | |
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| Qy | 10 | ATGAAGGATGTGGAGTGGGGCGGGGAGGGTGTCTGTGAACCTGGCAGCGCCAGGGGC 69 | | | | |
| Db | 1 | ATGAAGGATGTGGAGTGGGGCGGGGAGGGTGTCTGTGAACCTGGCAGCGCCAGGGGC 60 | | | | |
| Qy | 70 | GACGGCTGTCTACTGTGGGACCCCGCGCCACGGTGTGGTGGCGGGGGTGGCCTG 129 | | | | |
| Db | 61 | GACGGCTGTCTACTGTGGGACCCCGCGCCACGGTGTGGTGGCGGGGGTGGCCTG 120 | | | | |
| Qy | 130 | AGGGAGAGCGCCCGGGGCAAGCAGCGGGGCCCGGATGAGCTGTGGGAAAGCGCTCTCT 189 | | | | |
| Db | 121 | AGGGAGAGCGCCCGGGGCAAGCAGCGGGGCCCGGATGAGCTGTGGGAAAGCGCTCTCT 180 | | | | |
| Qy | 190 | TACACGAGTACCGAGAGCTGCCCGCGCAACCTCAAGTACCGCGGGTGCAGAACTACCTG 249 | | | | |
| Db | 181 | TACACGAGTACCGAGAGCTGCCCGCGCAACCTCAAGTACCGCGGGTGCAGAACTACCTG 240 | | | | |
| Qy | 250 | TACAACTGTGGGAGAGACCCCGGGCTTTCATCTACCAAGCTTTCTGTTTCTTC 309 | | | | |

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| Db | 241 | TACAA | CGTGTG | GAGAGAGACCCCGCGCTGGGCGTTTCATCTACACAGCTTTCGTTTTCTC | 300 |
| Qy | 310 | CTTGTCT | TTGGTTGCTTGATTTTGT | CAGTGTTTTCTACCATCCCTGAGCACACAAATTG | 369 |
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| Qy | 370 | GCCTCAAG | TTCCTCTTGATCTCGAGATTG | TGATGTCTTGGTTTGGAGTTC | 429 |
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| Qy | 430 | ATCATTCGAAT | CTGCTCTGGGGTTCGTGTCGATATAGAGATG | CGAAGGAAGACTG | 489 |
| Db | 421 | ATCATTCGAAT | CTGCTCTGGGGTTCGTGTCGATATAGAGATG | CGAAGGAAGACTG | 480 |
| Qy | 490 | AGGTTTCTCGAAAG | CCCTTCTGTGTATAGATA | CAATGTTCTTATCGCTTCAATAGCA | 549 |
| Db | 481 | AGGTTTCTCGAAAG | CCCTTCTGTGTATAGATA | CAATGTTCTTATCGCTTCAATAGCA | 540 |
| Qy | 550 | GTTGTCTTTCGAAAAC | TCAAGGTATATTTTGGCCAGCTCTGCACTCAGAA | GCTCCGT | 609 |
| Db | 541 | GTTGTCTTTCGAAAAC | TCAAGGTATATTTTGGCCAGCTCTGCACTCAGAA | GCTCCGT | 600 |
| Qy | 610 | TTCCTTACAGAT | CCCTCCGCATGTCGCGATGGACCGAAGGGGAGG | CACTTGGAAATTTACTG | 669 |
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| Db | 661 | GGTTCAGTGGTTTATG | CTCAGCAAGGAATTAATCACAGCTTGTGATAGGATTTT | TG | 720 |
| Qy | 730 | GTTCTTATTTTTT | CGTCTTTCTTGTCTATCTCGTGGAAAAGGATG | CCAAATAAGAGTTT | 789 |
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| Qy | 790 | TCTACATATGAGAT | GTCTCTGTGTGGGACAAATTTACATTTGACAACTATTGCGCTATGCA | 849 | |
| Db | 781 | TCTACATATGAGAT | GTCTCTGTGTGGGACAAATTTACATTTGACAACTATTGCGCTATGCA | 840 | |
| Qy | 850 | GACAAACTCCCTTAACT | TGGCTGGGAAGATTGCTTTCTGACGGCTTTCAC | TCTTGGC | 909 |
| Db | 841 | GACAAACTCCCTTAACT | TGGCTGGGAAGATTGCTTTCTGACGGCTTTCAC | TCTTGGC | 900 |
| Qy | 910 | ATTTCTTTCTTTTGCA | CTTCTCGCGCATCTTGGCTCAGTTTTGCATTTAAAGTACAA | 969 | |
| Db | 901 | ATTTCTTTCTTTTGCA | CTTCTCGCGCATCTTGGCTCAGTTTTGCATTTAAAGTACAA | 960 | |
| Qy | 970 | GAAACACCGCCAGAAAC | CACTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTTAC | 1029 | |
| Db | 961 | GAAACACCGCCAGAAAC | CACTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTTAC | 1020 | |
| Qy | 1030 | TGTGTTTGGCGTAGTTA | CGCAGCTGATGAGAAATCTGTTTCCATTGCAACTTGGAGGCCA | 1089 | |
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| Qy | 1090 | CACTTGAAAGGCTTGCAC | ACCTGACGCCCTACCAAGAAAAGAACCGGGAAGCATCAAGC | 1149 | |
| Db | 1081 | CACTTGAAAGGCTTGCAC | ACCTGACGCCCTACCAAGAAAAGAACCGGGAAGCATCAAGC | 1140 | |
| Qy | 1150 | AGTCAGAAGCTAAGTTT | TAAAGAGCGAGTGGCTATGCCCGAGGGCCAGATTT | 1209 | |
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| Db | 1201 | AAGAGCGGACAGCCT | CAGTGTGACGAGGAGTCCCAAGCACCGACATCACACCGCAG | 1260 | |
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| Qy | 1330 | TGCTGCGCCTCAAAAG | TCTCAGCCAAACCAAGTGTAGATGCTGACACAGCCCTTGGC | 1389 | |
| Db | 1321 | TGCTGCGCCTCAAAAG | TCTCAGCCAAACCAAGTGTAGATGCTGACACAGCCCTTGGC | 1380 | |

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| QY | 1390 | ACTGATGATGATATATGATCAAAAAGGATGCGCAGTGTGATGTATCAGTGGGAAGACCTCACC | 1449 |
| DB | 1381 | ACTGATGATGATATATGATGAAAAGGATGCGCAGTGTGATGTATCAGTGGGAAGACCTCACC | 1440 |
| QY | 1450 | CCACCACTTTAAAACTGTGCTATTGCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG | 1509 |
| DB | 1441 | CCACCACTTTAAAACTGTGCTATTGCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG | 1500 |
| QY | 1510 | AGGTTTAAAGGAACRTTACGTCCATATCATGTGTAAGATGTCAATTGAAACAATATTCGTCT | 1569 |
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| DB | 1621 | GGAAAAGGCAAAATCACATCAGATTAAGAGAGCCGAGAGAAAATAAACAAGCAACAATGAG | 1680 |
| QY | 1690 | ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAACAAGTACAGTCC | 1749 |
| DB | 1681 | ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAACAAGTACAGTCC | 1740 |
| QY | 1750 | ATAGATTCGAAGCTGAGTGCCTTACTAGACATCTATCAACAGGTCCTTCGGAAGAGGCTCT | 1809 |
| DB | 1741 | ATAGATTCGAAGCTGAGTGCCTTACTAGACATCTATCAACAGGTCCTTCGGAAGAGGCTCT | 1800 |
| QY | 1810 | GCCTCAGCCCTCGCTTTGGCTTCATTCAGGTTCCCAACCTTTTGAATGTGAACAGACATCT | 1859 |
| DB | 1801 | GCCTCAGCCCTCGCTTTGGCTTCATTCAGGTTCCCAACCTTTTGAATGTGAACAGACATCT | 1860 |
| QY | 1870 | GACTATCAAAGCCCTGTGGATAGCAAGATCTTTGGGTTTCGCAACAAAACAGTGGCTGC | 1929 |
| DB | 1861 | GACTATCAAAGCCCTGTGGATAGCAAGATCTTTGGGTTTCGCAACAAAACAGTGGCTGC | 1920 |
| QY | 1930 | TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCTCGAGTTCAATTCTGACGCCAAT | 1989 |
| DB | 1921 | TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCTCGAGTTCAATTCTGACGCCAAT | 1980 |
| QY | 1990 | GAGTTTCAGTGCAGACTTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG | 2049 |
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| QY | 2050 | GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCGAGCCCAACACCAATTGCAAAACCA | 2109 |
| DB | 2041 | GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCGAGCCCAACACCAATTGCAAAACCA | 2100 |
| QY | 2110 | ATAAATAGCGCACCCAGCAGAGCGCCCAACACTTTACAGATCCCACTCTCTCCCA | 2169 |
| DB | 2101 | ATAAATAGCGCACCCAGCAGAGCGCCCAACACTTTACAGATCCCACTCTCTCCCA | 2160 |
| QY | 2170 | GCATCAAGCATCTGCCACAGCCCAAGAACTCTGCAACCTTAACCTCGAGGCTTACAGGAA | 2229 |
| DB | 2161 | GCATCAAGCATCTGCCACAGCCCAAGAACTCTGCAACCTTAACCTCGAGGCTTACAGGAA | 2220 |
| QY | 2230 | AGCAATTCGAGCGTCAACAACCTGCTTGGCTTCAAGGAAATGTTCAAGTGTGCACAG | 2289 |
| DB | 2221 | AGCAATTCGAGCGTCAACAACCTGCTTGGCTTCAAGGAAATGTTCAAGTGTGCACAG | 2280 |
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| DB | 2281 | TCAAATCTCCAAAGACCGTTCTATGAGGAAAAGCTTGAATGGGAGAGAAACTCTG | 2340 |
| QY | 2350 | TTGTCCTCTGTGCCATAGTGTGCCGAAGAATTGGGCAAACTTTGCTGTGTCGAAAACCTG | 2409 |
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| LOCUS | AF202977 | 3137 bp mRNA linear PRI 01-AUG-2000 | | Db | 121 | AGGAGAGCCGCGCGGGCAAGCAGCGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT | 180 |
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| ACCESSION | AF202977 | | | Db | 181 | TACACGAGTAGCAGAGCTGCGCGGGCAACGTCAGGTACCGGCGGGTGCAGAACTACCTG | 240 |
| VERSION | AF202977.1 | GI:7798695 | | Qy | 250 | TACAACTGCTGGAGAGACCCCGCGCTGGCGGTTTCATCTACCAACGCTTTCGTTTTCTC | 309 |
| KEYWORDS | | | | Db | 241 | TACAACTGCTGGAGAGACCCCGCGCTGGCGGTTTCATCTACCAACGCTTTCGTTTTCTC | 300 |
| SOURCE | | Homo sapiens (human) | | Qy | 310 | CTTCTCTTTGGTCTGCTGATTTTCTCAGTGTGTTTCTACCATCCCTGAGCAGACAAAATG | 369 |
| ORGANISM | | Homo sapiens | | Db | 301 | CTTCTCTTTGGTCTGCTGATTTTCTCAGTGTGTTTCTACCATCCCTGAGCAGACAAAATG | 360 |
| REFERENCE | | KCNQ5, a novel potassium channel broadly expressed in brain, mediates M-type currents | | Qy | 370 | GCCTCAAGTTGCCTCTTGATCTCGAGTTCGTGATGATTCGTCTTTTGGTTTGGAGTTC | 429 |
| AUTHORS | | J. Biol. Chem. 275 (31), 24089-24095 (2000) | | Db | 361 | GCCTCAAGTTGCCTCTTGATCTCGAGTTCGTGATGATTCGTCTTTTGGTTTGGAGTTC | 420 |
| | | 2 (bases 1 to 3137) | | Qy | 430 | ATCATTCGAATCTCGTCTGCGGGTTCGTGTCGATATAGAGATGCAAGGAAGACTG | 489 |
| | | Schroeder, B.C., Hechenberger, M., Weinreich, F., Kubisch, C. and Jentsch, T.J. | | Db | 421 | ATCATTCGAATCTCGTCTGCGGGTTCGTGTCGATATAGAGATGCAAGGAAGACTG | 480 |
| TITLE | | KCNQ5, a novel potassium channel broadly expressed in brain, mediates M-type currents | | Qy | 490 | AGTTTCTGCTGAAAGCCCTCTTGTGTTATAGATACCATTTGTTTATCGTTCATATAGCA | 549 |
| JOURNAL | | Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinistrasse 85, Hamburg 20246, Germany | | Db | 481 | AGTTTCTGCTGAAAGCCCTCTTGTGTTATAGATACCATTTGTTTATCGTTCATATAGCA | 540 |
| MEDLINE | | Location/Qualifiers | | Qy | 550 | GTGTTTCTGCAAAAACCTCAGGGTAATATTTTTCGACGCTTCGACTCAGAACTCTCGT | 609 |
| PUBMED | | 1.3137 | | Db | 541 | GTGTTTCTGCAAAAACCTCAGGGTAATATTTTTCGACGCTTCGACTCAGAACTCTCGT | 600 |
| REFERENCE | | 1. 3137 | | Qy | 610 | TTCTTACAGATCTCTCCGATGTCGCGATGACCGAAGGGAGGACCTTGGAAATTTACTG | 669 |
| AUTHORS | | /gene="KCNQ5" | | Db | 601 | TTCTTACAGATCTCTCCGATGTCGCGATGACCGAAGGGAGGACCTTGGAAATTTACTG | 660 |
| | | 1..2694 | | Qy | 670 | GGTTTCTGCTGTTATGCTCAAGCAAGAAATTAATCAAGCTTCGATACATAGGATTTTGT | 729 |
| | | /note="splice variant 1" | | Db | 661 | GGTTTCTGCTGTTATGCTCAAGCAAGAAATTAATCAAGCTTCGATACATAGGATTTTGT | 720 |
| | | /product="potassium voltage-gated channel, KQT-like subfamily, member 5" | | Qy | 730 | GTTCCTATTTTTCGCTCTTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG | 789 |
| | | /protein_id="AAF69797.1" | | Db | 721 | GTTCCTATTTTTCGCTCTTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG | 780 |
| | | /db_xref="GI:7798696" | | Qy | 790 | TCTACATATGAGATGCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG | 849 |
| | | /translation="MKDVEGRVLLNSAARGDGLLLGTRATLGGGGGLRESR | | Db | 781 | TCTACATATGAGATGCTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG | 840 |
| | | RGQCARMSLIGPLSYTSSOSCRNVKRVONYLVNLEPRGMAFIVHAFVLIV | | Qy | 850 | GACAAAACCTCCCTAACTTGGCTGGGAGATTTGCTTTCTGACGCTTTTGCACTCCTTGGC | 909 |
| | | FGCLLSVFSTIPHTKLASSCLLILFVMIWVFLRFLIRWSAGCCCVRGWQGL | | Db | 841 | GACAAAACCTCCCTAACTTGGCTGGGAGATTTGCTTTCTGACGCTTTTGCACTCCTTGGC | 900 |
| | | RFAPKPCVIDTIVLIASIVVSAKTOGNIATSAISLRFLOLIRWVDRRGRTWK | | Qy | 910 | ATTTCTTTTCTTGGCACTTCTGCGGCAATTTTGGCTCAGGTTTTCGATTTAAAGTACAA | 969 |
| | | LGSVVVAHSELITAWYIGLVILFSSFLVLEKDNKEFSTYADALMWGITLIT | | Db | 901 | ATTTCTTTTCTTGGCACTTCTGCGGCAATTTTGGCTCAGGTTTTCGATTTAAAGTACAA | 960 |
| | | IGYDKTPTLWGLLSAGFALLGISFALPAGILSGFALKVQEHQKHFEKRRNP | | Qy | 970 | GAACAAACCTCCCTAACTTGGCTGGGAGATTTGCTTTCTGACGCTTTTGCACTCCTTGGC | 1029 |
| | | AANLIQCVRWSYAADEKSVSTATWPKHLKALHTCSPTKKEQGEASOKLSFKERV | | Db | 961 | GAACAAACCTCCCTAACTTGGCTGGGAGATTTGCTTTCTGACGCTTTTGCACTCCTTGGC | 1020 |
| | | ASPRGQSIKRSQASVGRSRSPTDITAGSPTKVQKWSFNDRFRPSLRSLKSSQPK | | Qy | 1030 | TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCTCAATTCGAACTGGAAGCCA | 1089 |
| | | PVIDADTALGDDVVDKGCOCVSDLTPLPLATVIRAIRIMEKHFVAKRKETLAP | | Db | 1021 | TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCTCAATTCGAACTGGAAGCCA | 1080 |
| | | YVNDVLEQVSAGHLMCLCRKLSLQTRVDQILGQITSDKSEKITAHEHTDDLS | | Qy | 1090 | CACCTTGAAGGCTTGCACACTGCGAGCCCTACCAAGAAAGAACAGGGAAGGATCAAGC | 1149 |
| | | MLGRVVKVQVSIKSLDCLDIYQVLRKGSALALASFPQIPPECEQTSQDYOS | | Db | 1081 | CACCTTGAAGGCTTGCACACTGCGAGCCCTACCAAGAAAGAACAGGGAAGGATCAAGC | 1140 |
| | | PVDSKLSGSAQNSGCLSRSTANSRLQFLTPNFSAGTVALSPETHSQATVP | | Qy | 1150 | AGTCAGAGCTTAAGTTTTTAAGGAGCGAGTGGCGATGCTAGCCCCAGGGGCGAGTATT | 1209 |
| | | ISQSDGSAVAATNTIAQINTAPKPAFTLIQIPPLFALKHLPRPRLTHPNAGLOE | | Db | 1141 | AGTCAGAGCTTAAGTTTTTAAGGAGCGAGTGGCGATGCTAGCCCCAGGGGCGAGTATT | 1200 |
| | | SISDVTTLVAKENVOVQNSLTKDRSMRKSFDMGSETLLSVCPMPVKDLGKLSVQ | | | | | |
| | | NLIRSTELNLIQLSRSSSSGSGSDPVPKWRSKLRTIDEEVGPETETDTPDAAPQ | | | | | |
| | | PARAAAFASDSLRTRGRSSQSIKAGESTDALSPLPHVCLK" | | | | | |
| ORIGIN | | | | | | | |
| Query Match | 99.0% | Score 3040.4; | DB 9; | Length 3137; | | | |
| Best Local Similarity | 99.9% | Pred. No. 0; | | | | | |
| Matches 3041; | Conservative | 1; | Mismatches | 2; | Indels | 0; | Gaps |
| Qy | 10 | ATGAAGGATGTGGAGTCGGGCGGCGAGGTGCTGCTGAACCTGCGACGCGCGAGGGGC | 69 | | | | |
| Db | 1 | ATGAAGGATGTGGAGTCGGGCGGCGAGGTGCTGCTGAACCTGCGACGCGCGAGGGGC | 60 | | | | |
| Qy | 70 | GACGCGCTGCTACTGCTGGGCAACCGCGCGGCACCGCTTGGTGGCGGGCGGTCGCTG | 129 | | | | |

| | | | | | | | |
|----|------|-------------|---------------|--------------|--------------|---------------------------|------|
| Qy | 2290 | TCAAAATCTCA | CGGTTCTATGAGG | AAAGCTTTG | CATGGGAGG | AAACTCTG | 2349 |
| Db | 2281 | TCAAAATCTCA | CGGTTCTATGAGG | AAAGCTTTG | CATGGGAGG | AAACTCTG | 2340 |
| Qy | 2350 | TTGTCGTCTG | TCCATGGTCCG | AAGACTTTGG | CAAACTCTTG | TGTCGAAAACCTG | 2409 |
| Db | 2341 | TTGTCGTCTG | TCCATGGTCCG | AAGACTTTGG | CAAACTCTTG | TGTCGAAAACCTG | 2400 |
| Qy | 2410 | ATCAGTTCGAC | CGAGGAACTGA | ATATACAACTTT | CAGGAGTGAGT | CAAGTGGCTCCAGA | 2469 |
| Db | 2401 | ATCAGTTCGAC | CGAGGAACTGA | ATATACAACTTT | CAGGAGTGAGT | CAAGTGGCTCCAGA | 2460 |
| Qy | 2470 | GGCAGCCAGAT | TTTTTATCCCA | ATGAGGGAAT | CCAAATTTG | TTTATTAACATGAAGAG | 2529 |
| Db | 2461 | GGCAGCCAGAT | TTTTTATCCCA | ATGAGGGAAT | CCAAATTTG | TTTATTAACATGAAGAG | 2520 |
| Qy | 2530 | GTGGTCCCGA | GAGACAGACG | ACACTTTTG | TGATGCGCAC | CGACGCTGCCAGGGAA | 2589 |
| Db | 2521 | GTGGTCCCGA | GAGACAGACG | ACACTTTTG | TGATGCGCAC | CGACGCTGCCAGGGAA | 2580 |
| Qy | 2590 | GCTGCTTTG | CATCAGACTCT | CTTAAGGACT | TGGAAGGT | ACGATCATCTCAGAGCA | 2649 |
| Db | 2581 | GCTGCTTTG | CATCAGACTCT | CTTAAGGACT | TGGAAGGT | ACGATCATCTCAGAGCA | 2640 |
| Qy | 2650 | AAGCAGAGG | AAAGTACAGAT | GCCCTCAG | CTTGCCCTCAT | TGTCAAACTGAAATTAAGTCTT | 2709 |
| Db | 2641 | AAGCAGAGG | AAAGTACAGAT | GCCCTCAG | CTTGCCCTCAT | TGTCAAACTGAAATTAAGTCTT | 2700 |
| Qy | 2710 | CATTTTCTT | CCAGGATACG | ATGCTTTAG | CCATACATAT | CATTGCGATGAACCTATTTG | 2769 |
| Db | 2701 | CATTTTCTT | CCAGGATACG | ATGCTTTAG | CCATACATAT | CATTGCGATGAACCTATTTG | 2760 |
| Qy | 2770 | AAAGCCCTCT | TAATAAGTTG | AAATTCAG | AATCGGGAAG | AAATGAAGGCGAGTTTATA | 2829 |
| Db | 2761 | AAAGCCCTCT | TAATAAGTTG | AAATTCAG | AATCGGGAAG | AAATGAAGGCGAGTTTATA | 2820 |
| Qy | 2830 | AGCCCGTTA | CTTTTAATG | ATGCAAAAT | TCATGCTTTAG | GATGGCTTAAATAATTCGAAGT | 2889 |
| Db | 2821 | AGCCCGTTA | CTTTTAATG | ATGCAAAAT | TCATGCTTTAG | GATGGCTTAAATAATTCGAAGT | 2880 |
| Qy | 2890 | GCATCGACAT | TAAACCCACT | CAATTTAGT | TAATGTACTCTT | GAGTTAAAAAGCCTGAGAAACCA | 2949 |
| Db | 2881 | GCATCGACAT | TAAACCCACT | CAATTTAGT | TAATGTACTCTT | GAGTTAAAAAGCCTGAGAAACCA | 2940 |
| Qy | 2950 | AACACAGCT | TAATGCTAT | CGGGTGAT | GAATATGT | CAAGTTAGGTCAATTTAGAGATTTC | 3009 |
| Db | 2941 | AACACAGCT | TAATGCTAT | CGGGTGAT | GAATATGT | CAAGTTAGGTCAATTTAGAGATTTC | 3000 |
| Qy | 3010 | ACACTGTAT | TTTGAATTTAT | CGGAGTAA | CAACACCTT | CAAAATTTCA | 3053 |
| Db | 3001 | ACACTGTAT | TTTGAATTTAT | CGGAGTAA | CAACACCTT | CAAAATTTCA | 3044 |

RESULT 4
BD275572 linear DNA 3718 bp PAT 17-JUL-2003
LOCUS BD275572 3718bp Catted Potassium Channel.

| | |
|-----------|--|
| ACCESSION | BD275572 |
| VERSION | BD275572.1 GI:33085340 |
| KEYWORDS | JP 2002543768-A/2. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| AUTHORS | 1 (bases 1 to 3718) |
| TITLE | Mezsker, M.L., Li, W., Petrukhin, K. and Caskey, T.C. |
| JOURNAL | Novel Human Voltage-Gated Potassium Channel |
| | Patent: JP 2002543768-A 2 24-DEC-2002; |
| | Merck and Co Inc |
| COMMENT | OS Homo Sapiens |
| | PN JP 2002543768-A/2 |
| | PD 24-DEC-2002 |
| | PF 10-APR-2000 JP 2000611548 |

| | | | | |
|---|--|------|---|------|
| y | | 1210 | AAGAGCCGACAAGCCTCAGTAGTGACAGAGTCCCACGAACCGACATCACAGCCGAG | 1269 |
| b | | 1201 | AAGAGCCGACAAGCCTCAGTAGTGACAGAGTCCCACGAACCGACATCACAGCCGAG | 1260 |
| y | | 1270 | GGCAGTCCCACCAAAAGTCGAGAAGCTTGAGCTTCAA CGA CGAA CCGGCTTCGGGCC | 1329 |
| b | | 1261 | GGCAGTCCCACCAAAAGTCGAGAAGCTTGAGCTTCAA CGA CGAA CCGGCTTCGGGCC | 1320 |
| y | | 1330 | TGCGTGGCCTCAAAAGTTCTCAGCCAAAACAGTGTATAGTCTGCACACAGCCCTTGCG | 1389 |
| b | | 1321 | TGCGTGGCCTCAAAAGTTCTCAGCCAAAACAGTGTATAGTCTGCACACAGCCCTTGCG | 1380 |
| y | | 1390 | ACTGATCATGTATGATGAAAAAGGATGCGAGTGTGATGATCATGFTGGGAAGACCTCAC | 1449 |
| b | | 1381 | ACTGATCATGTATGATGAAAAAGGATGCGAGTGTGATGATCATGFTGGGAAGACCTCAC | 1440 |
| y | | 1450 | CCACACTTAAACTGTCTATTCGAGCTATCAGAAATTATAAAATTTTCAATGTTGCAAAACGG | 1509 |
| b | | 1441 | CCACACTTAAACTGTCTATTCGAGCTATCAGAAATTATAAAATTTTCAATGTTGCAAAACGG | 1500 |
| y | | 1510 | AAGTTTAAGGAAACRTTACGTCCTCATATGATGTAAGAGATGTCAATGAAACAATATTCGCT | 1569 |
| b | | 1501 | AAGTTTAAGGAAACRTTACGTCCTCATATGATGTAAGAGATGTCAATGAAACAATATTCGCT | 1560 |
| y | | 1570 | GGTCACTCGGACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACAGCTGTGTATCAAAATCTT | 1629 |
| b | | 1561 | GGTCATCTGGACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACAGCTGTGTATCAAAATCTT | 1620 |
| y | | 1630 | GGAAAGGGCAAAATCAACATCAGATAAGAGAGCGAGAGAAAAATAACAGCAGAACATGAG | 1689 |
| b | | 1621 | GGAAAGGGCAAAATCAACATCAGATAAGAGAGCGAGAGAAAAATAACAGCAGAACATGAG | 1680 |
| y | | 1690 | ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAGGTTTGAAGACAGGTACAGTCC | 1749 |
| b | | 1681 | ACCAACAGACGATCTCAGTATGCTCGGTGGGTGTCAGGTTTGAAGACAGGTACAGTCC | 1740 |
| y | | 1750 | ATAGAAATCCAAGCTGGACTGACATCTAGACATCTATCAACAGGTCTTTCGAAAGGCTCT | 1809 |
| b | | 1741 | ATAGAAATCCAAGCTGGACTGACATCTAGACATCTATCAACAGGTCTTTCGAAAGGCTCT | 1800 |
| y | | 1810 | GGCTCAGCCCTCGCTTGGCTTCATTCAGAGTTCACACCTTTTGAATGTGAACAGACATCT | 1869 |
| b | | 1801 | GGCTCAGCCCTCGCTTGGCTTCATTCAGAGTTCACACCTTTTGAATGTGAACAGACATCT | 1860 |
| y | | 1870 | GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCGCGCAAAACAGTGGCTGC | 1929 |
| b | | 1861 | GACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCGCGCAAAACAGTGGCTGC | 1920 |
| y | | 1930 | TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTTCAATTCAGCGCAANT | 1989 |
| b | | 1921 | TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTTCAATTCAGCGCAANT | 1980 |
| y | | 1990 | GAGTTCAAGTCCAGACTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG | 2049 |
| b | | 1981 | GAGTTCAAGTCCAGACTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG | 2040 |
| y | | 2050 | GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTCGAAACCAA | 2109 |
| b | | 2041 | GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTCGAAACCAA | 2100 |
| y | | 2110 | ATAAATACGGGACCCCAAGCCAGCAGCCCCCAACACTTTTACAGATCCCACTCTCTCCCA | 2169 |
| b | | 2101 | ATAAATACGGGACCCCAAGCCAGCAGCCCCCAACACTTTTACAGATCCCACTCTCTCCCA | 2160 |
| y | | 2170 | GCCATCAAGCATCTGCCAGGCCAGAAATCTGTACCCCTAAACCTGTGAGGCTTACAGGAA | 2229 |
| b | | 2161 | GCCATCAAGCATCTGCCAGGCCAGAAATCTGTACCCCTAAACCTGTGAGGCTTACAGGAA | 2220 |
| y | | 2230 | AGCAATTTGACGTCAACAACCTGCTTGTGCTTCCAGAGGAAATGTTTCAGTTTGACAG | 2289 |
| b | | 2221 | AGCAATTTGACGTCAACAACCTGCTTGTGCTTCCAGAGGAAATGTTTCAGTTTGACAG | 2280 |

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|------------|---|--|-----|
| DEFINITION | | Sequence 3 from patent US 6767736. | |
| ACCESSION | AR565636 | | |
| VERSION | AR565636.1 | GI:53981669 | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 3111) | | |
| AUTHORS | Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T. | | |
| TITLE | Human ion channel protein and polynucleotides encoding the same | | |
| JOURNAL | Patent: US 6767736-A 3 27-JUL-2004; | | |
| FEATURES | Location/Qualifiers | | |
| | 1..3111 | | |
| | source | | |
| | /organism="unknown" | | |
| | /mol_type="genomic DNA" | | |
| ORIGIN | | | |
| | Query Match | 94.1%; Score 2890.8; DB 6; Length 3111; | |
| | Best Local Similarity | 98.9%; Pred. No. 0; | |
| | Matches 2951; Conservative | 1; Mismatches 3; Indels 29; Gaps 3; | |
| QY | 1 | GGCAGCGGCATGAAGAGTGTGGAGTCGGCCGGCGGCGAGGGTCTGCTGAACTCGGCAGCC | 60 |
| DB | 156 | GGCAGCGGCATGAAGAGTGTGGAGTCGGCCGGCGGCGAGGGTCTGCTGAACTCGGCAGCC | 215 |
| QY | 61 | GCCAGGGGCGACGGCTGCTACTGTGGGCACCCGGCGGCGCACGCTTGGTGGCGGCGGC | 120 |
| DB | 216 | GCCAGGGGCGACGGCTGCTACTGTGGGCACCCGGCGGCGCACGCTTGGTGGCGGCGGC | 275 |
| QY | 121 | GTTGGCTCAGGGAGAGCCGGCGGCGGCGAGCAGGGGGCCGGATGAGCTGCTGGGGAG | 180 |
| DB | 276 | GTTGGCTCAGGGAGAGCCGGCGGCGGCGAGCAGGGGGCCGGATGAGCTGCTGGGGAG | 335 |
| QY | 181 | CCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGGCGCAAGCTCAAGTACCGGGGGTGAG | 240 |
| DB | 336 | CCGCTCTCTTACACGAGTAGCCAGAGCTGCCGGCGGCGCAAGCTCAAGTACCGGGGGTGAG | 395 |
| QY | 241 | AATACCTGTACAACTGCTGGAGAGACCCGGCGGCGGCGCTTCACTACCACTCTTC | 300 |
| DB | 396 | AATACCTGTACAACTGCTGGAGAGACCCGGCGGCGGCGCTTCACTACCACTCTTC | 455 |
| QY | 301 | GTATTTCTCTCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT | 360 |
| DB | 456 | GTATTTCTCTCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT | 515 |
| QY | 361 | ACAAATTTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG | 420 |
| DB | 516 | ACAAATTTGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG | 575 |
| QY | 421 | TTGGAGTTTCATTCGAAATCTGCTCTCGGGTGTGCTTGTGCTATATAGAGGATGGCAA | 480 |
| DB | 576 | TTGGAGTTTCATTCGAAATCTGCTCTCGGGTGTGCTTGTGCTATATAGAGGATGGCAA | 635 |
| QY | 481 | GGAAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTTATATAGATACCATTTCTATCGCT | 540 |
| DB | 636 | GGAAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTTATATAGATACCATTTCTATCGCT | 695 |
| QY | 541 | TCAATAGCAGTTGTTTCTGCAAAAGCTCAGGTAATATTTTGGCAGCTCTGCACTCAGA | 600 |
| DB | 696 | TCAATAGCAGTTGTTTCTGCAAAAGCTCAGGTAATATTTTGGCAGCTCTGCACTCAGA | 755 |
| QY | 601 | AGTCTCCGTTTCTTACAGATCCTCCGATGCTGGCATGGCGCATGGAGGAGGAGGACTTGG | 660 |
| DB | 756 | AGTCTCCGTTTCTTACAGATCCTCCGATGCTGGCGCATGGCGCATGGAGGAGGAGGACTTGG | 815 |
| QY | 661 | AAATTAATCGGTTTGTGTTTATGCTCAGCAGCAAGGAAATTAATCAAGCTTGTGACATA | 720 |
| DB | 816 | AAATTAATCGGTTTGTGTTTATGCTCAGCAGCAAGGAAATTAATCAAGCTTGTGACATA | 875 |
| QY | 721 | GGATTTTGTGTTTGTGTTTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT | 780 |
| DB | 876 | GGATTTTGTGTTTGTGTTTATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT | 935 |

| | | | |
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| 2083 | QY | GCAGCCACCAACACCATTTGAAACCAAAATAAATACGGACCCCAAGCCAGCAGCCCCCAACA | 2142 |
| 2058 | DB | GCAGCCACCAACACCATTTGAAACCAAAATAAATACGGACCCCAAGCCAGCAGCCCCCAACA | 2117 |
| 2143 | QY | ACTTTACAGATCCACACTCTCTCTCCAGCCCATCAAGCATCTGCCACAGGCCAGAACTCTG | 2202 |
| 2118 | DB | ACTTTACAGATCCACACTCTCTCTCCAGCCCATCAAGCATCTGCCACAGGCCAGAACTCTG | 2177 |
| 2203 | QY | CACCTAACCCCTCAGCGTTTACAGGAAAGATTCTTGACGTACACACTGCTTGTGCC | 2262 |
| 2178 | DB | CACCTAACCCCTCAGCGTTTACAGGAAAGATTCTTGACGTACACACTGCTTGTGCC | 2237 |
| 2263 | QY | TCCAGGAAATGTTTCAGGTTTGACAGTCAAATCTCACCAGGACCGTTCTTATGAGAAA | 2322 |
| 2238 | DB | TCCAGGAAATGTTTCAGGTTTGACAGTCAAATCTCACCAGGACCGTTCTTATGAGAAA | 2297 |
| 2323 | QY | AGCTTTGACATGGAGGAGAAACTCTGTTGTCTGTCTGTCTCCATGTCGGAGGACTTG | 2382 |
| 2298 | DB | AGCTTTGACATGGAGGAGAAACTCTGTTGTCTGTCTGTCTCCATGTCGGAGGACTTG | 2357 |
| 2383 | QY | GGCAAACTTTTGTCTGTGCAAAAACCTGATCAGGTGACCGAGGAACTGTAATATACAAC | 2442 |
| 2358 | DB | GGCAAACTTTTGTCTGTGCAAAAACCTGATCAGGTGACCGAGGAACTGTAATATACAAC | 2417 |
| 2443 | QY | TCAGGAGTGTGAGTCAAGTGGCTCCAGAGGACGCAAGATTTTACCCCAATGGAGGAA | 2502 |
| 2418 | DB | TCAGGAGTGTGAGTCAAGTGGCTCCAGAGGACGCAAGATTTTACCCCAATGGAGGAA | 2477 |
| 2503 | QY | TCCAAATGTTTATTAACATGATGAAGAGTGGTCCCGAAGACAGAGACAGACACTTTT | 2562 |
| 2478 | DB | TCCAAATGTTTATTAACATGATGAAGAGTGGTCCCGAAGACAGAGACAGACACTTTT | 2537 |
| 2563 | QY | GATCGCGCACCGACCTGCCAGGGAAGCTGCTTTTGCATCAGACTCTCTTAAGACTGA | 2622 |
| 2538 | DB | GATCGCGCACCGACCTGCCAGGGAAGCTGCTTTTGCATCAGACTCTCTTAAGACTGA | 2597 |
| 2623 | QY | AGGTACAGTATCTCAGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCCCTCAGCTTG | 2682 |
| 2598 | DB | AGGTACAGTATCTCAGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCCCTCAGCTTG | 2657 |
| 2683 | QY | CCTCATGTCAAACCTGAAATTAAGTCTTCAATTTTCTCCAGGCTAGCAGTCTTTAGCC | 2742 |
| 2658 | DB | CCTCATGTCAAACCTGAAATTAAGTCTTCAATTTTCTCCAGGCTAGCAGTCTTTAGCC | 2717 |
| 2743 | QY | ATACATATCATTCGATGAACATTTTCGAAAGCCCTTCTAAAAGTTGAAATTCGAAGAAT | 2802 |
| 2718 | DB | ATACATATCATTCGATGAACATTTTCGAAAGCCCTTCTAAAAGTTGAAATTCGAAGAAT | 2777 |
| 2803 | QY | CGGGAAGAAATGAAAGGCGATTTATAGCCCGTTACCTTTTAAATGTCATGAAATGCTAT | 2862 |
| 2778 | DB | CGGGAAGAAATGAAAGGCGATTTATAGCCCGTTACCTTTTAAATGTCATGAAATGCTAT | 2837 |
| 2863 | QY | GTTTAGGATGGCTAAATTCGAAGTGCATGCAGATTAACCCACTCATTTAGTAATGTA | 2922 |
| 2838 | DB | GTTTAGGATGGCTAAATTCGAAGTGCATGCAGATTAACCCACTCATTTAGTAATGTA | 2897 |
| 2923 | QY | CTTTGAGTTAAAAGCCTGAGAAACCAACACAGCTTAATGCTATGGGTTGTAATGATG | 2982 |
| 2898 | DB | CTTTGAGTTAAAAGCCTGAGAAACCAACACAGCTTAATGCTATGGGTTGTAATGATG | 2957 |
| 2983 | QY | TCAAGTTTAGTCTATTTAGAGATTTGACACTGATTTTGAATATATGGGAGTAAACACC | 3042 |
| 2958 | DB | TCAAGTTTAGTCTATTTAGAGATTTGACACTGATTTTGAATATATGGGAGTAAACACC | 3017 |
| 3043 | QY | TTCAAATTTCA 3053 | |
| 3018 | DB | TTCAAATTTCA 3028 | |

| | | | | | |
|----------|----------|---------|-----|--------|-----------------|
| RESULT 5 | AR565636 | 3111 bp | DNA | linear | PAT 08-OCT-2004 |
| LOCUS | AR565636 | | | | |

QY 781 AAAGAGTTTCTACATATGACAGATGCTCTCTGGTGGGGCACAAATTACATTGACAACTATT 840
DB 936 AAAGAGTTTCTACATATGACAGATGCTCTCTGGTGGGGCACAAATTACATTGACAACTATT 995
QY 841 GGCTATGGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTCTTCTGACGGCTTTGCA 900
DB 996 GGCTATGGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTCTTCTGACGGCTTTGCA 1055
QY 901 CTCCTTGGCAATTTCTTTTTCACATTTCTGCGGCAATTTCTTGGCTCAGGTTTTCATTA 960
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QY 961 AAAGTACAAGAACACACCGCCAGAAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAAC 1020
DB 1116 AAAGTACAAGAACACACCGCCAGAAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAAC 1175
QY 1021 CTCATTTCAGTGTGTTTGGGTAGTTTACGCGCTGATGAGAAATCTGTTTCCATTTCAACC 1080
DB 1176 CTCATTTCAGTGTGTTTGGGTAGTTTACGCGCTGATGAGAAATCTGTTTCCATTTCAACC 1235
QY 1081 TGGAAAGCCACACTTGAAGGCTTTGCACACCTGCAGCCCTTACCAAGAAAGAAACAAGGGGAA 1140
DB 1236 TGGAAAGCCACACTTGAAGGCTTTGCACACCTGCAGCCCTTACCA 1279
QY 1141 GCATCAAGCAGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGGC 1200
DB 1280 -----TCAGAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGGC 1328
QY 1201 CAGAGTATTAAGAGCCGACAAGCCCTCAGTAGGTGACAGAGGTCCTCCAGCACCCACATC 1260
DB 1329 CAGAGTATTAAGAGCCGACAAGCCCTCAGTAGGTGACAGAGGTCCTCCAGCACCCACATC 1388
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AX253254
LOCUS AX253254 3074 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 1 from Patent WO0170811.
ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Lerche C., Scherer C., Seeborn G., Busch A. and Steimmeyer K.
Potassium channel protein kncls, a target for diseases of central
nervous system and cardiovascular system
Patent: WO 0170811-A 1 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
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Query Match 93.0%; Score 2857.4; DB 6; Length 3074;
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Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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 DEFINITION Sequence 5 from Patent WO0232960.
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 ACCESSION AX456864
 VERSION AX456864.1 GI:21715731
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 1 Argenti, T.M. and Sheldon, J.H.
 Methods of selecting compounds for modulation of bladder function
 Patent: WO 0232960-A 5 25-APR-2002;
 Wyeth (US)

FEATURES
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ORIGIN
 Query Match 93.0%; Score 2857.4; DB 6; Length 3074;
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RESULT 11

AF263835 2832 bp mRNA linear PRI 01-JUN-2000
LOCUS Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5); mRNA,
DEFINITION partial cds.

ACCESSION AF263835

VERSION AF263835.1 GI:8132996

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2832)
AUTHORS Kniazeva,M. and Han,M.

TITLE A new gene of the voltage-gated potassium channel KCNQ family,

REFERENCE 2 (bases 1 to 2832)

A new candidate gene for retinal disorders

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2832)

Knazeva,M. and Han,M.

Direct Submission

| | |
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| JOURNAL | Submitted (04-MAY-2000) MCDDB, University of Colorado at Boulder, |
| FEATURES | Porter Biosciences Bldg., Boulder, CO 80309, USA |
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| Db | 1321 GAAGACCTCACCCCAACCACTTAAACCTGCTCATTCGAGCTATCAGAAATTTATGAAATTTTCA 1380 |
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| Qy | 1618 GATCAAAATTTCTTGGAAAGGGCAATCAATCAGTATGATGATGATGATGATGATGATGATGATGAT 1677 |
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| Qy | 1678 GCAGAACATGAGACCAAGCAGATCTCAGTATGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737 |

| | | | |
|----|------|--|------|
| Db | 1561 | GCAGAAACATGAGACACACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGAGTTGTAAGAAA | 1621 |
| Qy | 1738 | CAGGTCAGAGTCCATAGAGATCAAGCTGGACCTGACCTACTAGACATCTATCAACAGGCTCCTT | 1797 |
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| Db | 1681 | CGGAAAGGCTCTGCTCTCAGCCCTCGCTTTGGCTTTCATCTCCAGATCCCAACCTTTTGAATGT | 1740 |
| Qy | 1858 | GACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGATCTTTTGGGTTTCGGGTTCCGCACAA | 1917 |
| Db | 1741 | GAAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGATCTTTTGGGTTTCGGGTTCCGCACAA | 1800 |
| Qy | 1918 | AACAGTGGCTCTTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTTGCAGTTTCATT | 1977 |
| Db | 1801 | AACAGTGGCTCTTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTTGCAGTTTCATT | 1860 |
| Qy | 1978 | CTGACGGCCAAATGAGTTCAAGTCCAGATCTTCTACGGCTTACGCTTACCTATATGACACAGT | 2037 |
| Db | 1861 | CTGACGGCCAAATGAGTTCAAGTCCAGATCTTCTACGGCTTACGCTTACCTATATGACACAGT | 1920 |
| Qy | 2038 | CAAGCAACACAGGTCGCCAATTAGTCAAAAGCATGGCTCAGCAGTGGCAGGCCACCAACACC | 2097 |
| Db | 1921 | CAAGCAACACAGGTCGCCAATTAGTCAAAAGCATGGCTCAGCAGTGGTAGTCACCAACACC | 1980 |
| Qy | 2098 | ATTGCAAAACCAATTAATACGGCACCCCAAGCCAGCAGCCCCCAACATTTTACAGATCCCCA | 2157 |
| Db | 1981 | ATTGCAAAACCAATTAATACGGCACCCCAAGCCAGCAGCCCCCAACATTTTACAGATCCCCA | 2040 |
| Qy | 2158 | CCTCCTCTCCAGCCATCAAGCATCTGCCAGGCGAGAAATCTTCGACCCCTAACCCCTGCA | 2217 |
| Db | 2041 | CCTCCTCTCCAGCCATCAAGCATCTGCCAGGCGAGAAATCTTCGACCCCTAACCCCTGCA | 2100 |
| Qy | 2218 | GGCTTACAGGAAGCATTTCTGACGTACACACCTGCTGTTGCTCTCAAGGAAAATGTT | 2277 |
| Db | 2101 | GGCTTACAGGAAGCATTTCTGACGTACACACCTGCTGTTGCTCTCAAGGAAAATGTT | 2160 |
| Qy | 2278 | CAGGTTGCACAGTCAAAATCTCACCACAGACCGTTCTATGAGGAAGAACTTTGACATGGGA | 2337 |
| Db | 2161 | CAGGTTGCACAGTCAAAATCTCACCACAGACCGTTCTATGAGGAAGAACTTTGACATGGGA | 2220 |
| Qy | 2338 | GGAGAAATCTGTTGTCTGTCTGTCCATGGTGTCCGAGGACCTTGGGCAAACTTTGTCT | 2397 |
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| Qy | 2458 | AGTGGCTCCAGAGCAGCCAGATTTTTACCCCAATGGAGGAATCCAAATTTGTTTATA | 2517 |
| Db | 2341 | AGTGGCTCCAGAGCAGCCAGATTTTTACCCCAATGGAGGAATCCAAATTTGTTTATA | 2400 |
| Qy | 2518 | ACTGATGAAGAGTGGGTCCCGAAGACACAGACACACTTTTGATGCCGACCCGAG | 2577 |
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| Qy | 2578 | CCTGCCAGGGAAGCTGCTTTTGATACAGACTCTCTAAAGGACTGGAAGGTCAAGATCATCT | 2637 |
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| Qy | 2638 | CAGAGCATTTGTAAGGACGAGGAAGTACAGATGCCCTCAGCTTGCCTCATGTCAACTG | 2697 |
| Db | 2521 | CAGAGCATTTGTAAGGACGAGGAAGTACAGATGCCCTCAGCTTGCCTCATGTCAACTG | 2580 |
| Qy | 2698 | AAATAAGTCTTTCATTTTTCTTCCAGGCAATAGCAGTTCTTTAGGCATACATATCATGCA | 2757 |
| Db | 2581 | AAATAAGTCTTTCATTTTTCTTCCAGGCAATAGCAGTTCTTTAGGCATACATATCATGCA | 2640 |
| Qy | 2758 | TGAACATAATTCGAAAGCCCTTCTAAAAAGTTGAAATTTGCAAGAAATCGGGAAGAACATGAA | 2817 |

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| Db | 2641 | TGAAC | TTTTCGAAAGCCCTCTTAA | AAAGTTGAAATTCGGAAGAACATGAA | 2700 | |
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| DEFINITION | AX322509 | Accession | | | | |
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| SOURCE | | Homo sapiens (human) | | | | |
| ORGANISM | | Homo sapiens | | | | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| AUTHORS | | Dworetzky, S.I., Ramanathan, C.S., Trojnecki, J.T., Boissard, C.G. and Gribkoff, V.K. | | | | |
| TITLE | | Human kcnq5 potassium channel, methods and compositions thereof | | | | |
| JOURNAL | | Patent: WO 0192526-A 1 06-DEC-2001; | | | | |
| FEATURES | | Bristol-Myers Squibb Company (US) | | | | |
| source | | Location/Qualifiers | | | | |
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| Query Match | | 87.6% | Score 2690,4; | DB 6; | Length 2694; | |
| Best Local Similarity | | 99.9% | Pred. No. 0; | | | |
| Matches 2691; | | Conservative 1; | Mismatches 2; | Indels 0; | Gaps 0; | |
| Qy | 10 | ATGAAGGATGTGGAGTCGGGCGGGGAGGGTCTGCTGAACTCGGCGAGCCGCGAGGGGC | 69 | | | |
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| Qy | 70 | GACGGCTGTACTGTGTGGGCACCCGCGCGGCACCGCTTGGTGGCGCGCGCGTGGCGCTG | 129 | | | |
| Db | 61 | GACGGCTGTACTGTGTGGGCACCCGCGCGGCACCGCTTGGTGGCGCGCGCGTGGCGCTG | 120 | | | |
| Qy | 130 | AGGGAGAGCCGCGGGGACAGAGGGGGCCGGATGAGCTGTCTGGGAGCCGCTCTCT | 189 | | | |
| Db | 121 | AGGGAGAGCCGCGGGGACAGAGGGGGCCGGATGAGCTGTCTGGGAGCCGCTCTCT | 180 | | | |
| Qy | 190 | TACACGAGTAGCCAGAGCTGCCGCGCGCAACGCTCAAGTACCGCGCGGTGCAGAACTACCTG | 249 | | | |
| Db | 181 | TACACGAGTAGCCAGAGCTGCCGCGCGCAACGCTCAAGTACCGCGCGGTGCAGAACTACCTG | 240 | | | |
| Qy | 250 | TACAACTGTGTGAGAGACCCCGCGCGGTGGCGCTTCACTACACGCTTTCGTTTTC | 309 | | | |
| Db | 241 | TACAACTGTGTGAGAGACCCCGCGCGGTGGCGCTTCACTACACGCTTTCGTTTTC | 300 | | | |
| Qy | 310 | CTTGTCTTTCGTTGCTTGAATTTTGTCAAGTGTTCCTACCTGAGCAGACAAATTC | 369 | | | |
| Db | 301 | CTTGTCTTTCGTTGCTTGAATTTTGTCAAGTGTTCCTACCTGAGCAGACAAATTC | 360 | | | |
| Qy | 370 | GCCTCAAGTTGCTCTTGATCCTCGAGTTCGTCATGATGTCCTCTTTGTTGGAGTTC | 429 | | | |
| Db | 361 | GCCTCAAGTTGCTCTTGATCCTCGAGTTCGTCATGATGTCCTCTTTGTTGGAGTTC | 420 | | | |
| Qy | 430 | ATCATTCGAACTCTGGTTCGGGTTCGCTGTTGTGCATATAGAGGATTCGCAAGGAAGCTG | 489 | | | |

QY 2650 AAGCGAGGAGAAAGTACAGATCCCTCAGCTTGCTCATGTCAAAGTAAATAA 2703
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AR565635
LOCUS AR565635 2772 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6767736.
ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2772)
AUTHORS Hu, Y., Kieck, J. A., Turner, C. A. Jr., Nehls, M. C., Friedrich, G.,
Zambrowicz, B. and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
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ORIGIN

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QY 61 GCCAGGGCGAGCGGCTCTACTGCTGGGCAACCCGCGGGCAGCGCTTGGTGGGGCGGC 120
DB 157 GCCAGGGCGAGCGGCTCTACTGCTGGGCAACCCGCGGGCAGCGCTTGGTGGGGCGGC 216

QY 121 GGTGGCTGAGGGAGAGCGCGCGGGCAAGCAGGGGGCCGGATGAGCGCTCTGGGGAG 180
DB 217 GGTGGCTGAGGGAGAGCGCGCGGGCAAGCAGGGGGCCGGATGAGCGCTCTGGGGAG 276

QY 181 CCGCTCTCTTACAGAGTAGCAGAGCTGCGGGCGGCAACGTCAGTAGCCGGGGGTGCAG 240
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QY 241 AACTACCTGTACAAGCTGCTGGAGAGACCCCGCGGCTGGGGTTCATCTACACGCTTTC 300
DB 337 AACTACCTGTACAAGCTGCTGGAGAGACCCCGCGGCTGGGGTTCATCTACACGCTTTC 396

QY 301 GTTTTCTCTGCTTGGTGTGCTTGAATTTGTCAGGTTTTCTACCATCCCTGAGCAC 360
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QY 361 ACAAAATGGCTCAAGTGGCTCTTGATCTGAGTTCGAGTTCGATGCTGCTTTGGT 420
DB 457 ACAAAATGGCTCAAGTGGCTCTTGATCTGAGTTCGAGTTCGATGCTGCTTTGGT 516

QY 421 TTGGAGTTCATCATTCGAATCTGCTCTGCGGGTTCGCTTCTCGATATAGAGGATGGCAA 480
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QY 481 GGAAGACGTAGGTTGCTCGAAAGCCCTTCTGTTTATAGATACATTTGTTCTTATCGCT 540
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QY 541 TCAATACAGTGTCTCGAAAGAACTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGA 600
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QY 1441 GACCTCACCCACACCTTAAACCTGCTCATTTCCAGCTATCAGAAATATGAATTTTCACTTT 1500
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LOCUS
DEFINITION Sequence 1 from Patent WO0175108.
2772 bp DNA linear PAT 29-OCT-2001

AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B.,
Zambrowicz, B. and Sands, A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
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RESULT 15

AF263836
LOCUS AF263836 3108 bp mRNA linear ROD 01-JUN-2000
DEFINITION Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
partial cds.
ACCESSION AF263836
VERSION AF263836.1 GI:8132998
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 23:15:31 ; Search time 1674 Seconds
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

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Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 3040.4 | 99.0 | 3137 | 18 | US-10-661-629-1 |
| 3 | 2890.8 | 94.1 | 3111 | 9 | US-09-825-147-3 |
| 4 | 2890.8 | 94.1 | 3111 | 18 | US-10-803-268-3 |
| 5 | 2857.4 | 93.0 | 3074 | 9 | US-09-813-148-1 |
| 6 | 2690.4 | 87.6 | 2694 | 9 | US-09-866-020-1 |
| 7 | 2690.4 | 87.6 | 2694 | 9 | US-09-810-796-2 |
| 8 | 2690.4 | 87.6 | 2694 | 19 | US-10-948-493-1 |
| 9 | 2635.4 | 85.8 | 2772 | 9 | US-09-825-147-1 |
| 10 | 2635.4 | 85.8 | 2772 | 18 | US-10-803-268-1 |
| 11 | 2626.4 | 85.5 | 2667 | 9 | US-09-810-796-3 |

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| 12 | 518 | 16.9 | 2335 | 17 | US-10-353-690-55 | Sequence 55, Appl |
| 13 | 518 | 16.9 | 2335 | 19 | US-10-850-928-1 | Sequence 1, Appl |
| 14 | 517.6 | 16.9 | 2273 | 16 | US-10-096-578-88 | Sequence 88, Appl |
| 15 | 511.6 | 16.7 | 2169 | 13 | US-10-128-870-22 | Sequence 22, Appl |
| 16 | 511.6 | 16.7 | 2169 | 14 | US-10-131-685-22 | Sequence 22, Appl |
| 17 | 509.8 | 16.6 | 582 | 15 | US-10-313-542-303 | Sequence 303, Appl |
| 18 | 499 | 16.2 | 7411 | 18 | US-10-335-053-6 | Sequence 6, Appl |
| 19 | 499 | 16.2 | 7420 | 17 | US-10-295-027-281 | Sequence 281, Appl |
| 20 | 499 | 16.2 | 7420 | 18 | US-10-643-795A-75 | Sequence 75, Appl |
| 21 | 499 | 16.2 | 7420 | 19 | US-10-948-518-75 | Sequence 75, Appl |
| 22 | 499 | 16.2 | 7863 | 15 | US-10-084-817-335 | Sequence 335, Appl |
| 23 | 480 | 15.6 | 5595 | 18 | US-10-820-307-8 | Sequence 8, Appl |
| 24 | 474 | 15.4 | 548 | 10 | US-09-826-734-269 | Sequence 269, Appl |
| 25 | 467 | 15.2 | 2766 | 18 | US-10-820-307-6 | Sequence 6, Appl |
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| 29 | 460.8 | 15.0 | 2565 | 13 | US-10-128-870-26 | Sequence 26, Appl |
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| 32 | 457.4 | 14.9 | 2755 | 18 | US-10-820-307-4 | Sequence 4, Appl |
| 33 | 455.8 | 14.8 | 1848 | 18 | US-10-744-796-5 | Sequence 5, Appl |
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| 35 | 452 | 14.7 | 575 | 15 | US-10-313-542-305 | Sequence 305, Appl |
| 36 | 432.2 | 14.1 | 1878 | 18 | US-10-744-796-3 | Sequence 3, Appl |
| 37 | 432.2 | 14.1 | 4596 | 18 | US-10-723-860-7636 | Sequence 7636, Ap |
| 38 | 425.4 | 13.9 | 455 | 17 | US-10-242-535A-25396 | Sequence 25396, A |
| 39 | 425.4 | 13.9 | 455 | 17 | US-10-085-783A-25396 | Sequence 25396, A |
| 40 | 425 | 13.8 | 3287 | 13 | US-10-128-870-19 | Sequence 19, Appl |
| 41 | 425 | 13.8 | 3287 | 14 | US-10-131-685-19 | Sequence 19, Appl |
| 42 | 423.4 | 13.8 | 1425 | 10 | US-09-960-706-511 | Sequence 511, Appl |
| 43 | 423.4 | 13.8 | 1425 | 10 | US-09-873-313-313 | Sequence 313, Appl |
| 44 | 423.4 | 13.8 | 1425 | 16 | US-10-116-712-662 | Sequence 662, Appl |
| 45 | 423.4 | 13.8 | 1932 | 18 | US-10-744-796-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1

US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a NO. US20020102677A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
US-09-810-796-1

Query Match 100.0%; Score 3070.6; DB 9; Length 3071;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-810-796-1

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| Db | 961 | AAAGTACAAAGAACACACCGCGAGAAACATTTTGAGAAAGGAAGAACCCAGCTGCCAAC | 1020 |
| QY | 1021 | CTCATTCAGTGTGTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTCCAAACC | 1080 |
| Db | 1021 | CTCATTCAGTGTGTTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTCCAAACC | 1080 |
| QY | 1081 | TGGAAGCCACATTTGAAGGCTTGGCACACCTGCGAGCCCTTACCAAGAAAGAACCAAGGGAA | 1140 |
| Db | 1081 | TGGAAGCCACATTTGAAGGCTTGGCACACCTGCGAGCCCTTACCAAGAAAGAACCAAGGGAA | 1140 |
| QY | 1141 | GCATCAAGCAGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCCAGGGGC | 1200 |
| Db | 1141 | GCATCAAGCAGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCCAGGGGC | 1200 |
| QY | 1201 | CAGAGTATTAAGAGCCGCAAGCCCTCAGTACAGGAGGTCCCAAGCAGCAGCATC | 1260 |
| Db | 1201 | CAGAGTATTAAGAGCCGCAAGCCCTCAGTACAGGAGGTCCCAAGCAGCAGCATC | 1260 |
| QY | 1261 | ACAGCGGAGGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACAGCCGGAACCCGC | 1320 |
| Db | 1261 | ACAGCGGAGGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACAGCCGGAACCCGC | 1320 |
| QY | 1321 | TTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCCAAAACCAAGTATAGATGCTGACACA | 1380 |
| Db | 1321 | TTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCCAAAACCAAGTATAGATGCTGACACA | 1380 |
| QY | 1381 | GGCCTTGGCAGTGTATATGATGATAAAGATGCCAGTGTGATGATCAGTGAA | 1440 |
| Db | 1381 | GGCCTTGGCAGTGTATATGATGATAAAGATGCCAGTGTGATGATCAGTGAA | 1440 |
| QY | 1441 | GACCTCACCCACCACTTAAAGCTGTCAATCGAGCTATCAGAAATTTATGAAATTTTTCATGTT | 1500 |
| Db | 1441 | GACCTCACCCACCACTTAAAGCTGTCAATCGAGCTATCAGAAATTTATGAAATTTTTCATGTT | 1500 |
| QY | 1501 | GCAAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGATAAAGATGTCAATGAA | 1560 |
| Db | 1501 | GCAAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGATAAAGATGTCAATGAA | 1560 |
| QY | 1561 | TATTCGCTGGTTCATCTGGACATGTTGTAGAAATTTAAAGCTTCAAAACAGTGTGAT | 1620 |
| Db | 1561 | TATTCGCTGGTTCATCTGGACATGTTGTAGAAATTTAAAGCTTCAAAACAGTGTGAT | 1620 |
| QY | 1621 | CAAAATCTTGGAAAAAGGGCAATCAATCAGATAGAAAGAGCCGAGAGAAATTAACAGCA | 1680 |
| Db | 1621 | CAAAATCTTGGAAAAAGGGCAATCAATCAGATAGAAAGAGCCGAGAGAAATTAACAGCA | 1680 |
| QY | 1681 | GAAATGAGACACACAGACGATCTCAGTATGCTCGGTCGGTCTCAAGGTTTCAAAAAACAG | 1740 |
| Db | 1681 | GAAATGAGACACACAGACGATCTCAGTATGCTCGGTCGGTCTCAAGGTTTCAAAAAACAG | 1740 |
| QY | 1741 | GTACAGTCCATAGAAATCCAAAGCTGGAGTCCCTACTAGACATCTATCAACAGGTCCTTCGG | 1800 |
| Db | 1741 | GTACAGTCCATAGAAATCCAAAGCTGGAGTCCCTACTAGACATCTATCAACAGGTCCTTCGG | 1800 |
| QY | 1801 | AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCCTTCCAGTTCCTTGAATGAA | 1860 |
| Db | 1801 | AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCCTTCCAGTTCCTTGAATGAA | 1860 |
| QY | 1861 | CAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTCGGGTTCCGCAAAAAAC | 1920 |
| Db | 1861 | CAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTCGGGTTCCGCAAAAAAC | 1920 |
| QY | 1921 | AGTGGCTGCTTATCCAGATCAACTAGTGCACAAATCTGAGAGGCTCGAGTTCATTCG | 1980 |
| Db | 1921 | AGTGGCTGCTTATCCAGATCAACTAGTGCACAAATCTGAGAGGCTCGAGTTCATTCG | 1980 |
| QY | 1981 | ACGCCAAATGAGTTCAGTCCCGAGATTTCTAGCGCTTAGCCCTACTATGACAGTCAA | 2040 |
| Db | 1981 | ACGCCAAATGAGTTCAGTCCCGAGATTTCTAGCGCTTAGCCCTACTATGACAGTCAA | 2040 |
| QY | 2041 | GCAACACAGGTGCAATTTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAT | 2100 |
| Db | 2041 | GCAACACAGGTGCAATTTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAT | 2100 |
| QY | 2101 | GCAAAACAAATTAATACGGCACCCAGCAGCCCAACACTTTTACAGATCCCACT | 2160 |
| Db | 2101 | GCAAAACAAATTAATACGGCACCCAGCAGCCCAACACTTTTACAGATCCCACT | 2160 |
| QY | 2161 | CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAAACTCTGCACCCCTAACCCCTGCAGGC | 2220 |
| Db | 2161 | CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAAACTCTGCACCCCTAACCCCTGCAGGC | 2220 |
| QY | 2221 | TTACAGGAAAGCAATTTCTGAGCTCACCACTGCTGCTTGGCTTCAAGGAAATGTTTCA | 2280 |


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Db 2221 TTAGGAAAGCAATTTCTGACGTCACCACTGCTTGTGCTCCAAAGGAAATGTTTCAG 2280
Qy 2281 GTTGCACAGTCAAAATCTCACCAAGCAGCGTCTCTATGAGGAAAGCTTTGACATGGGAGGA 2340
Db 2281 GTTGCACAGTCAAAATCTCACCAAGCAGCGTCTCTATGAGGAAAGCTTTGACATGGGAGGA 2340
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Qy 2521 GATGAAGAGTGGTCCGAGAGACAGACAGACTTTTGTATGCCGACCGACGCT 2580
Db 2521 GATGAAGAGTGGTCCGAGAGACAGACAGACTTTTGTATGCCGACCGACGCT 2580
Qy 2581 GCCAGGAGTGCCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAG 2640
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Db 2641 AGCAATTTGTAAGGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700
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Db 2821 CAGTTTATAGCCGCTTACCTTTTAAATGCAATGAAATGCAATGTTAGGAGTGCCTAAAA 2880
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Db 2881 TTCCAAGTGTCATCGACATTAACCCACTCAATTTAGTAAATGACCTTGAATGTTAAAAAGCCT 2940
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Db 2941 GAGAAACCAACACAGCTAATGCTATGGGTGATGAATATGTCAAGTTAGTCAATTTA 3000
Qy 3001 GAAGATTGACACTGTATTTTGAATTTATGGAGTAAACACCTTCAAAATTTCAAAAAAAA 3060
Db 3001 GAAGATTGACACTGTATTTTGAATTTATGGAGTAAACACCTTCAAAATTTCAAAAAAAA 3060
Qy 3061 AAAAAA 3071
Db 3061 AAAAAA 3071
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RESULT 2
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

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; LENGTH: 3137  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2691)  
US-10-661-629-1  
  
Query Match 99.0%; Score 3040.4; DB 18; Length 3137;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3041; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
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Db 1 ATGAAGATGTGAGTCCGGCCGGGCGCAGGGTGTCTGTGAATCTGGGAGCGCCGAGGGGC 60  
  
Qy 70 GAGCGCTGTACTGTCTGGGCAACCCGCGCGCCACGCTGTGTGGCGGCGGGTGGCTG 129  
Db 61 GAGCGCTGTACTGTCTGGGCAACCCGCGCGCCACGCTGTGTGGCGGCGGGTGGCTG 120  
  
Qy 130 AGGAGAGCCGCGGGGCAAGCAGGGGCGCCGGATGAGCCTGTCTGGGGAAGCCGCTCTCT 189  
Db 121 AGGAGAGCCGCGGGGCAAGCAGGGGCGCCGGATGAGCCTGTCTGGGGAAGCCGCTCTCT 180  
  
Qy 190 TACACGATGACACAGAGCTGCGGCGCAACGCTCAAGTACCGGCGGGTGCAGAACTACCTG 249  
Db 181 TACACGATGACACAGAGCTGCGGCGCAACGCTCAAGTACCGGCGGGTGCAGAACTACCTG 240  
  
Qy 250 TACAACTGTCTGGAGAGACCCCGCGCTGGCGCTTCACTACCAACGCTTTCGTTTCTC 309  
Db 241 TACAACTGTCTGGAGAGACCCCGCGCTGGCGCTTCACTACCAACGCTTTCGTTTCTC 300  
  
Qy 310 CTTGTCTTTGTTGCTTGTATTTTGTCTAGTGTCTTACCATCCCTGAGCACACAAAATTG 369  
Db 301 CTTGTCTTTGTTGCTTGTATTTTGTCTAGTGTCTTACCATCCCTGAGCACACAAAATTG 360  
  
Qy 370 GCCTCAAGTTGCCTCTTGATCTCGAGTTCTGTGATGATGTCTGCTTTGTTGGAGTTC 429  
Db 361 GCCTCAAGTTGCCTCTTGATCTCGAGTTCTGTGATGATGTCTGCTTTGTTGGAGTTC 420  
  
Qy 430 ATCAATTCGAATCTGGTCTGCGGGTGTCTGTTCGATATAGAGATGCGAAGGAACTG 489  
Db 421 ATCAATTCGAATCTGGTCTGCGGGTGTCTGTTCGATATAGAGATGCGAAGGAACTG 480  
  
Qy 490 AGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACCAATTTCTTATCGCTTCAATAGCA 549  
Db 481 AGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACCAATTTCTTATCGCTTCAATAGCA 540  
  
Qy 550 GTTGTTCGCAAAAACCTCAGGGTAATATTTTTCGCAAGTCTGCACTCAGAACTCTCGT 609  
Db 541 GTTGTTCGCAAAAACCTCAGGGTAATATTTTTCGCAAGTCTGCACTCAGAACTCTCGT 600  
  
Qy 610 TTCTACAGATCTCCGATGTCGCGATGCGACCGAAGGGGAGGACCTTGGAAATTTACTG 669  
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Qy 670 GGTTCAAGTGTATGCTCAGCAGCAAGAAATTAATCAAGTGTGATAGGATTTTGTG 729  
Db 661 GGTTCAAGTGTATGCTCAGCAGCAAGAAATTAATCAAGTGTGATAGGATTTTGTG 720  
  
Qy 730 GTTCTTATTTTTCGCTCTTCTTCTATCTGTGGTGGAAAGGATGCCAATAAAGAGTTT 789  
Db 721 GTTCTTATTTTTCGCTCTTCTTCTATCTGTGGTGGAAAGGATGCCAATAAAGAGTTT 780  
  
Qy 790 TCTACATATCAGATGCTCTCTGTGGGCGACAAATTAATGACAACTATTGGCTATGGA 849  
Db 781 TCTACATATCAGATGCTCTCTGTGGGCGACAAATTAATGACAACTATTGGCTATGGA 840  
  
Qy 850 GACAAAACTCCCTTAACCTTGGCTGGGGAAGATTTGCTTCTGACGCTTTTGCACTCCTTGGC 909  
Db 841 GACAAAACTCCCTTAACCTTGGCTGGGGAAGATTTGCTTCTGACGCTTTTGCACTCCTTGGC 900  
  
Qy 910 ATTTCTTTTTCGCACTTCTGCGGCAATTTCTTGGCTCAGGTTTTCGATTAAGATACAA 969
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| 1981 | GAGTTGAGTCCGAGCTTTTCTACGGCTTTAGCCCTACTATGACAGTCAAGCAACACAG | 2040 |
| 2050 | GTGCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCACCACCAACCTTTGCAAAACCAA | 2109 |
| 2041 | GTGCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCACCACCAACCTTTGCAAAACCAA | 2100 |
| 2110 | ATAAATACGGCACCACCAAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA | 2169 |
| 2101 | ATAAATACGGCACCACCAAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA | 2160 |
| 2170 | GCCATCAAGCATCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG | 2229 |
| 2161 | GCCATCAAGCATCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG | 2220 |
| 2230 | AGCATTTCTGACGTCACCACTGCTGCTTGTGCTTCCAAAGGAAATGTTTCAAGTTGACAG | 2289 |
| 2221 | AGCATTTCTGACGTCACCACTGCTGCTTGTGCTTCCAAAGGAAATGTTTCAAGTTGACAG | 2280 |
| 2290 | TCAAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG | 2349 |
| 2281 | TCAAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG | 2340 |
| 2350 | TTGCTCTGCTCTGCTCCATGCTGCGAAGGACTTGGGCAAACTCTTTGCTGCTGCAAAACCTG | 2409 |
| 2341 | TTGCTCTGCTCTGCTCCATGCTGCGAAGGACTTGGGCAAACTCTTTGCTGCTGCAAAACCTG | 2400 |
| 2410 | ATCAGGTGCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA | 2469 |
| 2401 | ATCAGGTGCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA | 2460 |
| 2470 | GGCAGCAGGATTTTACCCCAATGGAGGAACTCCAAATTTGTTTATTAACCTGATGAAGAG | 2529 |
| 2461 | GGCAGCAGGATTTTACCCCAATGGAGGAACTCCAAATTTGTTTATTAACCTGATGAAGAG | 2520 |
| 2530 | GTGGGTCCCGAAGACAGACAGACACTTTTGAATGCGCACCGCAGCCTGCCAGGAA | 2589 |
| 2521 | GTGGGTCCCGAAGACAGACAGACACTTTTGAATGCGCACCGCAGCCTGCCAGGAA | 2580 |
| 2590 | GCTGCTTTGCACTCAGACTCTTAAGGCTGGAAGGTCACGATCATCTCAGAGCATTTGT | 2649 |
| 2581 | GCTGCTTTGCACTCAGACTCTTAAGGCTGGAAGGTCACGATCATCTCAGAGCATTTGT | 2640 |
| 2650 | AAGCAGGAGAAAGTACAGATGCTTCAAGTGGCTCCTCATGTCAAACTGAAATTAAGTTCTT | 2709 |
| 2641 | AAGCAGGAGAAAGTACAGATGCTTCAAGTGGCTCCTCATGTCAAACTGAAATTAAGTTCTT | 2700 |
| 2710 | CATTTCTTTCCAGGATAGCAGTTCTTTAGGCATACATCATTTGCAATGAACTATTTCCG | 2769 |
| 2701 | CATTTCTTTCCAGGATAGCAGTTCTTTAGGCATACATCATTTGCAATGAACTATTTCCG | 2760 |
| 2770 | AAAGCCCTTCTAAGAAAGTTGAAATTCGAAGATCGGAAAGAACATGAAGGAGGATTTATA | 2829 |
| 2761 | AAAGCCCTTCTAAGAAAGTTGAAATTCGAAGATCGGAAAGAACATGAAGGAGGATTTATA | 2820 |
| 2830 | AGCCCGTTACCTTTTAAATGTCATGAAATGTCATGTTTAGGGATGGCTTAAATTTCCAGGT | 2889 |
| 2821 | AGCCCGTTACCTTTTAAATGTCATGAAATGTCATGTTTAGGGATGGCTTAAATTTCCAGGT | 2880 |
| 2890 | GCATCGACATTAACCCACTCATTTAGTATGATGCTTGAATGAAAGGCTGAGAAACCA | 2949 |
| 2881 | GCATCGACATTAACCCACTCATTTAGTATGATGCTTGAATGAAAGGCTGAGAAACCA | 2940 |
| 2950 | AACACAGCTAATGCTATGGGCTGTATGAATATGCTAAGTTTAGGTCATTTAGAGATTG | 3009 |
| 2941 | AACACAGCTAATGCTATGGGCTGTATGAATATGCTAAGTTTAGGTCATTTAGAGATTG | 3000 |
| 3010 | ACACTGTATTTGAAATTTATGGGATGAACACCTTCAAAATTTCA | 3053 |
| 3001 | ACACTGTATTTGAAATTTATGGGATGAACACCTTCAAAATTTCA | 3044 |

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; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Zands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-3

Query Match      94.1%; Score 2890.8; DB 9; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

1  GGCAGGCGCATGAAGGATGTGGAGTCGGGCGGGCGGAGGCTGCTGAACCTCGGAGCC 60
156  GGCAGGCGCATGAAGGATGTGGAGTCGGGCGGGCGGAGGCTGCTGAACCTCGGAGCC 215
61  GCCAGGGCGGAGCGCCCTGCTACTGCTGGGACCCGCGGCGGAGCTGTGGTGGCGGGC 120
216  GCCAGGGCGGAGCGCCCTGCTACTGCTGGGACCCGCGGCGGAGCTGTGGTGGCGGGC 275
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241  AACTACCTGTACAACTGCTGCTGAGAGACCCCGCGGCTGGGCGTTCACTACCAAGCTTTC 300
396  AACTACCTGTACAACTGCTGCTGAGAGACCCCGCGGCTGGGCGTTCACTACCAAGCTTTC 455
301  GTTTTCTCCTTGCTTGTGTTGCTTGAATTTGTCAGTGTTCCTACCACTCCCTGAGCAC 360
456  GTTTTCTCCTTGCTTGTGTTGCTTGAATTTGTCAGTGTTCCTACCACTCCCTGAGCAC 515
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636  GGAAGACTGAGGTTGCTCGAAGCCCTTCTGTTGTTATAGATACCATTTCTTATCGCT 695
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696  TCAATAGCAGTTGTTCTGCAAAACTCAGGTTAATATTTTGGCAGCTCTGCACTCAGA 755
601  AGTCTCGGTTTCTACAGATCCTCGCATGTGGCGCATGGACCGAAGGGGAGGCACTTGG 660
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Qy 721 GGATTTTGGTTCCTTATTTTGGTTCCTTCTCTATCTGGTGGAAAGATGCCAAT 780
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Qy 781 AAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGGCAAAATTAATTGACAACTATT 840
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Qy 961 AAAGTACAAGAACAAACCCGCGAGAAACATTTTGAGAAAAGAGAAACCCAGCTGCCAAC 1020
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Db 576 TTGAGTTTCATTCGATCTGGTCTGCGGGTGTGTTGTCGATATAGAGGATGGCAA 635
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Db 636 GGAAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCAATGTTCTTATCGCT 695
Qy 541 TCAATAGCAGTTGTTCTGCAAAAACCTCAGGGTAAATATTTTGGCAACGTCGCACTCAGA 600
Db 696 TCAATAGCAGTTGTTCTGCAAAAACCTCAGGGTAAATATTTTGGCAACGTCGCACTCAGA 755
Qy 601 AGTCTCGTTTCTTACAGATCCTCGCATGCTGCGATGGACCGAAGGGAGGCACTGG 660
Db 756 AGTCTCGTTTCTTACAGATCCTCGCATGCTGCGATGGACCGAAGGGAGGCACTGG 815
Qy 661 AAATTTACTGGGTTTCACTGAGTTTATGCTCACAGCAAGGAAATTAATCACAGCTTGGTACATA 720
Db 816 AAATTTACTGGGTTTCACTGAGTTTATGCTCACAGCAAGGAAATTAATCACAGCTTGGTACATA 875
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Qy 781 AAAGAGTTTCTACATATGAGATGCTCTGCTGGGGGCAAAATTAATCACAACTATT 840
Db 936 AAAGAGTTTCTACATATGAGATGCTCTGCTGGGGGCAAAATTAATCACAACTATT 995
Qy 841 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCA 900
Db 996 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCA 1055
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| Qy | 2641 | AGCATTGTGAAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAA | 2700 | 241 | AACTACCTGTACAACTGTGGAGAGACCCCGGGCTTGGCGTTCACTATACCAAGCTTTC | 300 |
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| Qy | 2701 | TAACTTCTTCATTTCTTTCCAGGCATAGCAGTTCCTTTAGCCATACATATCATGCA | 2760 | 301 | GTTTTTCTCTTGTCTTGTGGTTGCTGATTTTGTCACTGTTTCTACCACTCCCTGAGCAC | 360 |
| Db | 2829 | TAACTTCTTCATTTCTTTCCAGGCATAGCAGTTCCTTTAGCCATACATATCATGCA | 2888 | 506 | GTTTTTCTCTTGTCTTGTGGTTGCTGATTTTGTCACTGTTTCTACCACTCCCTGAGCAC | 565 |
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| Qy | 2881 | TTCCAAAGTGCATGACATTAACCACTCATTTAGTAATGATGACCTTCAGTTTAAAGCCT | 2940 | 481 | GGAACTGAGGTTTGTCTCGAAAGCCCTTCTGTATAGATACCACTGTTCTTATCGCT | 540 |
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| US-09-813-148-1 | | | | | | |
| ; Sequence 1. Application US/09813148 | | | | | | |
| ; Patent No. US20020076809A1 | | | | | | |
| ; GENERAL INFORMATION: | | | | | | |
| ; APPLICANT: STEINMEYER, Klaus | | | | | | |
| ; APPLICANT: LERCHE, Christian | | | | | | |
| ; APPLICANT: SCHERER, Constanze | | | | | | |
| ; APPLICANT: SEEBOM, Guisard | | | | | | |
| ; APPLICANT: BUSCH, Andreas E. | | | | | | |
| ; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN | | | | | | |
| ; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM | | | | | | |
| ; FILE REFERENCE: 38005-119 | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/813,148 | | | | | | |
| ; CURRENT FILING DATE: 2001-03-21 | | | | | | |
| ; PRIOR APPLICATION NUMBER: DE 100 13 732.6 | | | | | | |
| ; PRIOR FILING DATE: 2000-03-21 | | | | | | |
| ; PRIOR APPLICATION NUMBER: US 60/194,041 | | | | | | |
| ; PRIOR FILING DATE: 2000-04-03 | | | | | | |
| ; NUMBER OF SEQ ID NOS: 6 | | | | | | |
| ; SOFTWARE: Patentin version 3.0 | | | | | | |
| ; SEQ ID NO 1 | | | | | | |
| ; LENGTH: 3074 | | | | | | |
| ; TYPE: DNA | | | | | | |
| ; ORGANISM: Homo sapiens | | | | | | |
| US-09-813-148-1 | | | | | | |
| Query Match | | | | | | |
| Best Local Similarity 93.0%; Score 2857.4; DB 9; Length 3074; | | | | | | |
| Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0; | | | | | | |
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| Db | 206 | GGCAGCGCATGAAGGATGTGGAGTCGGGCGGGGCGAGGGTGTCTGTAACCTGGCAGCC | 265 | 1286 | TGGAAGCCACACTTTGAAGGCTTGCACACCTCGAGCCCTACCAAGAAAGAACAGGGGAA | 1345 |
| Qy | 61 | GCCAGGGGCGAGCGCTGTACTGTGGGCACTCGCGCGGCCACCGCTTGGTGGCGGGC | 120 | 1141 | GCATCAAGCAGTCAGAGCTTAAGTTTAAAGGCGAGTCGCGCATGGCTAGCCCCAGGGGC | 1200 |
| Db | 266 | GCCAGGGGCGAGCGCTGTACTGTGGGCACTCGCGCGGCCACCGCTTGGTGGCGGGC | 325 | 1346 | GCATCAAGCAGTCAGAGCTTAAGTTTAAAGGCGAGTCGCGCATGGCTAGCCCCAGGGGC | 1405 |
| Qy | 121 | GCTGGCTGAGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCCCTGCTGGGGAAG | 180 | 1201 | CAGAGTATTAAAGCCGACAAAGCCTCAGTAGTGTGACAGGAGGTCCCCAAGCACCGACATC | 1260 |
| Db | 326 | GCTGGCTGAGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCCCTGCTGGGGAAG | 385 | 1406 | CAGAGTATTAAAGCCGACAAAGCCTCAGTAGTGTGACAGGAGGTCCCCAAGCACCGACATC | 1465 |
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| Db | 386 | CCGCTCTCTTACAGAGTAGCCAGAGTGTCCGGCGGCAACGTCAAGTACCGCGGGTCCAG | 445 | 1466 | ACAGCCGAGGGCAGTCCCAACCAAGTGCAGAGCTGGAGCTTCAACGACCGAACCCGC | 1525 |
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RESULT 7
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jégia, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Query Match 87.6%; Score 2690.4; DB 9; Length 2694;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 1501 AAGTTTAAAGGAACGTTACGTCATATGATGATAAGAGTGCATTGAAACAATATTCGCT 1560
Qy 1570 GGTCACTCGACATGTTGTGTAGAAATTAAGAGCCCTTCAAAACAGCTGTTGTATCAAAATCTT 1629
Db 1561 GGTCACTCGACATGTTGTGTAGAAATTAAGAGCCCTTCAAAACAGCTGTTGTATCAAAATCTT 1620
Qy 1630 GGAAGAGGGCAATACATCAGATAGAAAGGCGAGAGAAATAACAGCAGAACATGAG 1689
Db 1621 GGAAGAGGGCAATACATCAGATAGAAAGGCGAGAGAAATAACAGCAGAACATGAG 1680
Qy 1690 ACCACAGACGATCTCAGTATGCTCGTGGGTGTCAAGGTTGAAAAACAGGTACAGTCC 1749
Db 1681 ACCACAGACGATCTCAGTATGCTCGTGGGTGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy 1750 ATAGAATCCAAGCTGGAATGCTTACTAGACATCTATCAACAGGTCCTTCGAAAGGCTCT 1809
Db 1741 ATAGAGTCCAAGCTGGAATGCTTACTAGACATCTATCAACAGGTCCTTCGAAAGGCTCT 1800
Qy 1810 GCCTCAGCCCTCGCTTTGGCTTCAATCCAGTTCACCTTTTGAATGTGAACAGACATCT 1869
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
Qy 1870 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCAACAAAACAGTGGCTGC 1929
Db 1861 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCAACAAAACAGTGGCTGC 1920
Qy 1930 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCAAGTTCATTCTCAACGCAAAAT 1989
Db 1921 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCAAGTTCATTCTCAACGCAAAAT 1980
Qy 1990 GAGTTCAGTCCGACACTTTTACGCGTTAGCCCTACTATGCAAGTCAAGCAACACAG 2049
Db 1981 GAGTTCAGTCCGACACTTTTACGCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040
Qy 2050 GTGCAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2109
Db 2041 GTGCAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2100
Qy 2110 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2169
Db 2101 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
Qy 2170 GCCATCAAGCATCTGCCAGCCAGCAAACTCTGCAACCTTAACCTTCGAGGCTTACAGAA 2229
Db 2161 GCCATCAAGCATCTGCCAGCCAGCAAACTCTGCAACCTTAACCTTCGAGGCTTACAGAA 2220
Qy 2230 AGCATTTCTGACGTCACCACTGCTGTTGTCCTTCAAGGAAATGTTTCAAGTTGCAAG 2289
Db 2221 AGCATTTCTGACGTCACCACTGCTGTTGTCCTTCAAGGAAATGTTTCAAGTTGCAAG 2280
Qy 2290 TCAAAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2349
Db 2281 TCAAAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
Qy 2350 TTGTCTGTCTGCCATGTTGCCAGAGGACTTGGGCAAACTCTTGTCTGTGTCGCAAAACCTG 2409
Db 2341 TTGTCTGTCTGCCATGTTGCCAGAGGACTTGGGCAAACTCTTGTCTGTGTCGCAAAACCTG 2400
Qy 2410 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTCCAGA 2469
Db 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTCCAGA 2460
Qy 2470 GGCAGCCAAAGTTTTTACCCCAATGGAGGAAATCCAAATGTTTATTAACATGATGAAGAG 2529
Db 2461 GGCAGCCAAAGTTTTTACCCCAATGGAGGAAATCCAAATGTTTATTAACATGATGAAGAG 2520
Qy 2530 GTGGGTCCGAGAGACAGAGACAGACTTTTTCATGTCGCAAGGCTTCAGCCGAGGAA 2589
Db 2521 GTGGGTCCGAGAGACAGAGACAGACTTTTTCATGTCGCAAGGCTTCAGCCGAGGAA 2580
Qy 2590 GCTCCCTTTGATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2649
Db 2581 GCTCCCTTTGATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy 2650 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2703
Db 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2694

RESULT 9
US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

Query Match 85.8%; Score 2635.4; DB 9; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 1 GGCAGCGGCATCAAGGATGTGAGTGGGCGGGGCGAGGCTGCTGAACTCGGCAGCC 60
Db 97 GGCAGCGGATGAGGATGTGAGTGGGCGGGGCGAGGCTGCTGAACTCGGCAGCC 156

Qy 61 GCCAGGGCGACGGCTGCTACTGTGGGCACCCCGCGGCGACCGCTTGGTGGCGGGC 120
Db 157 GCCAGGGCGACGGCTGCTACTGTGGGCACCCCGCGGCGACCGCTTGGTGGCGGGC 216

Qy 121 GGTGGCTCAGGAGAGCGCGCGGCGAGCAGAGGGGCGCGGATGAGCTCTGGGGAAG 180
Db 217 GGTGGCTCAGGAGAGCGCGCGGCGAGCAGAGGGGCGCGGATGAGCTCTGGGGAAG 276

Qy 181 CCGCTCTCTTACACGAGTAGCAGAGCTGCCGGCGCAAGCTCAAGTACCGCGGGTGCAG 240
Db 277 CCGCTCTCTTACACGAGTAGCAGAGCTGCCGGCGCAAGCTCAAGTACCGCGGGTGCAG 336

Qy 241 AACTACTGTACAACTGTGAGAGACCCCGCGGCTGGCGGCTTCACTACACCGCTTTC 300
Db 337 AACTACTGTACAACTGTGAGAGACCCCGCGGCTGGCGGCTTCACTACACCGCTTTC 396

Qy 301 GTTTTCTCCTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
Db 397 GTTTTCTCCTGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 456

Qy 361 ACAAAATGGCTCCTCAAGTGGCTTGTGATCTGGAGTTCGTGATGATGATGATGATGAT 420
Db 457 ACAAAATGGCTCCTCAAGTGGCTTGTGATCTGGAGTTCGTGATGATGATGATGATGAT 516

Qy 421 TTGAGTTTCATCATTCGATTCGTCTGGGTTGCTGTTGCTGATATAGAGATGGCAA 480
Db 517 TTGAGTTTCATCATTCGATTCGTCTGGGTTGCTGTTGCTGATATAGAGATGGCAA 576

Qy 481 GGAAGACTCAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCT 540
Db 577 GGAAGACTCAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCT 636

Qy 541 TCAATAGCAGTGTGTTTCTGCAAAAACTCAGGGTAATAATATTTTGGCCACGCTGCACCTACA 600
Db 637 TCAATAGCAGTGTGTTTCTGCAAAAACTCAGGGTAATAATATTTTGGCCACGCTGCACCTACA 696

Qy 601 AGTCTCCGTTTCTTACAGATCCTCCGCAATGCTCGCATGCGATGCGCAAGAGGGAGGCACTTGG 660
Db 697 AGTCTCCGTTTCTTACAGATCCTCCGCAATGCTCGCATGCGCAAGAGGGAGGCACTTGG 756

Qy 661 AAATTACTGGTTCAGTGGTGTATGCTCACAGCAGGAATTAATACAGCTTGGTACATA 720
Db 757 AAATTACTGGTTCAGTGGTGTATGCTCACAGCAGGAATTAATACAGCTTGGTACATA 816

Qy 721 GGATTTTGGTTCCTTATTTTTCGTTCTTCTGTTGCTATCTGTTGAAAGAGTGCAT 780
Db 817 GGATTTTGGTTCCTTATTTTTCGTTCTTCTGTTGCTATCTGTTGAAAGAGTGCAT 876

Qy 781 AAAGAGTTTTCATATGCAATGCTCTGTTGGGCGACAAATACATTGACAACTATT 840
Db 877 AAAGAGTTTTCATATGCAATGCTCTGTTGGGCGACAAATACATTGACAACTATT 936

Qy 841 GGCTATGGAGACAAAACTCCCTTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCA 900
Db 937 GGCTATGGAGACAAAACTCCCTTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCA 996

Qy 901 CTCCTTGGCAATTTCTTCTTGGCACTTCTGCGGCAATCTTGGCTCAGGTTTGGCATTA 960
Db 997 CTCCTTGGCAATTTCTTCTTGGCACTTCTGCGGCAATCTTGGCTCAGGTTTGGCATTA 1056

Qy 961 AAAGTACAGAAACAACAACCCGCAAGAACTTTGAGAAAGAGAAACCCAGCTGCCAAC 1020
Db 1057 AAAGTACAGAAACAACAACCCGCAAGAACTTTGAGAAAGAGAAACCCAGCTGCCAAC 1116

Qy 1021 CTCATTGAGTGTGTTTGGGCTAGTTACGCACTGTGATGAGAAATCTGTTTCCATTGCAACC 1080
Db 1117 CTCATTGAGTGTGTTTGGGCTAGTTACGCACTGTGATGAGAAATCTGTTTCCATTGCAACC 1176

Qy 1081 TGAAGCCACACTTGAAGGCTTGCACCTGCGAGCCCTACCAAGAAAGAAACAAGGGAA 1140
Db 1177 TGAAGCCACACTTGAAGGCTTGCACCTGCGAGCCCTACCAAGAAAGAAACAAGGGAA 1220

Qy 1141 GCATCAGCAGTGCAGAACTAAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCCAGGGC 1200
Db 1221 -----TCAGAACTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCCAGGGC 1269

Qy 1201 CAGAGTATTAAGAGCCGCAAGCCCTCAGTATGTTGACAGGAGTCCCCAAGCAGCGACATC 1260
Db 1270 CAGAGTATTAAGAGCCGCAAGCCCTCAGTATGTTGACAGGAGTCCCCAAGCAGCGACATC 1329

Qy 1261 ACAGCCGAGGCGAGTCCCAAGTGCAGAAAGTGCAGAGCTTCAACGACCGAACCCGC 1320
Db 1330 ACAGCCGAGGCGAGTCCCAAGTGCAGAAAGTGCAGAGCTTCAACGACCGAACCCGC 1389

Qy 1321 TTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCAAAAACAGGATAGATGCTGACACA 1380
Db 1390 TTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCAAAAACAGGATAGATGCTGACACA 1449

Qy 1381 GCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1450 GCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509

Qy 1441 GACCTCACCCCACTTAAACCTGTCTATCGAGCTATCAGAAATATGAAATTTTCATGTT 1500
Db 1510 GACCTCACCCCACTTAAACCTGTCTATCGAGCTATCAGAAATATGAAATTTTCATGTT 1569

Qy 1501 GCAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGAT 1560
Db 1570 GCAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGAT 1629

Qy 1561 TATTCTGCTGCTCATCTGACATGTTGTTAGAAATTAAGCCCTTCAAAACGCTGTTGAT 1620
Db 1630 TATTCTGCTGCTCATCTGACATGTTGTTAGAAATTAAGCCCTTCAAAACGCTGTTGAT 1689

Qy 1621 CAAATTTCTTGGAAAGGGCAAAATCACATCAGATAGAAAGCCGAGAGAAATTAACAGCA 1680

Db 1690 CAAATCTTGGAAAGGGCAATACATCAGATAGAAAGCCGAGAGAAATAACAGCA 1749
Qy 1681 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAG 1740
Db 1750 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAG 1809
Qy 1741 GTACAGTCCATAGAAATCCAAAGTGGACTGCGCTACTAGACATCTATCAACAGGTCCTTCGG 1800
Db 1810 GTACAGTCCATAGAAATCCAAAGTGGACTGCGCTACTAGACATCTATCAACAGGTCCTTCGG 1869
Qy 1801 AAAGSCTCTGCTCAGCGCTCGCTTGGCTTCATTCAGATTCCCACTTTTGAATGAA 1860
Db 1870 AAAGSCTCTGCTCAGCGCTCGCTTGGCTTCATTCAGATTCCCACTTTTGAATGAA 1929
Qy 1861 CAGACATCTGACTATCAAGCCCTGTGATAGCAAGATCTTCGGGTTCGCGCAAAAC 1920
Db 1930 CAGACATCTGACTATCAAGCCCTGTGATAGCAAGATCTTCGGGTTCGCGCAAAAC 1989
Qy 1921 AGTGGCTGCTATCCAGATCAACTAGTGGCAACATCTCGAGGCGCTGCACTTCAATCTG 1980
Db 1990 AGTGGCTGCTATCCAGATCAACTAGTGGCAACATCTCGAGGCGCTGCACTTCAATCTG 2049
Qy 1981 ACGCAATGATGTCAGTCCGACACTTCTACGCGCTTAGCCCTACTATGCACAGTCAA 2040
Db 2050 ACGCAATGATGTCAGTCCGACACTTCTACGCGCTTAGCCCTACTATGCACAGTCAA 2109
Qy 2041 GCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCAATT 2100
Db 2110 GCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCAATT 2169
Qy 2101 GCAACCAAAATAATACGGACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACT 2160
Db 2170 GCAACCAAAATAATACGGACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACT 2229
Qy 2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGCCAATCCCTGCGAGGC 2220
Db 2230 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGCCAATCCCTGCGAGGC 2289
Qy 2221 TTACAGGAAAGCATTTCTGAGGTCAACACCTGCTTGTGTCTTCAAGGAAATGTTTCA 2280
Db 2290 TTACAGGAAAGCATTTCTGAGGTCAACACCTGCTTGTGTCTTCAAGGAAATGTTTCA 2349
Qy 2281 GTTGCAAGTCAAAATCTCAAGGACCGTCTATGAGGAAAGCTTTGAATGGAGGA 2340
Db 2350 GTTGCAAGTCAAAATCTCAAGGACCGTCTATGAGGAAAGCTTTGAATGGAGGA 2409
Qy 2341 GAAACTCTGTTGCTGCTGCTGCCATGCTGCGAGGACTTGGGCAATCTTTGCTGTG 2400
Db 2410 GAAACTCTGTTGCTGCTGCTGCCATGCTGCGAGGACTTGGGCAATCTTTGCTGTG 2469
Qy 2401 CAAACCTGATCAGGTCCGACGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGT 2460
Db 2470 CAAACCTGATCAGGTCCGACGAGGAACTGAATATACAACTTTCAGGGAGTGAGTCAAGT 2529
Qy 2461 GGCTCCAGAGGACCAAGATTTTTCACCAATGAGGGAATCCAAATGTTTATACT 2520
Db 2530 GGCTCCAGAGGACCAAGATTTTTCACCAATGAGGGAATCCAAATGTTTATACT 2589
Qy 2521 GATGAGAGGTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGCGCACCGAGCCT 2580
Db 2590 GATGAGAGGTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGCGCACCGAGCCT 2649
Qy 2581 GCCAGGGAAGTGCCTTTGCACTCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAG 2640
Db 2650 GCCAGGGAAGTGCCTTTGCACTCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAG 2709
Qy 2641 AGCATTTGTAAGGACGAGGAAAGTACAGATGCGCTCAGCTTCATGTCAAACTGAAA 2700
Db 2710 AGCATTTGTAAGGACGAGGAAAGTACAGATGCGCTCAGCTTCATGTCAAACTGAAA 2769
Qy 2701 TAA 2703
|||

Db 2770 TAA 2772
RESULT 10
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1
Query Match 85.8%; Score 2635.4; DB 18; Length 2772;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;
Qy 1 GGCAGCGCATGAAGGATGTGAGTCCGGCCGGGGCAGGGTGTGCTGAACTCGGCAGCC 60
Db 97 GGCAGCGCATGAAGGATGTGAGTCCGGCCGGGGCAGGGTGTGCTGAACTCGGCAGCC 156
Qy 61 GCCAGGGCGACGCTTGTCTACTCTGGGACACCGCGGGCCACGCTTGGTGGCGGGC 120
Db 157 GCCAGGGCGACGCTTGTCTACTCTGGGACACCGCGGGCCACGCTCGGTGGCGGGC 216
Qy 121 GGTGGCTGAGGGAGAGCCCGGGGCAAGCAGGGGCGCCGGATGAGCTCTCGGGGAAG 180
Db 217 GGTGGCTGAGGGAGAGCCCGGGGCAAGCAGGGGCGCCGGATGAGCTCTCGGGGAAG 276
Qy 181 CCGCTCTTTACAGAGTAGCCAGAGCTGCCGGCGCAACGTCAGTACCGGGGGTGCAG 240
Db 277 CCGCTCTTTACAGAGTAGCCAGAGCTGCCGGCGCAACGTCAGTACCGGGGGTGCAG 336
Qy 241 AACTACCTGTACACAGTGTGGAGAGACCCCGCGCTGGGGGTTTCATCTACACGCTTTC 300
Db 337 AACTACCTGTACACAGTGTGGAGAGACCCCGCGCTGGGGGTTTCATCTACACGCTTTC 396
Qy 301 GTTTTCTCTCTTGTCTTGTGTTGCTTGAATTTGTCAAGTGTCTTGTGATTTGTGAGCAC 360
Db 397 GTTTTCTCTCTTGTCTTGTGTTGCTTGAATTTGTCAAGTGTCTTGTGATTTGTGAGCAC 456
Qy 361 ACAAATTTGGCTCAAGTGTGCTTGTGATCTGAGTTCGATGATGTGCTTGTGCT 420
Db 457 ACAAATTTGGCTCAAGTGTGCTTGTGATCTGAGTTCGATGATGTGCTTGTGCT 516
Qy 421 TTGAGATTCATCATTCGAATCTGGTCTGGGGTGTGTTCTCGATATAGAGGATGGCAA 480
Db 517 TTGAGATTCATCATTCGAATCTGGTCTGGGGTGTGTTCTCGATATAGAGGATGGCAA 576
Qy 481 GGAAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCT 540
Db 577 GGAAGACTGAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCT 636
Qy 541 TCAATAGAGTGTGTTCTGCAAAACTCAGGGTAAATATTTTGGCACTGCTGCACTCAGA 600

| | | | |
|----|------|---|------|
| Db | 1690 | CAAAATCTTGGAAAGGGCAAAATCACATCAGATAAGAAAGAGCCGAGAGAGAAAATAACAGCA | 1749 |
| Qy | 1681 | GAACATGAGACCA CAGAGCATCTCAGTATGCTCGGTGGGTGGTCAAGGTGTAAGAAAACAG | 1740 |
| Db | 1750 | GAACATGAGACCA CAGAGCATCTCAGTATGCTCGGTGGGTGGTCAAGGTGTAAGAAAACAG | 1809 |
| Qy | 1741 | GTACAGTCCATAGAAATCAAGCTGGACTGCTCTAGACATCTATCAACAGGTCTCTTCGG | 1800 |
| Db | 1810 | GTACAGTCCATAGAAATCAAGCTGGACTGCTCTAGACATCTATCAACAGGTCTCTTCGG | 1869 |
| Qy | 1801 | AAAGGCTCTGCTCTCAGCCCTCGCTTTGGCTTCATTCGAGTCCACACTTTTGAATGTGAA | 1860 |
| Db | 1870 | AAAGGCTCTGCTCTCAGCCCTCGCTTTGGCTTCATTCGAGTCCACACTTTTGAATGTGAA | 1929 |
| Qy | 1861 | CAGACATCTGACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCGCGCAAAAAC | 1920 |
| Db | 1930 | CAGACATCTGACTATCAAGCCCTGTGATAGCAAGATCTTTGGGTTCGCGCAAAAAC | 1989 |
| Qy | 1921 | AGTGGCTGCTTATCCAGATCAACTAGTCCAAACATCTCGAGAGGCTCGAGTTCTATCTG | 1980 |
| Db | 2049 | AGTGGCTGCTTATCCAGATCAACTAGTCCAAACATCTCGAGAGGCTCGAGTTCTATCTG | 2049 |
| Qy | 1981 | AGCCAAATGAGTTGAGTCCGAGCTTTCTAGCGCTTAGCCCTACTATGACAGTCAA | 2040 |
| Db | 2050 | AGCCAAATGAGTTGAGTCCGAGCTTTCTAGCGCTTAGCCCTACTATGACAGTCAA | 2109 |
| Qy | 2041 | GCACACAGCTGCAATTAAGTCAAAAGCGATGCTCAGAGTGGCAGCCACCAACCACTT | 2100 |
| Db | 2110 | GCACACAGCTGCAATTAAGTCAAAAGCGATGCTCAGAGTGGCAGCCACCAACCACTT | 2169 |
| Qy | 2101 | GCAACCAAAATAAATAGGCAACCAAGCAGAGCCCAACCACTTACAGATCCCACT | 2160 |
| Db | 2170 | GCAACCAAAATAAATAGGCAACCAAGCAGAGCCCAACCACTTACAGATCCCACT | 2229 |
| Qy | 2161 | CTCTCCAGCCATCAAGCATCTGCCAGGCAGAAACTCTGCACCTAACCCCTGCAGGC | 2220 |
| Db | 2230 | CTCTCCAGCCATCAAGCATCTGCCAGGCAGAAACTCTGCACCTAACCCCTGCAGGC | 2289 |
| Qy | 2221 | TTACAGGAAGAGCAATTTCTGACGTCAACCTGCTGCTTTGGCTCCAGGAAATGTTTCA | 2280 |
| Db | 2290 | TTACAGGAAGAGCAATTTCTGACGTCAACCTGCTGCTTTGGCTCCAGGAAATGTTTCA | 2349 |
| Qy | 2281 | GTTGCACAGTCAAAATCTCCAGAGGACGTTCTATGAGGAAAGCTTTGACATGGGAGGA | 2340 |
| Db | 2350 | GTTGCACAGTCAAAATCTCCAGAGGACGTTCTATGAGGAAAGCTTTGACATGGGAGGA | 2409 |
| Qy | 2341 | GAAGCTCTGTTGCTGCTGCTCCATGGTGCAGAGCACTTGGGCAAAATCTTTGCTGTG | 2400 |
| Db | 2410 | GAAGCTCTGTTGCTGCTGCTCCATGGTGCAGAGCACTTGGGCAAAATCTTTGCTGTG | 2469 |
| Qy | 2401 | CAAAACCTGATCAGTTCGACCGAGGACGTTGAATATACACTTTTTCAGGAGTGAAGTCAAGT | 2460 |
| Db | 2470 | CAAAACCTGATCAGTTCGACCGAGGACGTTGAATATACACTTTTTCAGGAGTGAAGTCAAGT | 2529 |
| Qy | 2461 | GGCTCCAGAGGACGCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTAACT | 2520 |
| Db | 2530 | GGCTCCAGAGGACGCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTAACT | 2589 |
| Qy | 2521 | GATCAAGAGGTGGTCCGAGAGACAGACACTTTTGTATGATGCGGACCGCAGCCT | 2580 |
| Db | 2590 | GATCAAGAGGTGGTCCGAGAGACAGACACTTTTGTATGATGCGGACCGCAGCCT | 2649 |
| Qy | 2581 | GCCAGGAGGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCCAGATCATCTCAG | 2640 |
| Db | 2650 | GCCAGGAGGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCCAGATCATCTCAG | 2709 |
| Qy | 2641 | AGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAACTGAA | 2700 |
| Db | 2710 | AGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAACTGAA | 2769 |
| Qy | 2701 | TAA 2703 | |
| Db | 2770 | TAA 2772 | |

| | | | |
|----|------|--|------|
| Db | 637 | TCATATGAGATGTTGTTCTGCAAAACTCAGGTAATATTTTTCGACGCTGCACTCAGA | 696 |
| Qy | 601 | AGTCTCCGTTTCCACAGATCTCCGATGCTGGTGGCATGACCGAAGGGAGGACCTTGG | 660 |
| Db | 697 | AGTCTCCGTTTCCACAGATCTCCGATGCTGGTGGCATGACCGAAGGGAGGACCTTGG | 756 |
| Qy | 661 | AAATTAATCTGAGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATA | 720 |
| Db | 757 | AAATTAATCTGAGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATA | 816 |
| Qy | 721 | GGATTTTGGTCTTATTTTTCGCTTCCTGCTCTATCTGTTGGAAGAGATGCCAAT | 780 |
| Db | 817 | GGATTTTGGTCTTATTTTTCGCTTCCTGCTCTATCTGTTGGAAGAGATGCCAAT | 876 |
| Qy | 781 | AAAGAGTTTCTACATATGAGATGCTCTCTGTTGGGCAAAATTAATTAATGACACTATT | 840 |
| Db | 877 | AAAGAGTTTCTACATATGAGATGCTCTCTGTTGGGCAAAATTAATTAATGACACTATT | 936 |
| Qy | 841 | GGCTATGAGACAAAACTCCCTTAACCTTGGCTGGGAAGATTCCTTCTGAGGCTTTGCA | 900 |
| Db | 937 | GGCTATGAGACAAAACTCCCTTAACCTTGGCTGGGAAGATTCCTTCTGAGGCTTTGCA | 996 |
| Qy | 901 | CTCTCTGGATTTCTTTCTGCACTTCTGCGGCAATCTTGGCTCAGGTTTTTGCATTA | 960 |
| Db | 997 | CTCTCTGGATTTCTTTCTGCACTTCTGCGGCAATCTTGGCTCAGGTTTTTGCATTA | 1056 |
| Qy | 961 | AAAGTACAGAACCAACCGCCAGAAACACATTTGAGAAAGAGAAACCCAGCTGCCAAC | 1020 |
| Db | 1057 | AAAGTACAGAACCAACCGCCAGAAACACATTTGAGAAAGAGAAACCCAGCTGCCAAC | 1116 |
| Qy | 1021 | CTCATTCAGTGTGTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACC | 1080 |
| Db | 1117 | CTCATTCAGTGTGTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTTGCAACC | 1176 |
| Qy | 1081 | TGGAAGCCACATCTGAAGCCCTTGACACCTCCAGCCCTTACCAAGAAAGAAACAGGGGAA | 1140 |
| Db | 1177 | TGGAAGCCACATCTGAAGCCCTTGACACCTCCAGCCCTTACCAAGAAAGAAACAGGGGAA | 1220 |
| Qy | 1141 | GCATCAAGCAGTCAGAAAGTAAAGTTTAAAGGAGGAGTGCATGCTAGCCCGAGGGGC | 1200 |
| Db | 1221 | GCATCAAGCAGTCAGAAAGTAAAGTTTAAAGGAGGAGTGCATGCTAGCCCGAGGGGC | 1269 |
| Qy | 1201 | CAGAGTATTAAGAGCCGACAGCTCAGTGTGAGTGCAGAGGCTCCCAAGACCGACATC | 1260 |
| Db | 1270 | CAGAGTATTAAGAGCCGACAGCTCAGTGTGAGTGCAGAGGCTCCCAAGACCGACATC | 1329 |
| Qy | 1261 | ACAGCCGAGGCGAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCG | 1320 |
| Db | 1330 | ACAGCCGAGGCGAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCG | 1389 |
| Qy | 1321 | TTCCGGCCCTCGCTGGCCCTCAAAAGTCTCAGCCAAACCCAGTATGATGCTGACACA | 1380 |
| Db | 1390 | TTCCGGCCCTCGCTGGCCCTCAAAAGTCTCAGCCAAACCCAGTATGATGCTGACACA | 1449 |
| Qy | 1381 | GCCCTTGGCACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATGATG | 1440 |
| Db | 1450 | GCCCTTGGCACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATGATG | 1509 |
| Qy | 1441 | GACCTCACCCCAACCACTTAAACTGTCATTTGAGAGCTATCGAATTTAATTTCACTGT | 1500 |
| Db | 1510 | GACCTCACCCCAACCACTTAAACTGTCATTTGAGAGCTATCGAATTTAATTTCACTGT | 1569 |
| Qy | 1501 | GCAAAACGGAAGTTTAAAGAACTTACGTCCTATGATGATGAAAAAGATGCTATTGAACAA | 1560 |
| Db | 1570 | GCAAAACGGAAGTTTAAAGAACTTACGTCCTATGATGATGAAAAAGATGCTATTGAACAA | 1629 |
| Qy | 1561 | TATTCGTGCTCATCTGGACATCTGTGTAGAAATTAAGAGCTTTCAACACAGTGTGAT | 1620 |
| Db | 1630 | TATTCGTGCTCATCTGGACATCTGTGTAGAAATTAAGAGCTTTCAACACAGTGTGAT | 1689 |
| Qy | 1621 | CAAAATCTTGAAGAGGCAATCACATCAGATAAGAGAGCCGAGAGAGAAAATAACAGCA | 1680 |

| Query Match | 85.5%; | Score 2626.4; | DB 9; | Length 2667; |
|-----------------------|-----------------|---|------------|--------------|
| Best Local Similarity | 98.9%; | Pred. No. 0; | | |
| Matches 2664; | Conservative 1; | Mismatches 2; | Indels 27; | Gaps 1 |
| Qy | 10 | ATGAAGAGATGTGGAGTCGGGCGGGGCAAGGAGTGTCTGAAATCGGCAAGCCGCAAGGGGC | 69 | |
| Db | 1 | ATGAAGAGATGTGGAGTCGGGCGGGGCAAGGAGTGTCTGAAATCGGCAAGCCGCAAGGGGC | 60 | |
| Qy | 70 | GACGGCTCTACTGCTGGGCACCCGGCGGCGCAAGTGTGGTGGCGGGCGGCGGTGGCGCTG | 129 | |
| Db | 61 | GACGGCTCTACTGCTGGGCACCCGGCGGCGCAAGTGTGGTGGCGGGCGGCGGTGGCGCTG | 120 | |
| Qy | 130 | AGGAGAGAGCCCGCGGGGCAAGCAGGAGGGGCGCGGATGAGCTCTGCTGGGGAAGCGCTCTCT | 189 | |
| Db | 121 | AGGAGAGAGCCCGCGGGGCAAGCAGGAGGGGCGCGGATGAGCTCTGCTGGGGAAGCGCTCTCT | 180 | |
| Qy | 190 | TACACGATAGCCAGAGCTGCGCGGCGCAACGTCAGATACCGCGGGTGCAGAACTACCTG | 249 | |
| Db | 181 | TACACGATAGCCAGAGCTGCGCGGCGCAACGTCAGATACCGCGGGTGCAGAACTACCTG | 240 | |
| Qy | 250 | TACAACGTCGTCGAGAGACCCGGCGGTCGGGTTCACTACACGCTTCGTTTCTC | 309 | |
| Db | 241 | TACAACGTCGTCGAGAGACCCGGCGGTCGGGTTCACTACACGCTTCGTTTCTC | 300 | |
| Qy | 310 | CTTGCTTTTGGTTGCTTGATTTTGTCACTGTTTCTTACCATCCCTGAGCACACAAAATTG | 369 | |
| Db | 301 | CTTGCTTTTGGTTGCTTGATTTTGTCACTGTTTCTTACCATCCCTGAGCACACAAAATTG | 360 | |
| Qy | 370 | GCCTCAAGTTGCTCTTGATCTGTGAGTTGCTGATGATGCTCTTTGGTTGGAGTTC | 429 | |
| Db | 361 | GCCTCAAGTTGCTCTTGATCTGTGAGTTGCTGATGATGCTCTTTGGTTGGAGTTC | 420 | |
| Qy | 430 | ATCAATTCGAATCTGTCTGCGGTTGCTGTCGATATAGAGGATGCAAGGAGACCTG | 489 | |
| Db | 421 | ATCAATTCGAATCTGTCTGCGGTTGCTGTCGATATAGAGGATGCAAGGAGACCTG | 480 | |
| Qy | 490 | AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA | 549 | |
| Db | 481 | AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA | 540 | |
| Qy | 550 | GTTGTTTCTGCAAAACCTCAGGTTAATATTTTGGCACTGTGCACTCAGAAAGTCTCGGT | 609 | |
| Db | 541 | GTTGTTTCTGCAAAACCTCAGGTTAATATTTTGGCACTGTGCACTCAGAAAGTCTCGGT | 600 | |

| | | | |
|----|------|--|------|
| Db | 1654 | ACCACAGCGATCTCAGTATGCTCGGTGGGTCAAGGTTGAAAAACAGGTACAGTCC | 1713 |
| Qy | 1750 | ATAAATCCAAAGCTGACATGCCCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT | 1809 |
| Db | 1714 | ATAAGTCCAAAGCTGACATGCCCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT | 1773 |
| Qy | 1810 | GCCTCAGCCCTCGCTTTGGCTTCATTCCAGTTTCCACCTTTTGAATGTGAACAGACATCT | 1869 |
| Db | 1774 | GCCTCAGCCCTCGCTTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT | 1833 |
| Qy | 1870 | GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGTTCCGCACAAAACAGTGGCTGC | 1929 |
| Db | 1834 | GACTATCAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGTTCCGCACAAAACAGTGGCTGC | 1893 |
| Qy | 1930 | TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCATTCTGACGCCAAAT | 1989 |
| Db | 1894 | TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCATTCTGACGCCAAAT | 1953 |
| Qy | 1990 | GAGTTCAAGTCCCAAGCTTTCTACGGCTTTAGGCCCTATATGGAAGTCAAGCAACACAG | 2049 |
| Db | 1954 | GAGTTCAAGTCCCAAGCTTTCTACGGCTTTAGGCCCTATATGCAAGTCAAGCAACACAG | 2013 |
| Qy | 2050 | GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGCAGCACCAACACCATTCGAAACCAA | 2109 |
| Db | 2014 | GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGCAGCACCAACACCATTCGAAACCAA | 2073 |
| Qy | 2110 | ATAAATACGGCACCCAAAGCCAGCAGCCCCAACAACTTTTACAGATGCCACTCTCTCCCA | 2169 |
| Db | 2074 | ATAAATACGGCACCCAAAGCCAGCAGCCCCAACAACTTTTACAGATGCCACTCTCTCCCA | 2133 |
| Qy | 2170 | GCGATCAAGCATCTGCCAGGCAGAACTCTGCACCCCTAAACCCCTCAGGCTTACAGGAA | 2229 |
| Db | 2134 | GCGATCAAGCATCTGCCAGGCAGAACTCTGCACCCCTAAACCCCTCAGGCTTACAGGAA | 2193 |
| Qy | 2230 | AGCATTTCTCAGCTCACACCTGTCCTTTGTTCCTCCAAAGGAAAATGTTCAAGTTGCACAG | 2289 |
| Db | 2194 | AGCATTTCTCAGCTCACACCTGTCCTTTGTTCCTCCAAAGGAAAATGTTCAAGTTGCACAG | 2253 |
| Qy | 2290 | TCAAAATCTCAAGAGGACCGTTCTATGAGGAAAGCTTTCACATGGGAGGAGAACTCTG | 2349 |
| Db | 2254 | TCAAAATCTCAAGAGGACCGTTCTATGAGGAAAGCTTTCACATGGGAGGAGAACTCTG | 2313 |
| Qy | 2350 | TTGTCTGTCTGTCCCATGGTCCGAAAGCACTTGGGCAAACTTTTGTCTGTGCAAAACCTG | 2409 |
| Db | 2314 | TTGTCTGTCTGTCCCATGGTCCGAAAGCACTTGGGCAAACTTTTGTCTGTGCAAAACCTG | 2373 |
| Qy | 2410 | ATCAGGTCCGACGAGGAATCGAATATACAACTTTTCAGGAGTGAATCAAGTGCTCCAGA | 2469 |
| Db | 2374 | ATCAGGTCCGACGAGGAATCGAATATACAACTTTTCAGGAGTGAATCAAGTGCTCCAGA | 2433 |
| Qy | 2470 | GGCAGCCAAGATTTTTTACCCAAATGGAGGAAATCCAAATTTGTTTATAA CTGATGAAGAG | 2529 |
| Db | 2434 | GGCAGCCAAGATTTTTTACCCAAATGGAGGAAATCCAAATTTGTTTATAA CTGATGAAGAG | 2493 |
| Qy | 2530 | GTGGGTCCCGAAGACAGACAGACACTTTTGTATCCGCACCCGACCTGCCAGGAA | 2589 |
| Db | 2494 | GTGGGTCCCGAAGACAGACAGACACTTTTGTATCCGCACCCGACCTGCCAGGAA | 2553 |
| Qy | 2590 | GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACCATCATCTCAGAGCATTTGT | 2649 |
| Db | 2554 | GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACCATCATCTCAGAGCATTTGT | 2613 |
| Qy | 2650 | AAGGCAGGAGAAAGTACAGATCCCTCAGTTTGCCTCATGTCAAACTGAATAA | 2703 |
| Db | 2614 | AAGGCAGGAGAAAGTACAGATCCCTCAGTTTGCCTCATGTCAAACTGAATAA | 2667 |

```

1  APPLICANT: Logan, Thomas Joseph
2  APPLICANT: Chun, Miyoung
3  APPLICANT: Galvin, Katherine M.
4  APPLICANT: Healy, Aileen
5  APPLICANT: Acton, Susan L.
6  APPLICANT: Donoghue, Mary
7  APPLICANT: Stagliano, Nancy
8  APPLICANT: Perodin, Jacqueline
9  APPLICANT: Rodrigue-Way, Amelie
10 TITLE OF INVENTION: Methods and compositions for treating
11 TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
12 TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
13 TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
14 TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
15 TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 44624, 84237, 8912, 2868,
16 TITLE OF INVENTION: 2837, 2544, 9464, 17799, 26686, 43848, 32135, 13208, 2914,
17 TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
18 TITLE OF INVENTION:
19 FILE REFERENCE: MPI02-018P1RNMNM
20 CURRENT APPLICATION NUMBER: US/10/353,690
21 CURRENT FILING DATE: 2003-01-29
22 PRIOR APPLICATION NUMBER: 60/353,224
23 PRIOR FILING DATE: 2002-02-01
24 PRIOR APPLICATION NUMBER: 60/364,529
25 PRIOR FILING DATE: 2002-03-15
26 PRIOR APPLICATION NUMBER: 60/373,861
27 PRIOR FILING DATE: 2002-04-19
28 PRIOR APPLICATION NUMBER: 60/376,287
29 PRIOR FILING DATE: 2002-04-29
30 PRIOR APPLICATION NUMBER: 60/388,080
31 PRIOR FILING DATE: 2002-06-12
32 PRIOR APPLICATION NUMBER: 60/390,971
33 PRIOR FILING DATE: 2002-06-24
34 PRIOR APPLICATION NUMBER: 60/394,130
35 PRIOR FILING DATE: 2002-07-03
36 PRIOR APPLICATION NUMBER: 60/394,797
37 PRIOR FILING DATE: 2002-07-10
38 PRIOR APPLICATION NUMBER: 60/404,904
39 PRIOR FILING DATE: 2002-08-21
40 PRIOR APPLICATION NUMBER: 60/405,450
41 PRIOR FILING DATE: 2002-08-23
42 Remaining Prior Application data removed - See File Wrapper or PALM.
43 NUMBER OF SEQ ID NOS: 126
44 SOFTWARE: FastSeq for Windows Version 4.0
45 SEQ ID NO 55
46 LENGTH: 2335
47 TYPE: DNA
48 ORGANISM: Homo Sapiens
49 US-10-353-690-55

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| | | | |
|----|------|--|------|
| Db | 440 | ACTATCCAGGAGCACAGGAACCTGCGCAACAGAGTGTCTCCTCATCTTGGAAATTCGTGATG | 499 |
| Qy | 406 | ATTGTCTGTTTGGAGTTCATCATTCGAATCTGGTCTGGGTTGCTGTGTGCGA | 465 |
| Db | 500 | ATCGTGGTTTGGGCTTGGAGTACATCGTCGGGTCTGGTCCGGCGAGTCTGTCGGC | 559 |
| Qy | 466 | TATAGAGATGGCAAGGAAGACTGAGGTTTGTCTCGAAGCCCTTCTGTGTATAGATACC | 525 |
| Db | 560 | TACCGAGGATGGCAGGTCGCTTCGGCTTTGCCAGAAAGCCCTTCTGTGTATCGACTTC | 619 |
| Qy | 526 | ATTGTTCTTATCGCTTCAATAGAGTGTCTTCTCAAAACTCAGGGTAAATATTTTGGC | 585 |
| Db | 620 | ATCGTGTTCGTGGCTCGGTGGCCGTCATCGCCGGGTACCCAGGGCAATCTTCGCC | 679 |
| Qy | 586 | ACGTCGCACTCAGAACTCCGTTTCTCAAGATCTCCGATGCTCGGATGGCCGATGACCGA | 645 |
| Db | 680 | ACGTCGGCTGCGCAGATGGCTTCTCGAGATCTCTGGCATGGTGGCATGGACCGC | 739 |
| Qy | 646 | AGGGAGGACATGGAATTAATCTGGGTTCACTGGGTTTATGCTCAGCAGGAAATTAATC | 705 |
| Db | 740 | CGCGCGGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGGGCATAGCAAGAGCTGATC | 799 |
| Qy | 706 | ACAGCTGCTATAGGATTTTGGTCTTATTTTCTCTTCTCTTCTCTCTCTCTCTCTCTG | 765 |
| Db | 800 | ACCGCTGTGTATACCGGTTCTGTGTCTCATCTCGCTCTCTCTCTCTCTCTCTCTCTG | 859 |
| Qy | 766 | GAAGAAGATGCCAATAAAGATTTTCTACATATGAGATGCTCTCTGTGGGGCACAATT | 825 |
| Db | 860 | GAGNAGGACCCAACTCCGACTTCTCTCTACGCGGACTCGCTCTGTGGGGGACGANT | 919 |
| Qy | 826 | ACATTGACAACTATTGGCTATGGACAAACTCCCTAACTGCTGGGGAAGATTGCTT | 885 |
| Db | 920 | ACATTGACAACTATGGCTATGGTACAGACACCGCAGACATGCTGGGAGGGTCTGT | 979 |
| Qy | 886 | TCTGAGGCTTGGCACTCTCTGGCAATTTCTTTTGTGCACTTCTCTGGCGCAATTTGGC | 945 |
| Db | 980 | CGTCTGGCTTGGCTTCTGGGCTCTCTCTTCTTCTTCTCTCTCTCTCTCTCTCTAGGC | 1039 |
| Qy | 946 | TCAGGTTTGGCTTAAAGTACAGAAACACCGCCAGAACACTTTTGAGAAAGAGG | 1005 |
| Db | 1040 | TCGGCTTTGGCTTGAAGTCCAGGAGCAGCAGCGGAGAGCACTTGAGAAAGCGGAGG | 1099 |
| Qy | 1006 | AACCCAGCTGCCAACCTCATTCAGTGTGTTGGGTAGTTACGCACTGATGAGAAATCT | 1065 |
| Db | 1100 | ATCGCGGCGCCAACTCATTCAGGCTGCTGGGCTGTACTCCACCGATATAGCCGG | 1159 |
| Qy | 1066 | GTCTTCCATTGCAACCTGGAAGCCACACTTGAAGGCTTGGCACCTGACG | 1116 |
| Db | 1160 | GCCTACTGACAGCCACCTGGTACTATGACAGTATCTCTCCCATCTTTCAGAGAGCTG | 1219 |
| Qy | 1117 | CTTACCAAGAAACAGAGGAGCATCAAGCAGTCAAGAGTCA | 1161 |
| Db | 1220 | GCCTCTTGTGAGCAGTGCACCGGCGCCGATGGGGCTACGGCCCTGGAGGTG | 1279 |
| Qy | 1162 | ----- | 1161 |
| Db | 1280 | CGGCGGCGCGGTACCCGAGGAGCACCTCCCGTTACCGCCCGCTGGCCACTGCCAC | 1339 |
| Qy | 1162 | -----AGTTTAAAGGAGCA | 1176 |
| Db | 1340 | CGGCGGCGCAGCCTCTTCTGCGCTGGGAAAGCAGCGGATGGGCATCAAGACCCG | 1399 |
| Qy | 1177 | GTGCGCATGGTACCCCGAGGGCCAGA-----GTATTAAGAGCCGACAAAGCTCAGTA | 1230 |
| Db | 1400 | ATCCGATGGCAGCTCCAGCGGCGACCGGTTCTTCCAGCAGCAGCTGGCACCTCCA | 1459 |
| Qy | 1231 | GGTGACAGGAGTCCCCAAGCACCGACATCAAGCCGAGG---GCAGTCCCAAAAGTG | 1287 |
| Db | 1460 | ACAATGCCACCTCCCCAAGCAGCAGCAGTGGGTGAGGCCACCAAGCCCAACCAAGGT | 1519 |
| Qy | 1288 | CAGAGAGCTGAGCTTCAAGCCGAGACCGGCTTCCGGCCCTCGCTGCGCCTCAAAAGT | 1347 |

| | | | |
|----|------|--|------|
| Db | 1520 | CAAAAGAGCTGGAGCTTCAATGACCGCACCGCTTCCGGGCATCTCTGAGATC----- | 1573 |
| Qy | 1348 | TCTCAGCCAAACACAGTATAGATGCTGACACAGCCCTTGGCACTGATGATATATGAT | 1407 |
| Db | 1574 | -----AAACCCCGCACCTTCTGCTGAGGATGCC-----CCTCAGAGAAAGTAGCAG | 1621 |
| Qy | 1408 | GAAGAAGATGCCAGTGTGATGATCAGTGAAGACCTCACCCCACTTAAACTGTC | 1467 |
| Db | 1622 | GAGAGAGTACCACTGTGAGCTCAGCGTGGACGACATCATGCTCTGTGTGAAGACATC | 1681 |
| Qy | 1468 | ATTCGAGCTATCAGAAATTTATGAAATTTCTGTTGAAACCGAAGTTTAAAGGAAACRTTA | 1527 |
| Db | 1682 | ATCCGCTCCATCAGGATTTCTCAAGTTCTGTGGTGGCAAAAGAAATTCAGAGACATCTG | 1741 |
| Qy | 1528 | CGTCCATATGATGTAAGATGCTCATGAAATAATTTCTGTGTGTCATCTGGACATGTTG | 1587 |
| Db | 1742 | CGACCGTACGAGTGAAGACCTCATTTGAGCAGTACTCAGCAGGCCACCTGGACATGCTG | 1801 |
| Qy | 1588 | TGTAGAAATTAAGGCTTCAAAACAGCTGTTGATCAAAATTTCTGGAAGAGGC-----AAATC | 1644 |
| Db | 1802 | GGCGGATCAAGAGCCCTGCAAACTCGGTGGACCAAAATTTGTGGTGGGGGGCCCGGGAC | 1861 |
| Qy | 1645 | ACATCAGATAAGAGCCGAGAGAAATAACAGCAGAAACATGAGACACACAGCATCTCT | 1704 |
| Db | 1862 | AGGAAGCCCGGAGAGGCGCAAGGGCCCTCCGACCGGAGGTGGTGAATAATC | 1921 |
| Qy | 1705 | AGTATGCTCGGTGGGTGTCAGGTTGAAAGACAGGTACAGTCCATAGAAATCCAGAGCTG | 1764 |
| Db | 1922 | AGCATGATGGACCGGTGTCAGGTTGAGAGACAGGTGTCAGTCCATCGAGCACAGCTG | 1981 |
| Qy | 1765 | GACTGCTTACTAGACATCTATCAAGGTCTTCGGAAGGCTCTCGGAAGGCTCTGCTCGCT | 1824 |
| Db | 1982 | GACCTGCTGTGGGCTTCTATTGCGCTGCTGCTG-----GCTCTGGCACTCGGCCAGC | 2035 |
| Qy | 1825 | TTGCTTCTATTCAGTTCACCTTTTGAATGTGAACAGACATCTCACTATCAAGCCCT | 1884 |
| Db | 2036 | CTGGGCGCTGCAAGTGGCTGTTTCGACCCCGACATCACTCCGACTTACCACAGCCCT | 2095 |
| Qy | 1885 | GTGATAGCAAGATCTTTCGGTTCGGCAAAA | 1918 |
| Db | 2096 | GTGACCAAGGACATCTCCGCTCTCCGACAGA | 2129 |

RESULT 14

US-10-096-578-88

; Sequence 88, Application US/10096578

; Publication No. US20030165874A1

; GENERAL INFORMATION:

; APPLICANT: Leppert, Mark F.

; APPLICANT: Singh, Nanda

; APPLICANT: Charlier, Carole

; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE

; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)

; FILE REFERENCE: 2323-160

; CURRENT APPLICATION NUMBER: US/10/096,578

; CURRENT FILING DATE: 2002-03-14

; PRIOR APPLICATION NUMBER: US 09/177,650

; PRIOR FILING DATE: 1998-10-23

; PRIOR APPLICATION NUMBER: US 60/063,147

; PRIOR FILING DATE: 1997-10-24

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 88

; LENGTH: 2273

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2271)

; NAME/KEY: misc_feature

; LOCATION: (1)..(2273)

; OTHER INFORMATION: n may be any nucleotide except at position

;; TITLE OF INVENTION: KNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;; FILE REFERENCE: DC58adiV
;; CURRENT APPLICATION NUMBER: US/10/128,870
;; CURRENT FILING DATE: 2002-04-24
;; PRIOR APPLICATION NUMBER: 09/105,058
;; PRIOR FILING DATE: June 26, 1998
;; PRIOR APPLICATION NUMBER: 60/055,599
;; PRIOR FILING DATE: August 12, 1997
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 22
;; LENGTH: 2169
;; TYPE: DNA
;; ORGANISM: MOUSE
US-10-128-870-22

Query Match 16.7%; Score 511.6; DB 13; Length 2169;
Best Local Similarity 58.2%; Pred. No. 1.5e-137;
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;

QY 73 GGCCTGCTACTGCTGGGCAACCGCGCGCCACGCTTGGTGGCGGCGGGCTGAGG 132
Db |||||
QY 67 GGCCTGCTGGGCTGGACCGCGCGCGCCGACTCCACACGCGAGCGCGCTACTATC 126
Db |||||
QY 133 GAGACCGCGGGCAAGCAGCGGCGCGGATGAGCTGCTGGGAGCGGCTCTTTAC 192
Db |||||
QY 127 GCGGGCTCGAGGCGCCCAAGCGCGCGAGCGTTTGGACAGCGCGAGCGGGCGCG 186
Db |||||
QY 193 ACGAGTAGCACAGCTGCGCGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACTGTAC 252
Db |||||
QY 187 GAGCGCGGAAGCCCGCGAGCGCAACGCTTCTACCGCAAGCTGCAGAAATTCCTCTAC 246
Db |||||
QY 253 AAGCTGCTGGAGAGACCGCGCGCTGGGGTTCATCTACCAAGCTTTCGTTTCTCTCT 312
Db |||||
QY 247 AAGCTGCTAGAGCGCGCGCGCTGGCGCTTCATCTACCAAGCTACGTTGCTCTTTTA 306
Db |||||
QY 313 GTCCTTGGTGTGATTTGTCAGTGTGTTTCTACATCCCTCGAGCACACAAATTTGCC 372
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QY 373 TCAAGTTGCTCTTGATCTGGAGTTCGATGATGCTGCTTCTTGGTGGAGTTTCAATC 432
Db |||||
QY 367 GAGGGGCGCTCTACATCTTGAATTCGTAATCTGCTGCTGATTCGCTGTTGAGTACTTT 426
Db |||||
QY 433 ATTCGATCTGCTCGGGTCTGCTGCTGATATAGAGATGCGAGAGAGTCTGAGG 492
Db |||||
QY 427 GTGAGATCTGGGCTCGAGCTGCTGCTGCGGATTCGAGGCTGAGGGCGAGGCTCAAG 486
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QY 493 TTTGCTCGAAAGCCCTTCTGTGTATAGATACCAATTTCTTATCGCTTCAATAGAGTT 552
Db |||||
QY 487 TTTGCCAGGAGCGCTTCTGTGTGATGATATCATGCTGCTGATTCCTCATTTGCTGTG 546
Db |||||
QY 553 GTTTCTGCAAAACTCAGGGTATATTTTGGCAGCTCTGCACTCAGAGTCTCGGTTTC 612
Db |||||
QY 547 CTGGCTGCTGGTTCCAGGAGCAATGCTTTGGCACAATCTGCGCTTCGGAGCTTGGCGTTC 606
Db |||||
QY 613 CTACAGATCTCGCATGGTCCCATGGACCGAAGGGGAGGCACTTGGAAATTTACTTGGGT 672
Db |||||
QY 607 TTGCAAACTTGGGATGATCCGTATGGACCGAGGGGTGGACCTGGAGTCTTTGGA 666
Db |||||
QY 673 TCAGTGGTTTATGCTCAACAGAGGAATTAATCAGAGCTTGGTATAGATATTTTGGTT 732
Db |||||
QY 667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGAATCTGCTGCTGTATATGCTCTGTC 726
Db |||||
QY 733 CTATATTTTTCGTTCTTCTGTTCTATCTGCTGGAAGAGTCCCAATTAAGAGTTTCT 792
Db |||||
QY 727 CTATCTCGGCTCATTTCTGTTGTACTTGGCAGAAAGGGTGAGATGACCACTTTGAC 786
Db |||||
QY 793 ACATATGCAGATGCTCTCTGGTGGGCAAAATTAATTAATGACATTAATGCTATGAGAC 852
Db |||||
QY 787 ACCTACGAGATGACCTCTGTTGGGTCTGATCACCTGACGACCAATGCTACGGGAC 846
Db |||||
QY 853 AAAACTCCCTAACTGGCTGGGAGAGTATGCTTCTGAGGCTTTGCACTCTCTTGGCAAT 912
Db |||||

Search completed: April 3, 2005, 06:38:13
Job time : 1683 secs

Db 847 AAGTACCTCAGACCTGGAACGGGAGGCTGCTGGCAGCGACCTTTACCTCTATTGGTGTG 906
QY |||||
QY 913 TCTTTCTTTGCACTTCTTCGCGGCAATCTTGGCTCAGGTTTGGCATTTAAAGTCAAGAA 972
Db |||||
Db 907 TCGTTCTTTTGTCTTCTCTGCTGGCATTTTGGGATTTGGGATTTGGCTTGAAGTCCAAG 966
QY |||||
QY 973 CAACACCGCGCAGAAACACTTTTGAAGAAAGAAAGAACCCAGCTGCGCAACCTCAATCAGTGT 1032
Db |||||
Db 967 CAGCATCGGCAAAACACTTTGAGAAACGGCGGAACCCCTGCGGCAAGTCTGATCCAGTCT 1026
QY |||||
QY 1033 GTTTGGCTGTAGTTACGACGCTGATGAGAAAT 1063
Db |||||
Db 1027 GCTGGAGATCTATGCTACTAATCTCTCAACGACCGACCTGCACTCCACGTTGGCAGTAC 1086
QY |||||
QY 1064 -----CTGTTTCCATTGCAACCTTGAAGCCACACTTGAAGSCCTTTGCAC 1107
Db |||||
Db 1087 TAGACGCGACAGTCTACTGTCTCCCATGTACAGACTATCCACCTCTGACAGCTGGAG 1146
QY |||||
QY 1108 ACCTGACGCGCTTACCAAGA-----AAGAAACAAGGGGAA 1140
Db |||||
Db 1147 CTGCTGAGGAATCTCAAGAGCAAACTCTGACTCACCTTCAGGAAGGAGCCACAGCCAGAG 1206
QY |||||
QY 1141 GCATCAAGCAGTCAAGAGCTAAGTTTAAAGGAGCGAG-----TGGCATGCTAGCCCCAG 1197
Db |||||
Db 1207 CCATCAACCAAGTCAAGAGTCAAGTTTGAAGATCGTCTTCTCCAGCCCCGAGGCATG 1266
QY |||||
QY 1198 GGCACAGATATTAAAGAGCCGACAAAGCTCAGTAGTGCAGAGGAGTCCCAAGCACCGAC 1257
Db |||||
Db 1267 GCTGCCAAGGAAAGGGTCTCCCCAGGCCAGACGCTCCGCGGTCTCCCTAGTGGGAT 1326
QY |||||
QY 1258 ATCAAGCAGGAGGAGTCCCAACAAAGTGCAGAGAGTGCAGCTTCAACGACCGAAC 1317
Db |||||
Db 1327 CAGAGTCTTGATGACAGCGCGAGCAAGGTGCCCCAGAGCTGGAGCTTTGGTGAAGCCAGC 1386
QY |||||
QY 1318 CGCTTCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCAAAACCACTGATAGATGCTGAC 1377
Db |||||
Db 1387 CGCACAGCGCAGGCTTTCGCGCATCAAGGTGCTGCTATCCCGGAGAAATTCAGAGCAAGC 1446
QY |||||
QY 1378 ACAGCCCTTGGCCTGATGATGATATGATGATAAAGAGTGCAGGTGTGATGATCAGTG 1437
Db |||||
Db 1447 C---TCCCTGGGAGGACATCGTAGAGGACAAACAGAGCTGTAACTCGAGTTTGTGACT 1503
QY |||||
QY 1438 GAAGCTCTACCCCAACCACTTAAACCTGCTCATTTGAGCTATCAGAAATTAATAATTCAT 1497
Db |||||
Db 1504 GAAGATCTTACCCCTGGCCTCAAAGTTAGCATCAGAGCTGTGTGTATGCGGTTCTTG 1563
QY |||||
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Db |||||
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QY |||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 21:32:07 ; Search time 9451 Seconds
(without alignments)
12368.572 Million cell updates/sec

Title: US-09-810-796-1

Perfect score: 3071

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsei:*

9: gb_gsei2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2115.4 | 68.9 | 2729 | 9 AY407015 | Mus muscu |
| 3 | 1818.6 | 59.2 | 2014 | 9 AY407014 | Pan trogl |
| 4 | 1630.8 | 53.1 | 2276 | 3 AK033079 | Mus muscu |
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| 7 | 683 | 22.2 | 732 | 6 CD629756 | 55049343J |
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| 9 | 657.4 | 21.4 | 717 | 6 CD629766 | 55049391J |
| 10 | 650.6 | 21.2 | 678 | 6 CD629758 | 55049351J |
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| 16 | 584 | 19.0 | 624 | 6 CD629751 | 55049303H |
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| 18 | 577.8 | 18.8 | 635 | 6 CD629759 | 55049359H |
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| 26 | 535.4 | 17.4 | 908 | 2 BF240146 | 601905649 |
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| 35 | 473.4 | 15.4 | 659 | 5 BX919587 | EX919587 |
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| 37 | 471.8 | 15.4 | 659 | 5 BX926684 | EX926684 |
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| 40 | 445.8 | 14.5 | 766 | 3 AK020325 | Mus muscu |
| 41 | 444 | 14.5 | 587 | 5 BX920263 | EX920263 |
| 42 | 434 | 14.1 | 446 | 6 CD629753 | 55049327H |
| 43 | 420.8 | 13.7 | 673 | 6 BY721135 | BY721135 |
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ALIGNMENTS

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DEFINITION Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407013
VERSION AY407013.1 GI:39762984
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2733)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 98.6%; Pred. No. 0;
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Db 118 GCCAGGGCGACGGCTGCTACTGCTGGGCAACCGCGCGCCAGCGCTGTGCTGGCGGC 177
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Db 298 AACTACCTGTACAACGTCGTGAGAGACCCCGCGGCTGGGCGTTCATCTACACGCTTTC 357
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DEFINITION genomic survey sequence.
ACCESSION AY407015
VERSION AY407015.1 GI:39762986
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2729)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 2729)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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| 2221 | QY | TTACAGGAAAGCAATTTCTGAGCTCACCACTGCCTTGTGCTCCAAAGAAAATGTTTCAG | 2280 |
| 2247 | DB | TTACAAGAGAGTAATTTCTGATGTCAACCACTGCCCTTGTGCTCCAAAGAAAATGTTTCAG | 2306 |
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| 2307 | DB | TTTGACAGATCAAACTGACCAAGGACCGTTCCCTGAGGAAAAGTTTCGACATGGGAGGA | 2366 |
| 2341 | QY | GAACCTCTGTCTGTCTGTCTGCCATGGTCCGAAAGCACTTGGGCAAAATCTTTGCTCTGTG | 2400 |
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| 2701 | QY | TAA | 2703 |
| 2727 | DB | TAA | 2729 |

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| SOURCE | Pan troglodytes (chimpanzee) | | | |
| ORGANISM | Pan troglodytes | | | |
| REFERENCE | Karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. | | | |
| AUTHORS | 1 (bases 1 to 2014) | | | |
| | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. | | | |
| | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios | | | |
| TITLE | Science 302 (5652), 1960-1963 (2003) | | | |
| JOURNAL | 14671302 | | | |
| PUNMED | 2 (bases 1 to 2014) | | | |
| REFERENCE | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., | | | |
| AUTHORS | | | | |

1834 CTTTCGGGTTCTGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCG 1893
Db

1960 AGAGCCCTGCAGTTCTTCTGACCCAAACAGTTCAGTGCAGACTTTCTACGGGCTT 2019
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Db

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AK033079.1 GI:26328812
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

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prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
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Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
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20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2276)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurthara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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Db 421 ATGATGAAAGAGTGCAGGCTGATGATGATGATGATGATGATGATGATGATGAT 480
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Db 541 CATTAAGCCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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Db 601 TGTGTGTAGAAATTAAGAGCTTCAACAGCGTGTGATGATGATGATGATGATGAT 660
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LOCUS 55049367J1 FLP Homo sapiens cDNA, mRNA sequence.
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ACCESSION CD629762
VERSION CD629762.1 GI:40278028
KEYWORDS EST.

SOURCE

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 797)
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)

JOURNAL

COMMENT

Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA

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| REFERENCE | 1 | (bases 1 to 734) |
| | | NIH-MGC http://mgs.nci.nih.gov/ . |
| | | National Institutes of Health, Mammalian Gene Collection (MGC) |
| | | Unpublished (1999) |
| AUTHORS | CONTACT | Robert Strausberg, Ph.D. |
| | EMAIL | cgabbs-remail.nih.gov |
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| | CDNA | Library Preparation: CLONETECH Laboratories, Inc. |
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ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 678)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel.: 6508454102
Email: gfu@incyte.com.

FEATURES
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REFERENCE 1 (bases 1 to 691)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel.: 6508454102
Email: gfu@incyte.com.

FEATURES
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QY 865 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACCTCTTGGCATTTCTTCTTGA 924
DB 61 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACCTCTTGGCATTTCTTCTTGA 120

QY 925 CTTCCTCGCGGCATTTCTTGGCTCAGGTTTTCGATTAAAGTACAAGAACACACGCCAG 984
DB 121 CTTCCTCGCGGCATTTCTTGGCTCAGGTTTTCGATTAAAGTACAAGAACACACGCCAG 180

QY 985 AAACACTTTGAGAAAAGGAAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGTAGT 1044
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QY 1105 CACACCTGCAGCCCTTACCAGAAAAGAACAGGGGAAGCATCAAGCAGTCAGAGCTAAAGT 1164
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QY 1165 TTTAAGGAGCGAGTGGCATGGCTAGCCCCAGGGGCCAGAGATTATTAAGAGCCGACAAGCC 1224
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QY 1225 TCAGTAGTGCAGGAGGTCCCAAGCACCCAGCATCACAGCCGA-GGCGAGTCCCAACAA 1283
DB 420 TCAGTAGTGCAGGAGGTCCCAAGCACCCAGCATCACAGCCGAGGGGCGAGTCCCAACAA 479

QY 1284 AGTCGAGAAGAGCTGGAGCTTCAACGACCGCAACCCGCTTCCGGCCCTCGCTGCGCTCAA 1343
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[illegible]

Site-2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

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Query Match      19.5%; Score 600.2; DB 2; Length 658;
Best Local Similarity 95.5%; Pred. No. 3.8e-154;
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QY 900 ACTCTTGGCATTTCTTCTTGGCACTTCTCTCCGGCATTCCTGGCTCAGGTTTGCATT 959
Db 77 ACTCTTGGCATTTCTTCTTGGCACTTCTCTCCGGCATTCCTGGCTCAGGTTTGCATT 136
QY 960 AAAAGTACAAGAACACCGCCGAGAACACTTTGAGAAAGAAAGAACCCAGCTGCCAA 1019
Db 137 AAAAGTACAAGAACACCGCCGAGAACACTTTGAGAAAGAAAGAACCCAGCTGCCAA 196
QY 1020 CCTCATTTGAGTGTGTTTGGCGTAGTTAGCGAGTGTGAGTAATCTGTTCCATTGCAAC 1079
Db 197 CCTCATTTGAGTGTGTTTGGCGTAGTTAGCGAGTGTGAGTAATCTGTTCCATTGCAAC 256
QY 1080 CTGGAAGCCACACTTTGAAGGCTTGCACACCTGACGCCCTACCAAGAAAGAACAGGGGA 1139
Db 257 CTGGAAGCCACACTTTGAAGGCTTGCACACCTGACGCCCTACCAAGAAAGAACAGGGGA 301
QY 1140 AGCATCAAGAGTCTAGAAGCTAAGTTTAAAGAGCGAGTGGCATGTTAGCCCCAGGGG 1199
Db 302 -----TCAGAAGCTAAGTTTAAAGAGCGAGTGGCATGTTAGCCCCAGGGG 349
QY 1200 CCAGAGTATTAAAGCCGACAGCCTCAGTAGTGACAGGAGTCCCAAGCCGAGCAT 1259
Db 350 CCAGAGTATTAAAGCCGACAGCCTCAGTAGTGACAGGAGTCCCAAGCCGAGCAT 409
QY 1260 CACAGCCGAGGCGAGTCCCAAGAGTGCAGAAAGTGGAGCTTCAACGACCGAACCCG 1319
Db 410 CACAGCCGAGGCGAGTCCCAAGAGTGCAGAAAGTGGAGCTTCAACGACCGAACCCG 469
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Db 470 CTTCCGGCCCTGCTGGCGCTCAAAAGTCTCAGCCAAAGAACAGTGTAGTGTGACAC 529
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Db 530 AGCCCTTGGCACTGATGTATATGATGAAAAGGATGCCAGTGTGATGATCAGTGA 589
QY 1440 AGACCTCACCCACCACTTAAACCTGTCAATTCAGCTATCAGAAATTATGAAATTCATGT 1499
Db 590 AGACCTCACCCACCACTTAAACCTGTCAATTCAGCTATCAGAAATTATGAAATTCATGT 649
QY 1500 TGCAAAACG 1508
Db 650 TGCAAAACG 658

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RESULT 14

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LOCUS 55049391H1 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
DEFINITION CD629765
ACCESSION CD629765.1 GI:40278031
VERSION CD629765.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 599)

```

AUTHORS

Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3150 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

source

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ORIGIN

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QY 865 ACTTGGCTGGGAAGATGCTTTCTGAGGCTTTGCATCTCTTGGCATTTCTTTTTCGCA 924
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QY 925 CTTCTGCGGCATTCCTGGCTCAGTTTTCATTTAAAGTACAGAACACACCGCCAG 984
Db 121 CTTCTGCGGCATTCCTGGCTCAGTTTTCATTTAAAGTACAGAACACACCGCCAG 180
QY 985 AAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTTCAGTGTGTTGGGTAGT 1044
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QY 1165 TTTAAGGAGCGAGTGGCGATGGCTAGCCCGAGGGCCAGAGTATTAAAGAGCGCAAGCC 1224
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Db 481 GTGCAGAGAGCTGGAGCTTCAAGCCGAAACCGCTTCCGGCCCTCGCTGGCTCAAA 540
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RESULT 15

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LOCUS 55049359J1 FLP Homo sapiens cDNA, mRNA linear EST 12-JAN-2004
DEFINITION CD629760
ACCESSION CD629760
VERSION CD629760.1 GI:40278026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 714)

REFERENCE
1 (bases 1 to 714)
Fu, G.K., Wang, J.T., Yang, J., Au-Yang, J. and Stuve, L.L.
AUTHORS
Circular rapid amplification of cDNA ends for high-throughput
TITLE
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
JOURNAL

COMMENT

Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| SOURCE | 1. .714 |

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1. .114
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/mol_type="mRNA"
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ORIGIN

| | | | | |
|---------------------------|--------|-------------------|-----------|-------------|
| Query Match | 19.1%; | Score 586.8; | DB 6; | Length 714; |
| Best Local Similarity | 96.3%; | Pred. No. 2e-150; | | |
| Matches 641: Conservative | 1; | Mismatches 17; | Indels 7; | Gaps 4; |

1077 AACCTGGAAGCCACA-CTTGAAGGCGTTGCA-CACCTGAGCCCTACC-----AAGAAAGA 1130

1131 ACAAGGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTAAAGAGCGAGTCGGCATGGCTAG 1190

628 AAAGGGGAGCATTCAAGCAGTCAGAACTAAGTTTAAAGGAGCGAGTCGCGCATGGCTAG 569

568 CCCAGGGCCAGATATTAGAGCCGCAAGCTCAGTAGTGACAGGAGTCCCCAAG 509

1251 CACCGACATCACAGCCGAGGCGAGTCCCTCCAAAGTCGACAGAGCTGGAGCTTCAA - CG 1307

1310 ACCGAACCGGTTCCGGCCCTCGGCTCGGCTCAAAGTTCTCAGCCAAACCAAGTGATG 1369

b

448 ACCGAACCCGGTTCGGGGCCCTCGGTCGGCCCAAAAGATCTTCAGCCCTTTTCTCCAGTGGTGGG
1429

b
388 ATGCTGACACAGCCCTTGGCACTGATGATATATGATGAAAAGGATGCCAGTGTGATG 329

128 TATCACTGGAGAGACCTCACCCACACTTAAACCTGTCATTCGAGCTATCAGAAATTATGA 269
1430 TATCAGTGGAGACCTCACCCACACTTAAACCTGTCATTCGAGCTATCAGAAATTATGA 269

1490 AATTTCATGTTGC AAAACGGAAGTTTAAGGAAACRTTACGTCATATGATGTAAAGATG 1549

1550 TCATTGAACACAAATTTCTGCTGGTCATCTGGACATGTTGTGTAGAAATAAAGCCCTTCAAA 1609

b
208 TCATTGAACAATATTCTGCTGGTCATCTGGACATGTTGTAGAAATTAAGCCCTTCAAA 149

148 CACGTTTGATCAAAATCTTTGAAAGGGGCAATCACATCAGATAAGAAAGAGCCGAGAGA 89

1670 AAATAACAGCAGAACATGAGACCCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGG 1723

1730 TTGAAAA 1737

28 TGAAAAACA 21

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 16:26:27 ; Search time 1546 Seconds
(without alignments)
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Perfect score: 3071
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
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- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 3070.6 | 100.0 | 3071 | 4 | AAS14651 Human cDN |
| 2 | 3040.4 | 99.0 | 3137 | 4 | AAC85414 Human KCN |
| 3 | 2936.2 | 95.6 | 3718 | 3 | AAC64371 Human KCN |
| 4 | 2890.8 | 94.1 | 3111 | 5 | AH43634 Human ion |
| 5 | 2857.4 | 93.0 | 3074 | 4 | AH49499 Human KCN |
| 6 | 2855.8 | 93.0 | 3074 | 10 | ADB78684 Human pot |
| 7 | 2690.4 | 87.6 | 2694 | 4 | AAS14652 Human cDN |
| 8 | 2690.4 | 87.6 | 2694 | 6 | AAD27192 Human pot |
| 9 | 2635.4 | 85.8 | 2772 | 5 | AH43633 Human ion |
| 10 | 2626.4 | 85.5 | 2667 | 4 | AAS14653 Human cDN |
| 11 | 1313.4 | 42.8 | 12510 | 3 | AAC64370 Human KCN |
| 12 | 518 | 16.9 | 2335 | 3 | AAA47618 KCN04 Pot |
| 13 | 517.6 | 16.9 | 2335 | 10 | ADE31698 Human 323 |
| 14 | 517.6 | 16.9 | 2273 | 2 | AAX57140 Mouse KCN |
| 15 | 511.6 | 16.7 | 2169 | 2 | AAX26588 Nucleotid |
| 16 | 509.8 | 16.6 | 582 | 8 | ACA04855 cDNA enco |
| 17 | 499 | 16.2 | 7407 | 10 | ADB78688 Human pot |
| 18 | 499 | 16.2 | 7407 | 10 | ADB78686 Human pot |
| 19 | 499 | 16.2 | 7407 | 10 | ADB78683 Human pot |
| 20 | 499 | 16.2 | 7407 | 10 | ADB78687 Human pot |

| | | | | | |
|----|-------|------|------|----|--------------------|
| 21 | 499 | 16.2 | 7411 | 10 | ADD29557 Human tum |
| 22 | 499 | 16.2 | 7420 | 11 | ADN38963 Cancer/an |
| 23 | 499 | 16.2 | 7420 | 11 | ADP65810 Human mRN |
| 24 | 499 | 16.2 | 7420 | 11 | ADP65731 Human pot |
| 25 | 499 | 16.2 | 7420 | 12 | ADL06495 Human tum |
| 26 | 499 | 16.2 | 7863 | 10 | ADJ56529 Human cDN |
| 27 | 497.4 | 16.2 | 7407 | 10 | ADB78685 Human pot |
| 28 | 480 | 15.6 | 5595 | 13 | ADS17851 Rattus no |
| 29 | 479 | 15.6 | 7413 | 5 | AAS74832 DNA encod |
| 30 | 475.4 | 15.5 | 2565 | 2 | AAX81548 Human bra |
| 31 | 475.4 | 15.5 | 3195 | 5 | AAS74831 DNA encod |
| 32 | 474 | 15.4 | 548 | 6 | ABA90234 Human ORF |
| 33 | 467 | 15.2 | 2766 | 13 | ADS17849 Rattus no |
| 34 | 465 | 15.1 | 3029 | 2 | AAX81547 Human bra |
| 35 | 463.6 | 15.1 | 2814 | 2 | AAX57141 Mouse KCN |
| 36 | 460.8 | 15.0 | 2565 | 2 | AAX26596 Nucleotid |
| 37 | 460.8 | 15.0 | 2914 | 2 | AAX57059 Human KCN |
| 38 | 460.8 | 15.0 | 2926 | 10 | ADB78690 Human pot |
| 39 | 460.8 | 15.0 | 2926 | 10 | ADB78682 Human pot |
| 40 | 460.8 | 15.0 | 2926 | 10 | ADB78691 Human pot |
| 41 | 459.2 | 15.0 | 2926 | 10 | ADB78689 Human pot |
| 42 | 457.4 | 14.9 | 2755 | 13 | ADS17847 Human KCN |
| 43 | 455.8 | 14.8 | 1848 | 12 | ADH51119 Potassium |
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| 45 | 452.6 | 14.7 | 4512 | 10 | ADJ56528 Rat cDNA |

ALIGNMENTS

RESULT 1
AAS14651

ID AAS14651 standard; cDNA; 3071 BP.

XX AAS14651;

AC AAS14651;

DT 18-DEC-2001 (first entry)

XX Human cDNA for voltage gated potassium channel hKVNQ5.

XX Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;

KW cerebroprotective; neurotropic; analgesic; vision disorder;

KW central nervous system disorder; epilepsy; migraine; hearing disorder;

KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;

KW pain; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

FN WO200170759-A1.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US009328.

XX 21-MAR-2000; 2000US-0190954P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2001-611467/70.

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for identifying a compound modulating ion flux in eukaryotic cell or cell membrane expressing the protein, comprises KCNQ approximately alpha-subunits.
PS Claim 5; Page 61-62; 79pp; English.
XX The invention relates to an isolated polypeptide comprising an alpha-subunit of a KCNQ potassium channel, with a subsequence having 65% sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence and forms a KCNQ potassium channel having the characteristic of voltage-gating with at least an additional KCNQ alpha-subunit. Also included in

Db 1801 AAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTCAGTCCACCTTTTGAATGTGAA 1860
Qy 1861 CAGACATCTGATATCAAAAGCCCTGTGATAGCAAAAGATCTTTTCGGTTCGGCAAAAC 1920
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Qy 1921 AGTGGCTCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCATCTG 1980
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Qy 1981 AGCCCAATGAGTTCAGTGCCAGACTTTTACGCGCTTAGCCCTACTATGCACAGTCAA 2040
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Qy 3061 AAAAAA 3071
Db 3061 AAAAAA 3071

RESULT 2
AAC85414
ID AAC85414 standard; cDNA; 3137 BP.
XX
AC AAC85414;
XX
DT 20-APR-2001 (first entry)
XX Human KCNQ5 potassium channel subunit coding sequence.
DE Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
KW compulsive behaviour; dementia; depression; Huntington's disease; mania;
KW memory impairment; memory dysfunction; spinal cord damage; phobia;
KW pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;
ds.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2694
FT /*tag= a
FT /product= "KCNQ5 subunit"
XX
XX WO200077035-A2.
XX
XX 21-DEC-2000.
XX
XX 29-MAY-2000; 2000WO-DK000289.
XX
XX 11-JUN-1999; 99DK-00000828.
XX (NEUR-) NEUROSEARCH AS.
XX
XX Jentsch TJ;
XX
XX WPI; 2001-080678/09.
XX P-PSDB; AAB47046.
XX
XX Novel genes encoding KCNQ5 potassium channel subunits, useful for
XX treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
XX depression, Huntington's disease, schizophrenia and Parkinson's disease.
XX
XX Claim 2; Page 44-48; 50pp; English.
XX
XX This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms
XX heteromeric channels with other KCNQ channel subunits, in particular
XX KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
XX chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5
XX are useful for diagnosis, treatment, prevention or alleviation of
XX diseases related to diseases or adverse conditions of the central nervous
XX system (CNS), including affective disorders, Alzheimer's disease,
XX anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative
XX illness, cognitive deficits, compulsive behavior, dementia, depression,
XX Huntington's disease, mania, memory impairment, memory disorders, memory
XX dysfunction, motor disorders, motor disorders, neurodegenerative
XX diseases, Parkinson's disease and Parkinson-like motor disorders,
XX phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,

[illegible]

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Db 2401 ATCAGTTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy 2470 GGCAGCCAGATTTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAG 2529
Db 2461 GGCAGCCAGATTTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAG 2520
Qy 2530 GTGGTCCGAGGAGACAGACAGACACTTTTGTAGTGGCAGCAGCCCTGCCAGGAA 2589
Db 2521 GTGGTCCGAGGAGACAGACAGACACTTTTGTAGTGGCAGCAGCCCTGCCAGGAA 2580
Qy 2590 GCTGCTTTGATCAGACTCTCTAGGACTGGAAGTCAAGTCAAGTCACTCAGAGATTTGT 2649
Db 2581 GCTGCTTTGATCAGACTCTCTAGGACTGGAAGTCAAGTCAAGTCACTCAGAGATTTGT 2640
Qy 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAAGTTCTT 2709
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAATAAGTTCTT 2700
Qy 2710 CATTTCTTTCCAGCATAGACTTTTAGCCATACATATCATGTGATGAATATTTTCG 2769
Db 2701 CATTTCTTTCCAGCATAGACTTTTAGCCATACATATCATGTGATGAATATTTTCG 2760
Qy 2770 AAAGCCCTTTAAAGTTGAAATTTGCAAGATCGGAAGAACATGAAAGCAGTTTATA 2829
Db 2761 AAAGCCCTTTAAAGTTGAAATTTGCAAGATCGGAAGAACATGAAAGCAGTTTATA 2820
Qy 2830 AGCCCGTTTACCTTTTAAATTTGCATGAAATGATGTTTAGGATGGCTAAAAATTTCAAGGT 2889
Db 2821 AGCCCGTTTACCTTTTAAATTTGCATGAAATGATGTTTAGGATGGCTAAAAATTTCAAGGT 2880
Qy 2890 GCATCGACATTAACCCACTCATTTAGTAAATGTAACCTTGAGTTAAAGCCCTGAGAAACCA 2949
Db 2881 GCATCGACATTAACCCACTCATTTAGTAAATGTAACCTTGAGTTAAAGCCCTGAGAAACCA 2940
Qy 2950 AACACAGCTAATGCTATGGGGTGATGAATATGCAAGTTTAGGTTCATTTAGAGATTG 3009
Db 2941 AACACAGCTAATGCTATGGGGTGATGAATATGCAAGTTTAGGTTCATTTAGAGATTG 3000
Qy 3010 ACATGTATTTTGAATTTATGGAGTAAACACCTTTCAAATTTCA 3053
Db 3001 ACATGTATTTTGAATTTATGGAGTAAACACCTTTCAAATTTCA 3044

RESULT 3
AAC64371
ID AAC64371 standard; cDNA; 3718 BP.
XX
AC
AAC64371;

DT 07-FEB-2001 (first entry)
XX Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardiocactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ss.
XX Homo sapiens.
XX WO200061606-A1.
XX 19-OCT-2000.
XX 10-APR-2000; 2000WO-US009587.
XX 14-APR-1999; 99US-0129274P.
XX (MERI) MERCK & CO INC.
XX Petrukhin K, Caskey CT, Li W, Metzker ML;
XX WPI; 2000-647417/62.
XX P-PSDB; AAB24241.
XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
XX inhibitors and activators which can treat e.g. Stargardt-like macular
XX dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX Claim 3; Fig 2; 99pp; English.
XX The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
XX which is a voltage-gated potassium channel protein. Human KCNQ5 has
XX ophthalmological, auditory, central nervous system (CNS), cardioactive,
XX anticonvulsant, gastrointestinal and muscular active activities.
XX Sequences and methods from the present invention are useful for
XX identifying activators or inhibitors of KCNQ5 protein. These activators
XX and inhibitors are useful for treating Stargardt-like macular dystrophy,
XX cone-rod dystrophy, Salla disease, age-related macular degeneration,
XX other forms of macular degeneration, deafness, epilepsy, and different
XX forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
XX Stargardt-like macular dystrophy and cone-rod dystrophies are located at
XX chromosome 6q
XX Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;
SQ Query Match 95.6%; Score 2936.2; DB 3; Length 3718;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2941; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy 103 ACGTTTGGTGGCGCGGTGGCTCAGGAGAGCCGCGGGGCAAGCAGCGGGCCCGG 162
Db 78 ACTCTGAGGACTCGCGCGGTGGCTCAGGAGAGCCGCGGGGCAAGCAGCGGGCCCGG 137
Qy 163 ATGAGCTCTGCGGAGAGCCGCTCTTACACGAGTAGCCAGAGTCGCCGCGCAACGTC 222
Db 138 ATGAGCTCTGCGGAGAGCCGCTCTTACACGAGTAGCCAGAGTCGCCGCGCAACGTC 197
Qy 223 AAGTACCGGGGTGCAGAACTACCTGTACAACTGCTGGAGAGACCCCGGCTGGCG 282
Db 198 AAGTACCGGGGTGCAGAACTACCTGTACAACTGCTGGAGAGACCCCGGCTGGCG 257
Qy 283 TTCACTACACGCTTTGCTTTTCTCTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 342
Db 258 TTCACTACACGCTTTGCTTTTCTCTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 317
Qy 343 TCTACCATCCCTGAGACACAAATTTGSCCTCAAGTTGCTTTGATCCTCGAGTTCTGTG 402
Db 318 TCTACCATCCCTGAGACACAAATTTGSCCTCAAGTTGCTTTGATCCTCGAGTTCTGTG 377

| | | | |
|----|------|--|------|
| Qy | 403 | ATGATTGTCGCTTTGGTTTGGAGTTTCATCATTCGAATCTGGTCTGGGGTGGCTGTGT | 462 |
| Db | 378 | ATGATTGTCGCTTTGGTTTGGAGTTTCATCATTCGAATCTGGTCTGGGGTGGCTGTGT | 437 |
| Qy | 463 | CGATATAGAGATGGCAAGGAAGACTGAGGTTTCTCGAAGCCCTTCTGTTGTTATAGAT | 522 |
| Db | 438 | CGATATAGAGATGGCAAGGAAGACTGAGGTTTCTCGAAGCCCTTCTGTTGTTATAGAT | 497 |
| Qy | 523 | ACCATGTTCTTATCGCTTCAATAGCAGTTGTTTCTCGAAGAACTCAGGGTAATATTTT | 582 |
| Db | 498 | ACCATGTTCTTATCGCTTCAATAGCAGTTGTTTCTCGAAGAACTCAGGGTAATATTTT | 557 |
| Qy | 583 | CCACGCTCTGCACTCAGAACTCTCGTTTCTACAGATCTCTCCGATGGTCCGATGGAC | 642 |
| Db | 558 | CCACGCTCTGCACTCAGAACTCTCGTTTCTACAGATCTCTCCGATGGTCCGATGGAC | 617 |
| Qy | 643 | CGAAGGGAGGCACTTGGAAATTAATCTGGTTTCAGTGTGTTATGTCTCAGCAAGAAATTA | 702 |
| Db | 618 | CGAAGGGAGGCACTTGGAAATTAATCTGGTTTCAGTGTGTTATGTCTCAGCAAGAAATTA | 677 |
| Qy | 703 | ATCAGAGCTTGGTACATAGGATTTTGGTTCTTATTTTTCGTTCTTCTTCTTATCTG | 762 |
| Db | 678 | ATCAGAGCTTGGTACATAGGATTTTGGTTCTTATTTTTCGTTCTTCTTCTTATCTG | 737 |
| Qy | 763 | GTGGAAGAGGATGCCAATAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGCACA | 822 |
| Db | 738 | GTGGAAGAGGATGCCAATAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGCACA | 797 |
| Qy | 823 | ATTACATTGCAACTATTGGTATGGAGCAAAACTCCCTTAACTTGGCTGGGAAGATTG | 882 |
| Db | 798 | ATTACATTGCAACTATTGGTATGGAGCAAAACTCCCTTAACTTGGCTGGGAAGATTG | 857 |
| Qy | 883 | CTTTCTGAGGCTTGGCACTCTTGGCAATTTCTTTCTTTGCACTTCTGCGGCAATCTT | 942 |
| Db | 858 | CTTTCTGAGGCTTGGCACTCTTGGCAATTTCTTTCTTTGCACTTCTGCGGCAATCTT | 917 |
| Qy | 943 | GGCTCAGGTTTGGCAATTAAGAGTCAAGAAACAACCGCCGAGAAACACTTTGAGAAAGA | 1002 |
| Db | 918 | GGCTCAGGTTTGGCAATTAAGAGTCAAGAAACAACCGCCGAGAAACACTTTGAGAAAGA | 977 |
| Qy | 1003 | AGGAACCCAGTGGCAACTCATTAGTGTGTTGGGTAGTGTACGAGCTGATGAGAAA | 1062 |
| Db | 978 | AGGAACCCAGTGGCAACTCATTAGTGTGTTGGGTAGTGTACGAGCTGATGAGAAA | 1037 |
| Qy | 1063 | TCTGTTTCCATTTGCAACCTGGAAGCCACATTTGAGGCTTGGCACTGAGCCCTACC | 1122 |
| Db | 1038 | TCTGTTTCCATTTGCAACCTGGAAGCCACATTTGAGGCTTGGCACTGAGCCCTACC | 1097 |
| Qy | 1123 | AAGAAAGAACAGGGGAAGCATCAAGCAGTCAGAACTAAGTTTAAAGAGCGAGTGGCC | 1182 |
| Db | 1098 | AAGAAAGAACAGGGGAAGCATCAAGCAGTCAGAACTAAGTTTAAAGAGCGAGTGGCC | 1157 |
| Qy | 1183 | ATGGCTAGCCCGAGGGCCAGAGTATTAAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGG | 1242 |
| Db | 1158 | ATGGCTAGCCCGAGGGCCAGAGTATTAAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGG | 1217 |
| Qy | 1243 | TCCCAAGCAGCGACATCAAGCCGAGGGAGTCCCAAGTGCAGAGCTGGAGC | 1302 |
| Db | 1218 | TCCCAAGCAGCGACATCAAGCCGAGGGAGTCCCAAGTGCAGAGCTGGAGC | 1277 |
| Qy | 1303 | TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCTTCAAAAGTTCTCAGCCAAAACCA | 1362 |
| Db | 1278 | TTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCTTCAAAAGTTCTCAGCCAAAACCA | 1337 |
| Qy | 1363 | GTGATAGATGTGACACAGCCCTTGGCACTGATGATGTATGATGAAAAAGGATGCCAG | 1422 |
| Db | 1338 | GTGATAGATGTGACACAGCCCTTGGCACTGATGATGTATGATGAAAAAGGATGCCAG | 1397 |
| Qy | 1423 | TGTGATGTATCAGTGGAGAGCTCACCCACCTTAAACTGTCTCATTTCCGAGCTATCAGA | 1482 |
| Db | 1398 | TGTGATGTATCAGTGGAGAGCTCACCCACCTTAAACTGTCTCATTTCCGAGCTATCAGA | 1457 |

| | | | |
|----|------|--|------|
| Qy | 1483 | ATTATGAAATTTTCATGTTGCAAAAACGGAAGTTTAAAGAAACRTTATCCTCATATGATGTA | 1542 |
| Db | 1458 | ATTATGAAATTTTCATGTTGCAAAAACGGAAGTTTAAAGAAACRTTATCCTCATATGATGTA | 1517 |
| Qy | 1543 | AAAGATGTCAATTGAAACATATTTCTGCTGGTCATCTGGACATGTTGTAGTAATAAAGC | 1602 |
| Db | 1518 | AAAGATGTCAATTGAAACATATTTCTGCTGGTCATCTGGACATGTTGTAGTAATAAAGC | 1577 |
| Qy | 1603 | CTTCAAAACAGTGTGATCAAAATTTCTTGGAAAAGGGCAAAATCACATCAGATAAGAGAGC | 1662 |
| Db | 1578 | CTTCAAAACAGTGTGATCAAAATTTCTTGGAAAAGGGCAAAATCACATCAGATAAGAGAGC | 1637 |
| Qy | 1663 | CGAGAGAAAATAACAGCAGAAATGAGACCAACAGACATCTCAGTATGCTCGGTGCGGTG | 1722 |
| Db | 1638 | CGAGAGAAAATAACAGCAGAAATGAGACCAACAGACATCTCAGTATGCTCGGTGCGGTG | 1697 |
| Qy | 1723 | GTCAAGGTTGAAAACAGGTACAGTCCATAGAACTCCAAAGCTGGACTGCCCTACTAGACATC | 1782 |
| Db | 1698 | GTCAAGGTTGAAAACAGGTACAGTCCATAGAACTCCAAAGCTGGACTGCCCTACTAGACATC | 1757 |
| Qy | 1783 | TATCAACAGGTCCTTTCGAAAAGGCTCTGCTCTCAGCCCTCGCTTTGGCTTCAATTCAGTTC | 1842 |
| Db | 1758 | TATCAACAGGTCCTTTCGAAAAGGCTCTGCTCTCAGCCCTCGCTTTGGCTTCAATTCAGTTC | 1817 |
| Qy | 1843 | CCACCTTTTGAATGTGAACAGACATCTGATATCAAAAGCCCTGTGGATAGCAAAAGATCTT | 1902 |
| Db | 1818 | CCACCTTTTGAATGTGAACAGACATCTGATATCAAAAGCCCTGTGGATAGCAAAAGATCTT | 1877 |
| Qy | 1903 | TCGGGTTTCCGCAACAAAACAGTGGCTGTTATCCAGATCAACTAGTGCACACATCTCAGA | 1962 |
| Db | 1878 | TCGGGTTTCCGCAACAAAACAGTGGCTGTTATCCAGATCAACTAGTGCACACATCTCAGA | 1937 |
| Qy | 1963 | GGCTCGAGTTCATTCTGACGCCAAATGAGTTTCAAGTCCAGAGCTTCTACGCGCTTAGC | 2022 |
| Db | 1938 | GGCTCGAGTTCATTCTGACGCCAAATGAGTTTCAAGTCCAGAGCTTCTACGCGCTTAGC | 1997 |
| Qy | 2023 | CCTACTATGACAGTCAAGCAACACAGGTGCGCAATTTAGTCAAAAGCGATGGCTCAGCAGTG | 2082 |
| Db | 1998 | CCTACTATGACAGTCAAGCAACACAGGTGCGCAATTTAGTCAAAAGCGATGGCTCAGCAGTG | 2057 |
| Qy | 2083 | GCAGCCACCAACCACTTGGCAACCAATTAATACGCAACCCAGCCAGCCAGAGCCCAACA | 2142 |
| Db | 2058 | GCAGCCACCAACCACTTGGCAACCAATTAATACGCAACCCAGCCAGAGCCCAACA | 2117 |
| Qy | 2143 | ACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGCCAGCAAACTCTG | 2202 |
| Db | 2118 | ACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGCCAGCAAACTCTG | 2177 |
| Qy | 2203 | CACCTTAACCTGTCAGGCTTACAGGAAAGCATTTCTGAGCTCACCATCTGCTTGTGCC | 2262 |
| Db | 2178 | CACCTTAACCTGTCAGGCTTACAGGAAAGCATTTCTGAGCTCACCATCTGCTTGTGCC | 2237 |
| Qy | 2263 | TCCAAGGAAATGTTTCAGGTTGCAAGTCAAACTCACCAGGACCGTTCTATCAGGAAA | 2322 |
| Db | 2238 | TCCAAGGAAATGTTTCAGGTTGCAAGTCAAACTCACCAGGACCGTTCTATCAGGAAA | 2297 |
| Qy | 2323 | AGCTTTGACATGGGAGGAGAACTCTGTTGCTCTGTTCTGCTCTGCTGCTGCTGCTGCTG | 2382 |
| Db | 2298 | AGCTTTGACATGGGAGGAGAACTCTGTTGCTCTGTTCTGCTCTGCTGCTGCTGCTGCTG | 2357 |
| Qy | 2383 | GGCAAAATTTTGTCTGTGCAAAACCTGATCAGGTGCAACGAGGAACTGAATATACAACTT | 2442 |
| Db | 2358 | GGCAAAATTTTGTCTGTGCAAAACCTGATCAGGTGCAACGAGGAACTGAATATACAACTT | 2417 |
| Qy | 2443 | TCAGGGATGAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGAGGGAA | 2502 |
| Db | 2418 | TCAGGGATGAGTCAAGTGGCTCCAGAGGAGCAAGATTTTACCCCAATGAGGGAA | 2477 |
| Qy | 2503 | TCCAATTTGTTTAACTGATGAAGAGTGGGTCCCGAAGAGACAGACACACATTTT | 2562 |
| Db | 2478 | TCCAATTTGTTTAACTGATGAAGAGTGGGTCCCGAAGAGACAGACACACATTTT | 2537 |
| Qy | 2563 | GATGCGCACCGCAGCCTGCCAGGGAAGCTGCCCTTTGATCAGACTCTCTAAGGACTGGA | 2622 |

Db 2538 GATGCGACCCAGCCTGCCAGGAAGTCTCTTGGATCAGACTCTTAAGGACTGGA 2597
QY 2623 AGGTCAACGATCATCTCAGAGCATTTGTTAAGCGAGGAGAAAGTACAGATGCCCTCAGCTTG 2682
Db 2598 AGGTCAACGATCATCTCAGAGCATTTGTTAAGCGAGGAGAAAGTACAGATGCCCTCAGCTTG 2657
QY 2683 CCTCATGTCMAACTGAATTAAGTCTCTTCAATTTCTTCCAGGCATAGCAGTCTTTAGCC 2742
Db 2658 CCTCATGTCMAACTGAATTAAGTCTCTTCAATTTCTTCCAGGCATAGCAGTCTTTAGCC 2717
QY 2743 ATACATATCATTCATGATGAATTAATTCGAAAGCCCTTCTAAAGTTGAAATTCGAAGAT 2802
Db 2718 ATACATATCATTCATGATGAATTAATTCGAAAGCCCTTCTAAAGTTGAAATTCGAAGAT 2777
QY 2803 CGGGAAGAACATGAAGGAGGTTTATAAGCCGTTTACCTTTTAAATTCATGAAATTCAT 2862
Db 2778 CGGGAAGAACATGAAGGAGGTTTATAAGCCGTTTACCTTTTAAATTCATGAAATTCAT 2837
QY 2863 GTTTAGGATGCTTAAATTCGAAGTGCATGACATTAACCCACTCATTTAGTAATGTA 2922
Db 2838 GTTTAGGATGCTTAAATTCGAAGTGCATGACATTAACCCACTCATTTAGTAATGTA 2897
QY 2923 CTTGAGTTAAAGCCCTGAGAAACCAACACAGCTTAATGCTATGGGTGTATGAATATG 2982
Db 2898 CTTGAGTTAAAGCCCTGAGAAACCAACACAGCTTAATGCTATGGGTGTATGAATATG 2957
QY 2983 TCAAGTTAGGTCATTTAGAAGATTGACACTGTATTTTGAATATTCGGAGTAAACACC 3042
Db 2958 TCAAGTTAGGTCATTTAGAAGATTGACACTGTATTTTGAATATTCGGAGTAAACACC 3017
QY 3043 TTCAAAATTCA 3053
Db 3018 TTCAAAATTCA 3028

RESULT 4

AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
XX AC AAH43634;
DT 21-JAN-2002 (first entry)
XX Human ion-channel forming protein coding sequence.
DE Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 59..2831
FT /*tag= a
FT /product= "Human ion-channel forming protein"
XX
XX WO200175108-A1.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010875.
XX
XX 03-APR-2000; 2000US-0194255P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
XX WPI; 2001-656987/75.
DR P-PSDB; AAB47678.
XX
XX New human ion channel protein and polynucleotides encoding the protein,

useful in diagnosing or treating diseases, in drug screening, and in clinical trial monitoring.

Disclosure; Page 37-38; 41pp; English.

The sequences in AAH43633-34 encode a novel ion-channel forming protein. The protein shares structural similarity with mammalian ion channel proteins, particularly voltage-gated potassium channel proteins. The protein is expressed in many human cell lines including fetal brain, brain, thymus, prostate, heart and skeletal muscle. The novel protein can be used in the diagnosis or treatment of diseases, in drug screening, and in clinical trial monitoring. The oligonucleotides may be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high throughput chip format). The nucleic acids and novel protein can also be used in the identification, selection and validation of novel molecular targets for drug discovery, to screen collections of genetic material from patients who have a particular medical condition, to identify mutations associated with a particular disease, as a diagnostic or prognostic assay, and to screen for drugs which can be used to treat symptomatic or phenotypic manifestations of perturbing the normal function of novel human protein. The polypeptides are further used in generating antibodies

Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;

Query Match 94.1%; Score 2890.8; DB 5; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

QY 1 GGCAGCGCATGAGGATGTGGAGTCGGCGCGGGCGAGGTCGTCTGAATCCGCGAGCC 60
Db 156 GGCAGCGCATGAGGATGTGGAGTCGGCGCGGGCGAGGTCGTCTGAATCCGCGAGCC 215
QY 61 GCCAGGGCGCAGCGCCTGCTACTCTGGGACACCGCGCGGCGACGCTTGGTGGCGGCGC 120
Db 216 GCCAGGGCGCAGCGCCTGCTACTCTGGGACACCGCGCGGCGACGCTTGGTGGCGGCGC 275
QY 121 GGTGGCCTGAGGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTCTGCGGGGAG 180
Db 276 GGTGGCCTGAGGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTCTGCGGGGAG 335
QY 181 CCGCTCTCTTACACGAGTAGCAGAGCTGCCCGCGCAACGTCAGTACCGGGGTGCAG 240
Db 336 CCGCTCTCTTACACGAGTAGCAGAGCTGCCCGCGCAACGTCAGTACCGGGGTGCAG 395
QY 241 AACTACCTGTACAACTGCTGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTC 300
Db 396 AACTACCTGTACAACTGCTGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTC 455
QY 301 GTTTTCTCTTGTCTTGTGTGTGATTTTGTTCAGTGTCTTCTACCATCCCTGAGCAC 360
Db 456 GTTTTCTCTTGTCTTGTGTGTGATTTTGTTCAGTGTCTTCTACCATCCCTGAGCAC 515
QY 361 ACAAAATGGCTCAAGTTCCTCTGATCTCGAGATTCGTCGATGATGTCGTCCTTTCGT 420
Db 516 ACAAAATGGCTCAAGTTCCTCTGATCTCGAGATTCGTCGATGATGTCGTCCTTTCGT 575
QY 421 TTGGAGTTTCATTCGAAATCTGGTCTCGGGGTTGCTGTCTCGATATAGAGGATGGCAA 480
Db 576 TTGGAGTTTCATTCGAAATCTGGTCTCGGGGTTGCTGTCTCGATATAGAGGATGGCAA 635
QY 481 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTGTTTATAGATACCATTTCTTATCGCT 540
Db 636 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTGTTTATAGATACCATTTCTTATCGCT 695
QY 541 TCAATAGCAGTTGTTCTGCAAAACCTCAGGGTAATATTTTGGCAGCTCTGCACTCAGA 600
Db 696 TCAATAGCAGTTGTTCTGCAAAACCTCAGGGTAATATTTTGGCAGCTCTGCACTCAGA 755
QY 601 AGTCTCGGTTTCTTACAGATCCTCCGATGTCGCGCATGGACCGAAGGGGAGGACATTGG 660
Db 756 AGTCTCGGTTTCTTACAGATCCTCCGATGTCGCGCATGGACCGAAGGGGAGGACATTGG 815

Db 2949 CAGTTTATAAGCCGTTACCTTTTAATTGTCATGAAATGCATGTTTAGGGATGGCTAATA 3008
QY 2881 TTCCAAGGTGCATGCACATTAACCCACATCACTATTAGTAATGACCTTGAATAAAGCCT 2940
Db 3009 TTCCAAGGTGCATGCACATTAACCCACTCA-TTAGTAATGACCTTGAATAAAGCCT 3067
QY 2941 GAGAAACCAACACACAGC-TAATGCTATGGGTGATGAATGT 2983
Db 3068 GAGAAACCAACACACAGCTTAATGCTATGGGGGTATGAATGT 3111

RESULT 5

AAH49499

ID AAH49499 standard; DNA; 3074 BP.

XX AC AAH49499;

XX DT 11-DEC-2001 (first entry)

XX DE Human KCNQ5 DNA.

XX KCNQ5; potassium channel protein; human; neurological; cardiovascular;
XX anticonvulsant; excitability modulator; membrane potential; neuron;
XX voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
XX screening; central nervous system disease; cardiovascular disease; ds.
XX Homo sapiens.

OS Key

XX Location/Qualifiers

XX 110..2908

XX /#tag= a

XX /product= "KCNQ5"

XX DE1013732-A1.

XX PN 27-SEP-2001.

XX 21-MAR-2000; 2000DE-01013732.

XX 21-MAR-2000; 2000DE-01013732.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AB;

XX WPI; 2001-571700/65.

XX P-PSDB; AAB86979.

XX New DNA sequence encoding potassium channel KCNQ5, useful in screening
XX for specific modulators, potential agents for treating central nervous
XX system and cardiovascular diseases.

XX Claim 2a; Page 9-10; 20pp; German.

XX This invention describes a novel DNA sequence (I) encoding: (i) a
XX polypeptide (ii) with potassium channel KCNQ5 activity; (iii) a
XX polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
XX the invention have neurological, cardiovascular and anticonvulsant
XX activity and act as modulators of the voltage-dependent KCNQ5 potassium
XX channel, a key regulator of membrane potential and modulator of
XX excitability of electrically activated cells such as neurons and
XX cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (ii)
XX are used to screen for compounds that modulate the activity of KCNQ5,
XX potentially useful for treating central nervous system (e.g. epilepsy)
XX and cardiovascular diseases. This sequence encodes the human potassium
XX channel KCNQ5 protein described in the invention

SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;

Query Match

Best Local Similarity 93.0%; Score 2857.4; DB 4; Length 3074;

Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGCAGGCGCATGAAGGATGTGAGTCGGGCGGGGCGAGGGTGCTGCTGAACCTCGGCAGCC 60
Db 206 GGCAGGCGCATGAAGGATGTGAGTCGGGCGGGGCGAGGGTGCTGCTGAACCTCGGCAGCC 265
QY 61 GCCAGGGCGCACGCGCTGCTACTGCTGGGCACCGCGGGCCACGCTTGGTGGCGGCGGC 120
Db 266 GCCAGGGCGCACGCGCTGCTACTGCTGGGCACCGCGGGCCACGCTTGGTGGCGGCGGC 325
QY 121 GGTGGCCTGAGGAGAGCGCGGGGGAAGCAGAGGGGCGCCGGGATGAGCCTGCTGGGGAAG 180
Db 326 GGTGGCCTGAGGAGAGCGCGGGGGAAGCAGAGGGGCGCCGGATGAGCCTGCTGGGGAAGC 385
QY 181 CCGCTCTCTTACACGAGTACGAGCTGCCCGGGGCAACGTCAGTACCGGGGGTGCAG 240
Db 386 CGCCTCTCTTACACGAGTACGAGCTGCCCGGGGCAACGTCAGTACCGGGGGTGCAG 445
QY 241 AACTACCTGTACAACTGCTGGAGAGACCCCGGGCTGGGGGCTTCATCTACACGCTTTC 300
Db 446 AACTACCTGTACAACTGCTGGAGAGACCCCGGGCTGGGGGCTTCATCTACACGCTTTC 505
QY 301 GTTTTCTCTCTGCTTTTGGTGTGCTGATTTTGTCAAGTTTGTCAAGTTTGTCAAGTTTGT 360
Db 506 GTTTTCTCTCTGCTTTTGGTGTGCTGATTTTGTCAAGTTTGTCAAGTTTGTCAAGTTTGT 565
QY 361 ACAAATTTGGCCTCAAGTTGCTTGTATCTGAGTTCTGAGTTCTGATGATGTTGCTTTGGT 420
Db 566 ACAAATTTGGCCTCAAGTTGCTTGTATCTGAGTTCTGAGTTCTGATGATGTTGCTTTGGT 625
QY 421 TTGCAGTTTCATCATTCGAACTGCTGCGGGTGTGCTGCTGATATAGAGGATGGCAA 480
Db 626 TTGCAGTTTCATCATTCGAACTGCTGCGGGTGTGCTGCTGATATAGAGGATGGCAA 685
QY 481 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTTATCGCT 540
Db 686 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTTATCGCT 745
QY 541 TCAATAGAGTTGTTTCTGCAAAACTCAGGGTAATATTTTTGGCAGCTGTCACATCAGA 600
Db 746 TCAATAGAGTTGTTTCTGCAAAACTCAGGGTAATATTTTTGGCAGCTGTCACATCAGA 805
QY 601 AGTCTCGGTTTCTACAGATCTCCGATGTCGCGCATGGACCGAAGGGGAGGACATTGG 660
Db 806 AGTCTCGGTTTCTACAGATCTCCGATGTCGCGCATGGACCGAAGGGGAGGACATTGG 865
QY 661 AAATTACTGGGTTTCAAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATA 720
Db 866 AAATTACTGGGTTTCAAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATA 925
QY 721 GGATTTTGGTTCTTATTTTTCGTTCTTCTGCTATCTGTTGGAAGGATGCCAAT 780
Db 926 GGATTTTGGTTCTTATTTTTCGTTCTTCTGCTATCTGTTGGAAGGATGCCAAT 985
QY 781 AAAGAGTTTCTACATATGAGATGCTCTGTTGGGGGCAATTAATACATTCACAACTATT 840
Db 986 AAAGAGTTTCTACATATGAGATGCTCTGTTGGGGGCAATTAATACATTCACAACTATT 1045
QY 841 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCA 900
Db 1046 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCA 1105
QY 901 CTCCTTGGCAATTTCTTTTGGCACTTCTGCGGGCAATCTTTGGCTCAGGTTTGGCAATA 960
Db 1106 CTCCTTGGCAATTTCTTTTGGCACTTCTGCGGGCAATCTTTGGCTCAGGTTTGGCAATA 1165
QY 961 AAAGTACAGAACCAACCGCCAGAACACTTTTCAGAAAGAAAGAACCCAGCTGCCAAC 1020
Db 1166 AAAGTACAGAACCAACCGCCAGAACACTTTTCAGAAAGAAAGAACCCAGCTGCCAAC 1225
QY 1021 CTCAATTCAGTGTGTTTGGCGTAGTTACGAGCTCATGAGAAATCTGTTTCAATTCGAACC 1080
Db 1226 CTCAATTCAGTGTGTTTGGCGTAGTTACGAGCTCATGAGAAATCTGTTTCAATTCGAACC 1285
QY 1081 TGGAAAGCCACTTTGAAGGCGCTTGCACACCTGCGAGCCCTACCAAGAAAGAAAGGGGAA 1140

| | | | |
|------|----|---|------|
| 1286 | Db | TGGAGCCACATTGAGGCGCTTGCACACCTGCAGCCCTACCAAGAAAGAACAAAGGGGAA | 1345 |
| 1141 | Qy | GCATCAAGCAGTCAGAAGCTAAAGTTTAAAGACGCGAGTGCATGCTAGCCGCCAGGGGC | 1200 |
| 1346 | Db | GCATCAGCAGTCAGAAGCTAAAGTTTAAAGACGCGAGTGCATGCTAGCCGCCAGGGGC | 1405 |
| 1201 | Qy | CAGAGTATTAAAGCCGACAAAGCCTCAGTATAGGTGA CAGAGAGTTCCTCCAGACCGGACATC | 1260 |
| 1406 | Db | CAGAGTATTAAAGCCGACAAAGCCTCAGTATAGGTGA CAGAGAGTTCCTCCAGACCGGACATC | 1465 |
| 1261 | Qy | ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCCGC | 1320 |
| 1466 | Db | ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCCGC | 1525 |
| 1321 | Qy | TTCCGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCAAACACAGCTGATAGATGCTGCACCA | 1380 |
| 1526 | Db | TTCCGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCAAACACAGCTGATAGATGCTGCACCA | 1585 |
| 1381 | Qy | GCCTTTGGCAGTCAGTATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAA | 1440 |
| 1586 | Db | GCCTTTGGCAGTCAGTATGATGTATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGGAA | 1645 |
| 1441 | Qy | GACCTCACCCACACACATTTAAAACTGTCAATTCGAGCTATCAGAAATTATGAAATTTCAATGTT | 1500 |
| 1646 | Db | GACCTCACCCACACACATTTAAAACTGTCAATTCGAGCTATCAGAAATTATGAAATTTCAATGTT | 1705 |
| 1501 | Qy | GCAAAACGGAAGTTTAAAGAAAARHTTACGTCCTATATGATGTAAAGATGTCATTGGAACAA | 1560 |
| 1706 | Db | GCAAAACGGAAGTTTAAAGAAAACATTAACGTCCTATGATGTAAAGATGTCATTGGAACAA | 1765 |
| 1561 | Qy | TATTCTGCTGGTCATCTGGACATGTTCTGTGTAGAAATTAAGAGCCTTCAACACAGTGTGAT | 1620 |
| 1766 | Db | TATTCTGCTGGTCATCTGGACATGTTCTGTGTAGAAATTAAGAGCCTTCAACACAGTGTGAT | 1825 |
| 1621 | Qy | CAAAATCTTGGAAAAGGCGAAATCAACATCAGATAAGAAAGCCGAGAGAAAAATAACAGCA | 1680 |
| 1826 | Db | CAAAATCTTGGAAAAGGCGAAATCAACATCAGATAAGAAAGCCGAGAGAAAAATAACAGCA | 1885 |
| 1681 | Qy | GAACATCAGACCA CAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAG | 1740 |
| 1886 | Db | GAACATCAGACCA CAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAG | 1945 |
| 1741 | Qy | GTA CAGTCCATAGAAATCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG | 1800 |
| 1946 | Db | GTA CAGTCCATAGAAATCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG | 2005 |
| 1801 | Qy | AAAGGCTCTGGCTCAGCGCCTGGCTTTGGCTTCATCTCCAGTTCGCCACCTTTTGAATGTGA | 1860 |
| 2006 | Db | AAAGGCTCTGGCTCAGCGCCTGGCTTTGGCTTCATCTCCAGTTCGCCACCTTTTGAATGTGA | 2065 |
| 1861 | Qy | CAGACATCTGACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGGTTCCGCGACAAAAC | 1920 |
| 2066 | Db | CAGACATCTGACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCCGGGTTCCGCGACAAAAC | 2125 |
| 1921 | Qy | AGTGGCTGCTTATCCAGATCAA CTAGTGGCCAAACATCTCGAGAGGCTCGAGTTTCATCTCG | 1980 |
| 2126 | Db | AGTGGCTGCTTATCCAGATCAA CTAGTGGCCAAACATCTCGAGAGGCTCGAGTTTCATCTCG | 2185 |
| 1981 | Qy | ACGCCAAATGAGTTTCAGTGGCCAGACCTTCTACGCGCTTAGCCCTACTATGTCACAGTCAA | 2040 |
| 2186 | Db | ACGCCAAATGAGTTTCAGTGGCCAGACCTTCTACGCGCTTAGCCCTACTATGTCACAGTCAA | 2245 |
| 2041 | Qy | GCAACACAGGTGCCAATTAAGTTCAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCAT | 2100 |
| 2246 | Db | GCAACACAGGTGCCAATTAAGTTCAAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCAT | 2305 |
| 2101 | Qy | GCAAACCAATTAATACGGCACCCCAAGCCAGCAGCCGCCCAACATTTTACAGATCCCACT | 2160 |
| 2306 | Db | GCAAACCAATTAATACGGCACCCCAAGCCAGCAGCCGCCCAACATTTTACAGATCCCACT | 2365 |
| 2161 | Qy | CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAGAAATCTCTGCACCCCTAAACCTTCGAGGC | 2220 |

| | | | |
|----------|---|--|------|
| Db | 2366 | CCTCTCCAGGCATCAAGCATCTGCCCGACGCCAGAAACTCTGCAACCTTAACCTTCGAGGC | 2424 |
| Qy | 2221 | TTACAGGAAGACATTTCTGACGTCAACCACTGCTCTGTTTGCCTCCAAAGGAAAAATGTTTCAG | 2280 |
| Db | 2426 | TTACAGGAAGACATTTCTGACGTCAACCACTGCTCTGTTTGCCTCCAAAGGAAAAATGTTTCAG | 2485 |
| Qy | 2281 | GTTGCACAGTCAAAATCTCACCAAGGACCGTTCTATGAGGAAAGAGCTTTGACATGGGAGGA | 2340 |
| Db | 2486 | GTTGCACAGTCAAAATCTCACCAAGGACCGTTCTATGAGGAAAGAGCTTTGACATGGGAGGA | 2545 |
| Qy | 2341 | GAAACTCTGTTGTCGTCTGCCATCGTCCCAAGGACCTTGGGCCAAATCTTTGTCCTGTG | 2400 |
| Db | 2546 | GAAACTCTGTTGTCGTCTGCCATCGTCCCAAGGACCTTGGGCCAAATCTTTGTCCTGTG | 2605 |
| Qy | 2401 | CAAAACCTGATCAGTGCACGAGGAAGTGAATATACAACTTTTCAGGAGTGAAGTCAAGT | 2460 |
| Db | 2606 | CAAAACCTGATCAGTGCACGAGGAAGTGAATATACAACTTTTCAGGAGTGAAGTCAAGT | 2665 |
| Qy | 2461 | GGCTCCAGAGGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTATAACT | 2520 |
| Db | 2666 | GGCTCCAGAGGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTATAACT | 2725 |
| Qy | 2521 | GATGAAGAGTGGGTCCCGAAGACAGACAGACACACTTTTGTATGCCGACCCGACGCT | 2580 |
| Db | 2726 | GATGAAGAGTGGGTCCCGAAGACAGACAGACACACTTTTGTATGCCGACCCGACGCT | 2785 |
| Qy | 2581 | GCCAGGGAAGTCGCTTTTGCATCAGAGCTCTTAAGGACTGGAAGGTCACGATCATCTCAG | 2640 |
| Db | 2786 | GCCAGGGAAGTCGCTTTTGCATCAGAGCTCTTAAGGACTGGAAGGTCACGATCATCTCAG | 2845 |
| Qy | 2641 | AGCAATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAA | 2700 |
| Db | 2846 | AGCAATTTGTAAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAA | 2905 |
| Qy | 2701 | TAAGTCTTCTCATTTTCTTTCCAGGCATAGCAGTCTTTTAGCCATACATATCATTTGCAATG | 2760 |
| Db | 2906 | TAAGTCTTCTCATTTTCTTTCCAGGCATAGCAGTCTTTTAGCCATACATATCATTTGCAATG | 2965 |
| Qy | 2761 | ACTATTTTCGAAAGCCCTTCTAAAAAGTTGAAATTCGAAGAATCGGGAAGAACATGAAAGG | 2820 |
| Db | 2966 | ACTATTTTCGAAAGCCCTTCTAAAAAGTTGAAATTCGAAGAATCGGGAAGAACATGAAAGG | 3025 |
| Qy | 2821 | CAGTTTATAGCCCGTACCTTTAAATTCATGATGAAATGCAATGCTTTAGG | 2869 |
| Db | 3026 | CAGTTTATAGCCCGTACCTTTAAATTCATGATGAAATGCAATGCTTTAGG | 3074 |
| RESULT 6 | | | |
| ADB78684 | | | |
| ID | ADB78684 standard; cdNA; 3074 BP. | | |
| XX | | | |
| AC | ADB78684; | | |
| XX | | | |
| DT | 04-DEC-2003 (first entry) | | |
| XX | | | |
| DE | Human potassium channel subunit mutant cdNA SEQ ID NO:55. | | |
| XX | | | |
| KW | ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic; | | |
| KW | neuroprotective; inotropic; antipyrctic; antiarhythmic; antimigraine; | | |
| KW | antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic; | | |
| KW | nephrotropic; antidiabetic; ophthalmological; epilepsy; | | |
| KW | ion channel dysfunction; human. | | |
| XX | | | |
| OS | Synthetic. | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | WO2003008574-A1. | | |
| XX | | | |
| PD | 30-JAN-2003. | | |
| XX | | | |
| PF | 08-JUL-2002; 2002WO-AU000910. | | |
| XX | | | |
| PR | 18-JUL-2001; 2001AU-00006452. | | |


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PR 05-MAR-2002; 2002AU-00000910.
XX 13-MAY-2002; 2002AU-00002292.
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX WPI; 2003-239332/23.
XX
XX Identifying predisposition to an ion channel dysfunction, such as
XX periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
XX schizophrenia, anxiety and depression, by detecting encoding-gene
XX mutation events.
XX
XX Claim 6; SEQ ID NO 55; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyretic,
XX antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
XX neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
XX ophthalmological activity. A polynucleotide of the invention acts as an
XX ion channel agonist, or ion channel antagonist. The methods, isolated
XX nucleic acids, polypeptides, antibody, selective agonist, antagonist or
XX modulator of an ion channel, cells and genetically modified non-human
XX animal, are useful for the diagnosis and treatment of epilepsy and/or a
XX disorder associated with ion channel dysfunction, such as hyper- or hypo-
XX kalemic periodic paralysis, myotonias, malignant hyperthermia,
XX myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
XX disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
XX depression, phobic obsessional symptoms, neuropathic pain, inflammatory
XX pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
XX Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
XX fibrosis, congenital stationary night blindness and total colour
XX blindness. The present sequence represents a mutant cDNA of the
XX invention. The sequence data for this patent is not represented in the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;
XX
XX Query Match 93.0%; Score 2855.8; DB 10; Length 3074;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 2860; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
XX
XX 1 GCGAGCGCGATGAGGATGTGGAGTGTGGGCGGGGCGAGGGTGTCTGAACTGGCGAGCC 60
XX 206 GCGAGCGCGATGAGGATGTGGAGTGTGGGCGGGGCGAGGGTGTCTGAACTGGCGAGCC 265
XX
XX 61 GCCAGGGCGAGCGGCTCTACTGCTGGGACCCGCGGCGGCGAGCTGGTGGCGGGCG 120
XX 266 GCCAGGGCGAGCGGCTCTACTGCTGGGACCCGCGGCGGCGAGCTGGTGGCGGGCG 325
XX
XX 121 GGTGGCTGTAGGAGAGCGCGGGGCAAGCAGGGGGGCGCGGATGAGCTGTGGGGAAG 180
XX 326 GGTGGCTGTAGGAGAGCGCGGGGCAAGCAGGGGGGCGCGGATGAGCTGTGGGAGC 385
XX
XX 181 CGGTCTCTTACAGAGTAGCAGAGCTGCGGGCGCAACGTCAGTACCGCGGGGTGCAG 240
XX 386 CGCTCTCTTACAGAGTAGCAGAGCTGCGGGCGCAACGTCAGTACCGCGGGGTGCAG 445
XX
XX 241 AACTACCTGTACAGCTGTGGAGAGACCCCGCGCTGGGCTTCATCTACACGCTTTC 300
XX 446 AACTACCTGTACAGCTGTGGAGAGACCCCGCGCTGGGCTTCATCTACACGCTTTC 505
XX
XX 301 GTTTTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
XX 506 GTTTTCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 565
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1441 GACCTCACCCACCACTTAAACCTGTCTATTCGAGCTATCAGAAATTAACAAATTCATGTT 1500
1446 GACCTCACCCACCACTTAAACCTGTCTATTCGAGCTATCAGAAATTAACAAATTCATGTT 1705
1501 GCAAAACGGAAGTTTAAAGAAACCTTACGTCCATATGATGTAAGATGTCATTGAAACAA 1560
1706 GCAAAACGGAAGTTTAAAGAAACCTTACGTCCATATGATGTAAGATGTCATTGAAACAA 1765
1561 TATTCTGCTGTCATCTGGACATGCTGTGTAGAAATTAAGAGCTTCAAAACAGGTGTTGAT 1620
1766 TATTCTGCTGTCATCTGGACATGCTGTGTAGAAATTAAGAGCTTCAAAACAGGTGTTGAT 1825
1621 CAATTTCTGGAAGGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1680
1826 CAATTTCTGGAAGGGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1885
1681 GAAATGAGACCAAGAGCATCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAACACAG 1740
1886 GAAATGAGACCAAGAGCATCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAACACAG 1945
1741 GTACAGTCCATAGAAATCAAGCTGACTGCTTCTAGACATCTATCAACAGGTCTCTCGG 1800
1946 GTACAGTCCATAGAAATCAAGCTGACTGCTTCTAGACATCTATCAACAGGTCTCTCGG 2005
1801 AAAGCTCTGCTCTCAGCCCTCGCTTTGGCTTCAITTCAGATTCCACACCTTTTGAATGAA 1860
2006 AAAGCTCTGCTCTCAGCCCTCGCTTTGGCTTCAITTCAGATCCCAACCTTTTGAATGAA 2065
1861 CAGACATCTGACTATCAAGCCCTGTGATGAGCAAGATCTTTCGGTTCGGCAACAAAC 1920
2066 CAGACATCTGACTATCAAGCCCTGTGATGAGCAAGATCTTTCGGTTCGGCAACAAAC 2125
1921 AGTGGCTCTTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTCGAGTTCATCTG 1980
2126 AGTGGCTCTTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTCGAGTTCATCTG 2185
1981 AGCCAAATGAGTTCAGTCCAGACTTCTACGGCTTACGCTTACCTATCATCAGAGTCAA 2040
2186 AGCCAAATGAGTTCAGTCCAGACTTCTACGGCTTACGCTTACCTATCATCAGAGTCAA 2245
2041 GCAACACAGGTGCTGATTAAGTTCAGTTCAGGAGGCTCAGAGTGGCCAGCCACCAACCAAT 2100
2246 GCAACACAGGTGCTGATTAAGTTCAGTTCAGGAGGCTCAGAGTGGCCAGCCACCAACCAAT 2305
2101 GCAAAACCAATTAATACGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2160
2306 GCAAAACCAATTAATACGGCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2365
2161 CCTCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
2366 CCTCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2425
2221 TTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2280
2426 TTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2485
2281 GTTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340
2486 GTTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2545
2341 GAAATCTGTTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2546 GAAATCTGTTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605
2401 CAATACCTGATCAGGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2460
2606 CAATACCTGATCAGGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2665
2461 GGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2520
2666 GGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2725
2521 GATGAAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2580

2726 GATGAAGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2785
2581 GCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2640
2786 GCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2845
2641 AGCATTTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
2846 AGCATTTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2905
2701 TAGTTTCTTCATTTTCTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2760
2906 TAGTTTCTTCATTTTCTTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2965
2761 ACTATTTCGAAAGCCCTTCTTAAAGAGTTCGAAAGTTCGAAAGTTCGAAAGTTCGAAAGTTCGAAAG 2820
2966 ACTATTTCGAAAGCCCTTCTTAAAGAGTTCGAAAGTTCGAAAGTTCGAAAGTTCGAAAGTTCGAAAG 3025
2821 CAGTTTATAGCCCGTTTACCTTTTAAATTCGATGATGATGATGATGATGATGATGATGATGATGAT 2869
3026 CAGTTTATAGCCCGTTTACCTTTTAAATTCGATGATGATGATGATGATGATGATGATGATGATGAT 3074

RESULT 7

AAS14652

ID AAS14652 standard; cdna; 2694 BP.

XX AAS14652;

AC AAS14652;

XX 18-DEC-2001 (first entry)

XX Human cdna encoding a voltage gated potassium channel hKvN05-1.

XX Human; ss; voltage-gated potassium channel; hKvN05-1; nootropic;

XX cerebrotective; neurotropic; analgesic; vision disorder;

XX central nervous system disorder; epilepsy; migraine; hearing disorder;

XX psychotic disorder; seizure; learning disorder; memory disorder; stroke;

XX pain; gene therapy; splice variant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..2994

XX /*tag= a

XX /product= "hKvN05-1"

XX WO200170759-A1.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US009328.

XX 21-MAR-2000; 2000US-0190954P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2001-611467/70.

XX P-PSDB; AAU03020.

XX Polypeptides and polynucleotides of potassium channel KvN05 for

XX identifying a compound modulating ion flux in eukaryotic cell or cell

XX membrane expressing the protein, comprises KvN05 approximately 1-1

XX Claim 5; Page 62-63; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-

XX subunit of a KvN05 potassium channel, with a subsequence having 65

XX sequence identity to amino acids 343-640 of hKvN05-1 amino acid sequence

XX and forms a KvN05 potassium channel having the characteristic of voltage-

XX gating with at least an additional KvN05 alpha-subunit. Also included in

the scope of the invention are the nucleic acids encoding hKNQ5 (including splice variants encoding hKNQ5-1 and hKNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a KCNQ containing potassium channel and modulate ion flux through the channel. The KCNQ polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the KCNQ nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of KCNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of KCNQ5. The present sequence is a splice variant of hKNQ5 encoding hKNQ5-1.

SQ Sequence 2694 BP; 714 A; 671 C; 569 G; 540 T; 0 U; 0 Other;

Query Match 87.6%; Score 2690.4; DB 4; Length 2694;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

10 ATGAGGATGAGTGGAGTCGGCGCGGGCAGGCTGCTGTAACCTGGGAGCGCCAGGGGC 69
 1 ATGAGGATGAGTGGAGTCGGCGCGGGCAGGCTGCTGTAACCTGGGAGCGCCAGGGGC 60

70 GACGGCTGCTACTGCTGGGACCGCGCGGCCACGCTTGTGTGGCGGGGGTGGCTG 129
 61 GACGGCTGCTACTGCTGGGACCGCGCGGCCACGCTTGTGTGGCGGGGGTGGCTG 120

130 AGGAGAGCCCGCGGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGAAAGCCCTCTCT 189
 121 AGGAGAGCCCGCGGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGAAAGCCCTCTCT 180

190 TACAGGATACCGAGCTGCGGGCGGCAACGTCAGTACCGGGGGTGCAGACTACCTG 249
 181 TACAGGATACCGAGCTGCGGGCGGCAACGTCAGTACCGGGGGTGCAGACTACCTG 240

250 TACAGGCTGCTGGAGAGACCCCGGGCTGGCGCTTCACTACCGCTTTCGTTTTCTC 309
 241 TACAGGCTGCTGGAGAGACCCCGGGCTGGCGCTTCACTACCGCTTTCGTTTTCTC 300

310 CTGTGCTTTGGTGTGCTGATTTGTGAGTGTGTTTCTACCATCCCTGAGCACACAAATG 369
 301 CTGTGCTTTGGTGTGCTGATTTGTGAGTGTGTTTCTACCATCCCTGAGCACACAAATG 360

370 GCCTCAAGTGGCTCTTGAATCTGAGTGTGAGTGTGCTTGTGTTGGTTGGAGTTC 429
 361 GCCTCAAGTGGCTCTTGAATCTGAGTGTGAGTGTGCTTGTGTTGGTTGGAGTTC 420

430 ATCATTCGAATCTGCTGCGGGTGTGCTGATATAGGATGCGAAGGAGACTG 489
 421 ATCATTCGAATCTGCTGCGGGTGTGCTGATATAGGATGCGAAGGAGACTG 480

490 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCAATTGTTTATCGCTTCAATAGCA 549
 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCAATTGTTTATCGCTTCAATAGCA 540

550 GTTGTGCTGCAAAACCTCAGGGTAATATTTTGGCCAGCTGTGCACTCAGAAATCTCGGT 609
 541 GTTGTGCTGCAAAACCTCAGGGTAATATTTTGGCCAGCTGTGCACTCAGAAATCTCGGT 600

610 TTCTTACAGATCTCCGATGGCGCATGAGCCGAGGGGAGGACCTTGGAAATTAATCTG 669
 601 TTCTTACAGATCTCCGATGGCGCATGAGCCGAGGGGAGGACCTTGGAAATTAATCTG 660

670 GGTTCAGTGGTTTATGCTCACAGCAAGGAAATTAATCACAGCTTGGTACATAGGATTTTG 729
 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAAATTAATCACAGCTTGGTACATAGGATTTTG 720

730 GTTCTTATTTTTCGCTTTTCTGCTCTATCTGGTGGAAAGGATGCGCAATAAAGAGTTT 789

Db 721 GTTCTTATTTTTCGCTTTTCTGCTCTATCTGGTGGAAAGGATGCGCAATAAAGAGTTT 780
 Qy 790 TCTACATATGCAGATGCTCTCTGTGGGGCAATATACATTGACAACATTTGGCTATGGA 849
 Db 781 TCTACATATGCAGATGCTCTCTGTGGGGCAATATACATTGACAACATTTGGCTATGGA 840
 Qy 850 GACAAAACCTCCCTAACCTTGGCTGGGAAGATTGCTTCTGCGAGCTTTGCACTCCTTGGC 909
 Db 841 GACAAAACCTCCCTAACCTTGGCTGGGAAGATTGCTTCTGCGAGCTTTTGGCACTCCTTGGC 900
 Qy 910 ATTTCTTTTCTTTGACATTTCTGCGCGCATTTCTGCGCTCAGCTTTTGGCAATAAAGTACAA 969
 Db 901 ATTTCTTTTCTTTGACATTTCTGCGCGCATTTCTGCGCTCAGCTTTTGGCAATAAAGTACAA 960
 Qy 970 GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1029
 Db 961 GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1020
 Qy 1030 TGTGTTTGGGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCACTGCAACCTGGAAGCCA 1089
 Db 1021 TGTGTTTGGGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
 Qy 1090 CACTTGAAGGCTTTGACACCTGCGAGCCCTACCAAGAAAGAAACAAAGGGAAGCATCAAGC 1149
 Db 1081 CACTTGAAGGCTTTGACACCTGCGAGCCCTACCAAGAAAGAAACAAAGGGAAGCATCAAGC 1140
 Qy 1150 AGTCAGAAGCTTAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCCAGGGGCGCAGATATT 1209
 Db 1141 AGTCAGAAGCTTAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCCAGGGGCGCAGATATT 1200
 Qy 1210 AAGAGCGCAGCAAGCCTCAGTAGTGCAGAGAGTCCCGAAGCAGCAGCATCACAGCCGAG 1269
 Db 1201 AAGAGCGCAGCAAGCCTCAGTAGTGCAGAGAGTCCCGAAGCAGCAGCATCACAGCCGAG 1260
 Qy 1270 GGCACTCCCAACCAAGTGCAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1329
 Db 1261 GGCACTCCCAACCAAGTGCAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1320
 Qy 1330 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACCAAGTGTAGTGTGACACAGCCCTTGGC 1389
 Db 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACCAAGTGTAGTGTGACACAGCCCTTGGC 1380
 Qy 1390 ACTGATGATATATGATGAAAAAGGATGCGAGTGTGATGTATCAGTGGAAAGACTCACC 1449
 Db 1381 ACTGATGATATATGATGAAAAAGGATGCGAGTGTGATGTATCAGTGGAAAGACTCACC 1440
 Qy 1450 CCACCACTTAAACCTGCTATTGAGCTATCAGATTTATGAAATTTTCAATTTGCAAAACGG 1509
 Db 1441 CCACCACTTAAACCTGCTATTGAGCTATCAGATTTATGAAATTTTCAATTTGCAAAACGG 1500
 Qy 1510 AAGTTTAAAGGAAACCTTACGCTCCATATGATGTAAGATGTCAATTGAAACATATTTCTCT 1569
 Db 1501 AAGTTTAAAGGAAACCTTACGCTCCATATGATGTAAGATGTCAATTGAAACATATTTCTCT 1560
 Qy 1570 GGTCACTGGAACATGTTGTGATGATTTAAAGCCCTTCAACACAGCTGTTGATCAAAATCTT 1629
 Db 1561 GGTCACTGGAACATGTTGTGATGATTTAAAGCCCTTCAACACAGCTGTTGATCAAAATCTT 1620
 Qy 1630 GGAAAGGGCAAAATCAATCAGATAAGAGCCGAGAGGAAATAACAGCAGAACATGAG 1689
 Db 1621 GGAAAGGGCAAAATCAATCAGATAAGAGCCGAGAGGAAATAACAGCAGAACATGAG 1680
 Qy 1690 ACCACAGACCATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1749
 Db 1681 ACCACAGACCATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1740
 Qy 1750 ATAGAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGCTCTTTCGGAAGGCTCT 1809
 Db 1741 ATAGAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGCTCTTTCGGAAGGCTCT 1800
 Qy 1810 GCCTCAGCCCTCGCTTTGGCTTCAATCCAGTTCCTCCACTTTTGAATGTGAACAGACATCT 1869

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Db 1801 GCCTCAGCCCTCGCTTTGGCTTCTATTCAGATCCACCTTTTGAATGGAACAGACATCT 1860
Qy 1870 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGGACACAAAACAGTGGCTGC 1929
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGGACACAAAACAGTGGCTGC 1920
Qy 1930 TTATCCAGATCAACTAGTAGGCCAAATCTTCGAGAGCCCTGCACTTCTTCAACGCCAAAT 1989
Db 1921 TTATCCAGATCAACTAGTAGGCCAAATCTTCGAGAGCCCTGCACTTCTTCAACGCCAAAT 1980
Qy 1990 GAGTTCAAGTCCGACACTTTTACGGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2049
Db 1981 GAGTTCAAGTCCGACACTTTTACGGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040
Qy 2050 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACATTTGCAAAACAA 2109
Db 2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACATTTGCAAAACAA 2100
Qy 2110 ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2169
Db 2101 ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2160
Qy 2170 GCCATCAAGCATCTGCCAGCCGCAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGAA 2229
Db 2161 GCCATCAAGCATCTGCCAGCCGCAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGAA 2220
Qy 2230 AGCATTTCTGACGTCACCACTGCTTGTTCGCTCCAGGAAATGTTTCAGGTTGCACAG 2289
Db 2221 AGCATTTCTGACGTCACCACTGCTTGTTCGCTCCAGGAAATGTTTCAGGTTGCACAG 2280
Qy 2290 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAACTCTG 2349
Db 2281 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAACTCTG 2340
Qy 2350 TTGTCTGTCTGCCATGGTCCGAGGACTGTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2409
Db 2341 TTGTCTGTCTGCCATGGTCCGAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2400
Qy 2410 ATCAGGTCGCGAGGAACTCAATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2469
Db 2401 ATCAGGTCGCGAGGAACTCAATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460
Qy 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATAACTGTATGAAGAG 2529
Db 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATAACTGTATGAAGAG 2520
Qy 2530 GTGGTCCGAGAGACAGACAGACACTTTTGAATGCCGACCGAGCTGCAGGAGAA 2589
Db 2521 GTGGTCCGAGAGACAGACAGACACTTTTGAATGCCGACCGAGCTGCAGGAGAA 2580
Qy 2590 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCATCTCAGACATTTGT 2649
Db 2581 GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCATCTCAGACATTTGT 2640
Qy 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGTTGCTCATGTCAAACTGAATAA 2703
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGTTGCTCATGTCAAACTGAATAA 2694
```

RESULT 8

AAD27192

ID AAD27192 standard; cDNA; 2694 BP.

XX AC AAD27192;

XX DT 09-APR-2002 (first entry)

XX DE Human potassium channel polypeptide, KCNQ5 cDNA.

XX KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;

XX KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;

XX KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;

XX KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;

KW

KW

KW

KW

KW

KW

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XX

XX

FH

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PN

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PD

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addiction; myokymia; Alzheimer's disease; age-associated memory loss; learning deficiency; cognitive disorder; motor disease; neuron disease; neurophysiological disorder; neuropsychological disorder; asthma; neuron cell death; brain tumour; gene therapy; antisense therapy; synaptic transmission; electrical excitability; ss.

Homo sapiens.

Location/Qualifiers

1. .2694

/*tag= a

/product= "Human KCNQ5 protein"

WO200192526-A1.

06-DEC-2001.

24-MAY-2001; 2001WO-US017314.

26-MAY-2000; 2000US-0207389P.

(BRIM) BRISTOL-MYERS SQUIBB CO.

Dworetzky SI, Ramanathan CS, Trojnecki JT, Boissard CG;

Gribkoff VK;

WPI; 2002-122069/16.

P-PSDB; AAE16599.

Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding it, for diagnosing, treating and identifying modulators useful in treating neurological, neurophysiological and neuropsychological diseases.

Claim 3; Fig 1; 128pp; English.

The invention relates to potassium channel polypeptides referred to as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5 polypeptides are useful for identifying compounds that modulate their biological activity. The compounds identified and KCNQ5 polynucleotides are useful for treating acute and chronic pain, migraine, acute stroke, dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders, depression, bipolar disorder, sleep disorders, eating disorders, addiction, myokymia, Alzheimer's disease, age-associated memory loss, learning deficiencies, cognitive disorders and motor neuron diseases. The nucleic acid molecules of the invention are further useful for treating neurophysiological, neuropsychological disorders, asthma, neuron cell death and brain tumours. They are also used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical excitability in the brain and are useful for generating antibodies. They are also useful to affinity purify biological effectors from biological materials e.g. disease tissues or cells. The present sequence is human KCNQ5 cDNA

Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Query Match 87.6%; Score 2690.4; DB 6; Length 2694;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 ATGAAGGATGTGGAGTCGGGCCGGGCGAGGGTGTCTGTAACTCGGCAGCGCCAGGGGC 69

Db 1 ATGAAGGATGTGGAGTCGGGCCGGGCGAGGGTGTCTGTAACTCGGCAGCGCCAGGGGC 60

Qy 70 GACGGCTGTACTGTCTGGGCAACCGCGCGGCCACGCTTGTGTGGCGGGCGGTGGCGCTG 129.

Db 61 GACGGCTGTACTGTCTGGGCAACCGCGCGGCCACGCTTGTGTGGCGGGCGGTGGCGCTG 120

Qy 130 AGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGAGACCGCTCTCT 189

Db 121 AGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGAGACCGCTCTCT 180

| | | | |
|----|------|--|------|
| Qy | 190 | TACACGAGTAGCTGCAGAGCTGCGCGCAACGTCAAGTACCGGCGGTGCAGAACTACCTG | 249 |
| Db | 181 | TACACGAGTAGCCAGAGCTGCGCGCAACGTCAAGTACCGGCGGTGCAGAACTACCTG | 240 |
| Qy | 250 | TACAACTGCTGGAGAGACCCCGCGCTGGCGTTCACTACCAACGCTTTCGTTTTCTC | 309 |
| Db | 241 | TACAACTGCTGGAGAGACCCCGCGCTGGCGTTCACTACCAACGCTTTCGTTTTCTC | 300 |
| Qy | 310 | CTTGCTTTGGTTGCTTGAATTTGTCAAGTGTTTTCTACCATCCCTGAGCACAAAAATTG | 369 |
| Db | 301 | CTTGCTTTGGTTGCTTGAATTTGTCAAGTGTTTTCTACCATCCCTGAGCACAAAAATTG | 360 |
| Qy | 370 | GCCTCAAGTTGCCCTTGTATCCTGGAGTTCGTGATGATTCGTCTTTGGTGGAGTTC | 429 |
| Db | 361 | GCCTCAAGTTGCCCTTGTATCCTGGAGTTCGTGATGATTCGTCTTTGGTGGAGTTC | 420 |
| Qy | 430 | ATCAATCGAATCTGCTTCGCGGTTCGTTCGTATATAGATACCAATGTTCTTATCGCTTCAATAGCA | 489 |
| Db | 421 | ATCAATCGAATCTGCTTCGCGGTTCGTTCGTATATAGATACCAATGTTCTTATCGCTTCAATAGCA | 480 |
| Qy | 490 | AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA | 549 |
| Db | 481 | AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA | 540 |
| Qy | 550 | GTTGTTTCTCGAAAACTCAGGTAATATTTTGGCCACGTCGCACTCAGAAAGTCTCCGT | 609 |
| Db | 541 | GTTGTTTCTCGAAAACTCAGGTAATATTTTGGCCACGTCGCACTCAGAAAGTCTCCGT | 600 |
| Qy | 610 | TTCTCAGAGATCCTCCGATGGTCGATGAGCCGAGGGGAGGCACTTCGAAATTAAGTTC | 669 |
| Db | 601 | TTCTCAGAGATCCTCCGATGGTCGATGAGCCGAGGGGAGGCACTTCGAAATTAAGTTC | 660 |
| Qy | 670 | GGTTCAAGTGGTTATGCTCAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTTC | 729 |
| Db | 661 | GGTTCAAGTGGTTATGCTCAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTTC | 720 |
| Qy | 730 | GTTCCTAATTTTTCGTTCTTCCCTTTCATCTGGTGGAAAGGATGCCAATAAAGAGTTT | 789 |
| Db | 721 | GTTCCTAATTTTTCGTTCTTCCCTTTCATCTGGTGGAAAGGATGCCAATAAAGAGTTT | 780 |
| Qy | 790 | TCTACATATCGAGATGCTCTCTGGTGGGACAAATTAATGACACTATTCGCTATGGA | 849 |
| Db | 781 | TCTACATATCGAGATGCTCTCTGGTGGGACAAATTAATGACACTATTCGCTATGGA | 840 |
| Qy | 850 | GACAAAACCTCCCTTAACTTGGCTGGGAAGATTGCTTCTCGAGCTTTGCACCTCTGGC | 909 |
| Db | 841 | GACAAAACCTCCCTTAACTTGGCTGGGAAGATTGCTTCTCGAGCTTTGCACCTCTGGC | 900 |
| Qy | 910 | ATTTCTTTTCTTTCGACTTCCTGCGGCAATTCCTGGCTCAGGTTTTCGATTTAAAGTACAA | 969 |
| Db | 901 | ATTTCTTTTCTTTCGACTTCCTGCGGCAATTCCTGGCTCAGGTTTTCGATTTAAAGTACAA | 960 |
| Qy | 970 | GAACAACACCGCCAGAAACCTTTGAGAAAAGGAACCCAGCTGCCACCTCATTCAG | 1029 |
| Db | 961 | GAACAACACCGCCAGAAACCTTTGAGAAAAGGAACCCAGCTGCCACCTCATTCAG | 1020 |
| Qy | 1030 | TGTTGTTGGGTAGTTACGACAGCTGATGAGAAATCTGTTTCCATTCGCAACTCGAAGCCA | 1089 |
| Db | 1021 | TGTTGTTGGGTAGTTACGACAGCTGATGAGAAATCTGTTTCCATTCGCAACTCGAAGCCA | 1080 |
| Qy | 1090 | CACTTGAAGCCTTTGCACACCTGCAGCCCTACCAAGAAGAAACAAGGGGAGCATCAAGC | 1149 |
| Db | 1081 | CACTTGAAGCCTTTGCACACCTGCAGCCCTACCAAGAAGAAACAAGGGGAGCATCAAGC | 1140 |
| Qy | 1150 | AGTCAGAAAGCTAAGTTTAAAGGCGAGTGGCATTGCTAGCCCGAGGGGCCAGAGTATT | 1209 |
| Db | 1141 | AGTCAGAAAGCTAAGTTTAAAGGCGAGTGGCATTGCTAGCCCGAGGGGCCAGAGTATT | 1200 |
| Qy | 1210 | AAGAGCCGCAAGCCTCAGTAGGTGACAGAGAGTCCCAAGCAACCGACATCAGACCGGAG | 1269 |
| Db | 1201 | AAGAGCCGCAAGCCTCAGTAGGTGACAGAGAGTCCCAAGCAACCGACATCAGACCGGAG | 1260 |
| Qy | 1270 | GGCAGTCCCACAAAGTGCAGAAAGCTGGAGTTTCAACAGACCGAAACCCGCTTCCGGCCC | 1329 |

Db 2341 TTGCTGTCTGCCANGTCCGAGGACTTGGCAAAATCTTTGTCTGTGCAAAACCTG 2400
Oy 2410 ATCAGGTCGACCGAGGAATCAATATACAACTTTTCAGGGAGTGAAGTCAAGTGGCTCCAGA 2469
Db 2401 ATCAGGTCGACCGAGGAATCAATATACAACTTTTCAGGGAGTGAAGTCAAGTGGCTCCAGA 2460
Oy 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAAATCATGATGAAGAG 2529
Db 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAAATCATGATGAAGAG 2520
Oy 2530 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGCGCACCGCAGCTGCCAGGAA 2589
Db 2521 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGCGCACCGCAGCTGCCAGGAA 2580
Oy 2590 GCTGCTTTGCATCAGACTCTCTAAGGACTCGAAGGTCAAGTCAATCATCTCAGAGCATTTGT 2649
Db 2581 GCTGCTTTGCATCAGACTCTCTAAGGACTCGAAGGTCAAGTCAATCATCTCAGAGCATTTGT 2640
Oy 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAATAA 2703
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAATAA 2694

RESULT 9

AAH43633
ID AAH43633 standard; cDNA; 2772 BP.

XX AC AAH43633;

XX DT 21-JAN-2002 (first entry)

XX XX

DE Human ion-channel forming protein ORF.

XX KW

KW Ion-channel forming protein; voltage-gated potassium channel; fetal;
brain; thymus; prostate; heart; skeletal muscle; probe; ss.

XX OS

XX PN Homo sapiens.

XX PD WO200175108-A1.

XX PF 11-OCT-2001.

XX PR 03-APR-2001; 2001WO-US010875.

XX PR 03-APR-2000; 2000US-0194255P.

XX PR (LEXI-) LEXICON GENETICS INC.

XX PI

PI Hu Y, Kiekie JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;

PI Sands AT;

XX WPI;

XX DR 2001-656987/75.

XX DR P-PSDB; AAB47678.

XX PT

PT New human ion channel protein and polynucleotides encoding the protein,
useful in diagnosing or treating diseases, in drug screening, and in
clinical trial monitoring.

XX PS

PS Claim 1; Page 34-35; 41pp; English.

XX CC

CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
The protein shares structural similarity with mammalian ion channel
proteins, particularly voltage-gated potassium channel proteins. The
protein is expressed in many human cell lines including fetal brain,
brain, thymus, prostate, heart and skeletal muscle. The novel protein can
be used in the diagnosis or treatment of diseases, in drug screening, and
in clinical trial monitoring. The oligonucleotides may be used as
hybridization probes for screening libraries, and assessing gene
expression patterns (particularly using a micro array or high throughput
chip format). The nucleic acids and novel protein can also be used in the
identification, selection and validation of novel molecular targets for
drug discovery, to screen collections of genetic material from patients
who have a particular medical condition, to identify mutations associated

CC with a particular disease, as a diagnostic or prognostic assay, and to
screen for drugs which can be used to treat symptomatic or phenotypic
manifestations of perturbing the normal function of novel human protein.
CC The polypeptides are further used in generating antibodies
XX
SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;

Query Match 85.8%; Score 2635.4; DB 5; Length 2772;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Oy 1 GGCAGCGGCATGAAGGATGTGGAGTCGGCGCGGGGAGGGTCTGCTGAACCTGGGAGCC 60

Db 97 GGCAGCGGCATGAAGGATGTGGAGTCGGCGCGGGGAGGGTCTGCTGAACCTGGGAGCC 156

Oy 61 GCCAGGGGCGACGCGCTTACTGCTGGGCACCCGCGCGCCAGCGTGTGGCGCGCGGC 120

Db 157 GCCAGGGGCGACGCGCTTACTGCTGGGCACCCGCGCGCCAGCGTGTGGCGCGCGGC 216

Oy 121 GGTGGCCTGAGGGAGAGCCCGCGGGCAAGCAGGGGCGCGGGATGAGCCTGCTGGGGAAG 180

Db 217 GGTGGCCTGAGGGAGAGCCCGCGGGCAAGCAGGGGCGCGGGATGAGCCTGCTGGGGAAG 276

Oy 181 CCGCTCTTTACAGGATAGCAGAGCTGCGGGGCGCAACGTCAAGTACCGCGCGGTGCAG 240

Db 277 CCGCTCTTTACAGGATAGCAGAGCTGCGGGGCGCAACGTCAAGTACCGCGCGGTGCAG 336

Oy 241 AACTTACCTGTACAACTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCAAGCTTTC 300

Db 337 AACTTACCTGTACAACTGCTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCAAGCTTTC 396

Oy 301 GTTTTCTCCTTGTCTTTGGTGTCTGATTTGTGCTGCTTCTTACCATCCCTGAGCAC 360

Db 397 GTTTTCTCCTTGTCTTTGGTGTCTGATTTGTGCTGCTTCTTACCATCCCTGAGCAC 456

Oy 361 ACAAATTTGGCTCAAGTTCGCTTCTGATCTCGAGTTCGCTGATGATGCTGCTTTGGT 420

Db 457 ACAAATTTGGCTCAAGTTCGCTTCTGATCTCGAGTTCGCTGATGATGCTGCTTTGGT 516

Oy 421 TTGGAGTTTCATTCGAAATCTGCTGCGGTTGCTGTTGTCGATATAGAGGATGCAAA 480

Db 517 TTGGAGTTTCATTCGAAATCTGCTGCGGTTGCTGTTGTCGATATAGAGGATGCAAA 576

Oy 481 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTTTATAGATACCATTTGTTTATCGCT 540

Db 577 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTTTATAGATACCATTTGTTTATCGCT 636

Oy 541 TCAATAGCAGTTGTTTCTGCAAAAACCTCAGGTTAATATTTTGGCAGCTCTGCACTCAGA 600

Db 637 TCAATAGCAGTTGTTTCTGCAAAAACCTCAGGTTAATATTTTGGCAGCTCTGCACTCAGA 696

Oy 601 AGTCTCGGTTTCTTACAGATCTCCGCAATGCTGGCGCATGACCAAGGAGGAGGCACTTGG 660

Db 697 AGTCTCGGTTTCTTACAGATCTCCGCAATGCTGGCGCATGACCAAGGAGGAGGCACTTGG 756

Oy 661 AAATTTACTGGGTTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTACATA 720

Db 757 AAATTTACTGGGTTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTACATA 816

Oy 721 GGATTTTGGTTCTTATTTTCTGCTTCTTCTGCTTCTATCTGGTGGAAAGGATGCCAAT 780

Db 817 GGATTTTGGTTCTTATTTTCTGCTTCTTCTGCTTCTATCTGGTGGAAAGGATGCCAAT 876

Oy 781 AAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGCGCAAAATTAATTCACAACTATT 840

Db 877 AAAGAGTTTCTACATATGAGATGCTCTCTGGTGGGCGCAAAATTAATTCACAACTATT 936

Oy 841 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAAGATTGCTTTCTGAGGCTTTGCA 900

Db 937 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAAGATTGCTTTCTGAGGCTTTGCA 996

Oy 901 CTCCTTGGCATTTCTTTCTTTGGCAATTCCTGCGCGCATCTTGGCTCAGGTTTGGCATT 960

Db 997 CTCCTTGGCATTTCTTTCTTGCACTTCCTGCGGCGATTCCTGGCTCAGGTTTTCATTA 1056
Qy 961 AAAGTACAAGAACAAACACCGCCAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAAC 1020
Db 1057 AAAGTACAAGAACAAACACCGCCAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAAC 1116
Qy 1021 CTCATTCACTGTTTGGCGTAGTTACGCGCTGATGAGAAATCTGTTTCATTTGCAACC 1080
Db 1117 CTCATTCACTGTTTGGCGTAGTTACGCGCTGATGAGAAATCTGTTTCATTTGCAACC 1176
Qy 1081 TGAAGCCACACTTGAAGCCCTTGACACCTTGACACCTTGACACCTTGACACCTTGACACCT 1140
Db 1177 TGAAGCCACACTTGAAGCCCTTGACACCTTGACACCTTGACACCTTGACACCTTGACACCT 1220
Qy 1141 GCATCAAGCAGTCAGAACCTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCCAGGGGC 1200
Db 1221 -----TCAGAACCTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCCAGGGGC 1269
Qy 1201 CAGAGTATTAGAGCCGACAGCCCTCAGTAGGTGACAGAGGTGCCCAAGCACCGACATC 1260
Db 1270 CAGAGTATTAGAGCCGACAGCCCTCAGTAGGTGACAGAGGTGCCCAAGCACCGACATC 1329
Qy 1261 ACAGCCGAGGCGAGTCCACCAAGTGCAGAGAGCTCGAGCTTCAACGACCGAACCCGC 1320
Db 1330 ACAGCCGAGGCGAGTCCACCAAGTGCAGAGAGCTCGAGCTTCAACGACCGAACCCGC 1389
Qy 1321 TTCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAACAGTGTAGATGCTGACACA 1380
Db 1390 TTCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAACAGTGTAGATGCTGACACA 1449
Qy 1381 GCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1450 GCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
Qy 1441 GACCTCACCCACCACTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1510 GACCTCACCCACCACTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
Qy 1501 GCAAAACGGAAGTTTAAAGAAACRTTACGTCCATATGATGATGATGATGATGATGATGATGAT 1560
Db 1570 GCAAAACGGAAGTTTAAAGAAACRTTACGTCCATATGATGATGATGATGATGATGATGATGAT 1629
Qy 1561 TATTCGTGCTCATCTGGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1630 TATTCGTGCTCATCTGGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689
Qy 1621 CAATTTCTGGAAGGCAATACATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1690 CAATTTCTGGAAGGCAATACATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1749
Qy 1681 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 1740
Db 1750 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 1809
Qy 1741 GTACAGTCCATAGATCCAGCTGACATGCTGCTAGACATCTATCAACAGCTGCTTCGG 1800
Db 1810 GTACAGTCCATAGATCCAGCTGACATGCTGCTAGACATCTATCAACAGCTGCTTCGG 1869
Qy 1801 AAAGCTCTGCTCAGCCCTCGCTTGGCTTCATTCAGTTCCCACTTTTGAATGTA 1860
Db 1870 AAAGCTCTGCTCAGCCCTCGCTTGGCTTCATTCAGTTCCCACTTTTGAATGTA 1929
Qy 1861 CAGACATCTGACTATCAAGCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
Db 1930 CAGACATCTGACTATCAAGCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1989
Qy 1921 AGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCAATTCG 1980
Db 1990 AGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCAATTCG 2049
Qy 1981 ACGCCAAATAGTTTCAAGTCCAGACTTTTACGCGCTTAGCCCTACTATGCAGTCA 2040
Db 2050 ACGCCAAATAGTTTCAAGTCCAGACTTTTACGCGCTTAGCCCTACTATGCAGTCA 2109

Qy 2041 GCAACACAGGTGCGCAATTTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTT 2100
Db 2110 GCAACACAGGTGCGCAATTTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTT 2169
Qy 2101 GCAACACAAATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCACCT 2160
Db 2170 GCAACACAAATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCACCT 2229
Qy 2161 CCTCTCCAGCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTAAACCTTCGAGGC 2220
Db 2230 CCTCTCCAGCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTAAACCTTCGAGGC 2289
Qy 2221 TTA CAGGAAAGCATTTCTGACGT CCA CACTGCTTGTGTGCT CCAAGGAAATGTTT CAG 2280
Db 2290 TTA CAGGAAAGCATTTCTGACGT CCA CACTGCTTGTGTGCT CCAAGGAAATGTTT CAG 2349
Qy 2281 GTTGCACAGTCAAATCTCACCAGGACCGTCTATGAGGAAAGCTTTGACATGGGAGGA 2340
Db 2350 GTTGCACAGTCAAATCTCACCAGGACCGTCTATGAGGAAAGCTTTGACATGGGAGGA 2409
Qy 2341 GAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2410 GAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2469
Qy 2401 CAAACCTGATCAGGTGACAGGAACTGGAATATACAACTTT CAGGAGTGAAGT CAAAGT 2460
Db 2470 CAAACCTGATCAGGTGACAGGAACTGGAATATACAACTTT CAGGAGTGAAGT CAAAGT 2529
Qy 2461 GGCTCCAGAGCCAGCAAGATTTTACCCAAATGGAGGAACTCCAAATTCGTTATTA 2520
Db 2530 GGCTCCAGAGCCAGCAAGATTTTACCCAAATGGAGGAACTCCAAATTCGTTATTA 2589
Qy 2521 GATGAAGAGTGGTCCCGAAGACAGACAGACAGACACTTTTGATGCGCACCGCAGCCT 2580
Db 2590 GATGAAGAGTGGTCCCGAAGACAGACAGACAGACACTTTTGATGCGCACCGCAGCCT 2649
Qy 2581 GCCAGGAAAGCTGCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCATCTCAG 2640
Db 2650 GCCAGGAAAGCTGCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCATCTCAG 2709
Qy 2641 AGCATTTGTAAGCAGCAGGAAAGTACAGATCCCTCAGCTGCTCATGTCAAACTGAAA 2700
Db 2710 AGCATTTGTAAGCAGCAGGAAAGTACAGATCCCTCAGCTGCTCATGTCAAACTGAAA 2769
Qy 2701 TAA 2703
Db 2770 TAA 2772

RESULT 10
AAS14653

ID AAS14653 standard; cDNA; 2667 BP.

XX AAS14653;

AC AAS14653;

XX 18-DEC-2001 (first entry)

XX Human cDNA encoding a voltage gated potassium channel hKVNQ5-2.

XX Human; ss; voltage-gated potassium channel; KVNQ5-2; nootropic;
cerebroprotective; neurotropic; analgesic; vision disorder;
central nervous system disorder; epilepsy; migraine; hearing disorder;
psychotic disorder; seizure; learning disorder; memory disorder; stroke;
pain; gene therapy; splice variant.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..2667

FT /*tag= a

FT /product= "hKVNQ5-2"

1450 CCACACCTTAAACCTGCTCATTCGAGCTATCAGATTATGAATTTTCATGTTGCAAAACGG 1509
Db CCACACCTTAAACCTGCTCATTCGAGCTATCAGATTATGAATTTTCATGTTGCAAAACGG 1473
1510 AAGTTTAAAGGAAACCTTACGTCCTATATGATGTAAGAGATGTCATTGAACAATATTCCTGCT 1569
Db AAGTTTAAAGGAAACCTTACGTCCTATATGATGTAAGAGATGTCATTGAACAATATTCCTGCT 1533
1570 GGTATCTGGAATGCTGTTGTAGAAATTAAGAGCCTTCAAAACGCTGTTGATCAAAATCTT 1629
Db GGTATCTGGAATGCTGTTGTAGAAATTAAGAGCCTTCAAAACGCTGTTGATCAAAATCTT 1593
1630 GGAAGGCGCAATCAGATCAGATGAGAGAGCGAGAGAAATTAACAGCAGAACTCAG 1689
Db GGAAGGCGCAATCAGATCAGATGAGAGAGCGAGAGAAATTAACAGCAGAACTCAG 1653
1690 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1749
Db ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1713
1750 ATAGATCCAAAGCTGGAATGCTGCTAGATCTATCAACAGGTCCTTTCGAAAGGCTCT 1809
Db ATAGATCCAAAGCTGGAATGCTGCTAGATCTATCAACAGGTCCTTTCGAAAGGCTCT 1773
1810 GCCTCAGCCCTCGCTTTCGCTTTCATTCAGTTCCTCCACCTTTTGAATGTGAACAGACATCT 1869
Db GCCTCAGCCCTCGCTTTCGCTTTCATTCAGTTCCTCCACCTTTTGAATGTGAACAGACATCT 1833
1870 GACTATCAAAAGCCTGTGATAGCAAAAGATCTTTGCGGTTCGCAACAAACAGTGGCTGC 1929
Db GACTATCAAAAGCCTGTGATAGCAAAAGATCTTTGCGGTTCGCAACAAACAGTGGCTGC 1893
1930 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCTGCGAGTTCAATTCACGCGCAAT 1989
Db TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCTGCGAGTTCAATTCACGCGCAAT 1953
1990 GAGTTGAGTCCGAGACTTTTACGCGCTTAGCCCTACTATGACAGTCAAGCAGACACAG 2049
Db GAGTTGAGTCCGAGACTTTTACGCGCTTAGCCCTACTATGACAGTCAAGCAGACACAG 2013
2050 GTGCCAATTAGTCAAAAGCGGTGCTCAGCAGTGGCAGCACAACACCATTTGCAAAACCA 2109
Db GTGCCAATTAGTCAAAAGCGGTGCTCAGCAGTGGCAGCACAACACCATTTGCAAAACCA 2073
2110 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2169
Db ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2133
2170 GCCATCAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCTGCGAGGCTTACAGGAA 2229
Db GCCATCAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCTGCGAGGCTTACAGGAA 2193
2230 AGCATTTCTGACGTCACCACTGCTGCTGCTCAGAGGAAATGTTTCAGGTTGCACAG 2289
Db AGCATTTCTGACGTCACCACTGCTGCTGCTCAGAGGAAATGTTTCAGGTTGCACAG 2253
2290 TCAATCTCAACAGACCGTTCTATAGGAAAAAGCTTTTGAATGGAGGAGAACTCTG 2349
Db TCAATCTCAACAGACCGTTCTATAGGAAAAAGCTTTTGAATGGAGGAGAACTCTG 2313
2350 TTGCTGCTCTCCCATGTCGCGAGGACCTTGGCAATCTTTGCTGTCGCAAAACCTG 2409
Db TTGCTGCTCTCCCATGTCGCGAGGACCTTGGCAATCTTTGCTGTCGCAAAACCTG 2373
2410 ATCAGGTCGACCGAGGAACTGAATATCAAACTTTTCAGGAGTGAAGTGGCTCCAGA 2469
Db ATCAGGTCGACCGAGGAACTGAATATCAAACTTTTCAGGAGTGAAGTGGCTCCAGA 2433
2470 GGCAGCCAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAACATGATGAAGAG 2529
Db GGCAGCCAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAACATGATGAAGAG 2493
2530 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCGCGCACCGCAGCCTGCCAGGAA 2589

2494 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGACGCTGCCAGGGAA 2553
Qy GCTGCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAGAGCATTTGT 2649
Db GCTGCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAGAGCATTTGT 2613
2650 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2703
Db AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2667

RESULT 11
AAC64370
ID AAC64370 standard; DNA; 125910 BP.
XX AAC64370;
AC
XX 07-FEB-2001 (first entry)
DT
XX Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1.
DE
XX Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;
KW Salla disease; ophthalmological; auditory; central nervous system;
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;
KW age-related macular degeneration; macular degeneration; deafness;
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
KW gastrointestinal disorder; ds.
XX Homo sapiens.
XX WO200061606-A1.
FN
XX 19-OCT-2000.
PD
XX 10-APR-2000; 2000WO-US009587.
PF
XX 14-APR-1999; 99US-0129274P.
PR
XX (MERI) MERCK & CO INC.
PA
XX Petrukhin K, Caskey CT, Li W, Metzker ML;
PI
XX WPI; 2000-647417/62.
DR P-PSDB; AAB24241.
XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
PT inhibitors and activators which can treat e.g. Stargardt-like macular
XX dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
PS Claim 3; Fig 1; 99pp; English.
XX The present sequence represents the human KCNQ5 (also called KCN6q) gene,
XX which encodes a voltage-gated potassium channel protein. Human KCNQ5 has
XX ophthalmological, auditory, central nervous system (CNS), cardioactive,
XX anticonvulsant, gastrointestinal and muscular active activities.
XX Sequences and methods from the present invention are useful for
XX identifying activators or inhibitors of KCNQ5 protein. These activators
XX and inhibitors are useful for treating Stargardt-like macular dystrophy,
XX cone-rod dystrophy, Salla disease, age-related macular degeneration,
XX other forms of macular degeneration, deafness, epilepsy, and different
XX forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
XX Stargardt-like macular dystrophy and cone-rod dystrophies are located at
XX chromosome 6q
XX
XX Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

Query Match 42.8%; Score 1313.4; DB 3; Length 125910;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1739 AGGTACAGTCCATAGATCCAGCTGACTGCTACTAGACATATCAACAGGTCCTTC 1798

| | | | |
|----|--------|---|--------|
| Db | 123624 | AGGTACAGTCCATAGAAATCCAAAGCTGGAGTGCTACTAGACATCTATCAACAGGTCTTC | 123683 |
| Qy | 1799 | GGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCAGTTCCTCCACCTTTTGAATGTG | 1858 |
| Db | 123684 | GGAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCAGCTTTTGAATGTG | 123743 |
| Qy | 1859 | AACAGACATCTGACATATCAAAAGCCCTGTGGATAGCAAAAGATCTCTTCGGGTTCCGACAAA | 1918 |
| Db | 123744 | AACAGACATCTGACATATCAAAAGCCCTGTGGATAGCAAAAGATCTCTTCGGGTTCCGACAAA | 123803 |
| Qy | 1919 | ACAGTGGCTGCTTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTCGAGTTCATTC | 1978 |
| Db | 123804 | ACAGTGGCTGCTTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTCGAGTTCATTC | 123863 |
| Qy | 1979 | TGACGCCAAATAGATTAGTGGCCAGACTTTCTACGCGCTTAGCGCTTACTATGCACAGTC | 2038 |
| Db | 123864 | TGACGCCAAATAGATTAGTGGCCAGACTTTCTACGCGCTTAGCGCTTACTATGCACAGTC | 123923 |
| Qy | 2039 | AAGCAACACAGGTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACA | 2098 |
| Db | 123924 | AAGCAACACAGGTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACA | 123983 |
| Qy | 2099 | TTGCAAAACCAATAAATACGCCACCAAGCCAGCAGCCCCCAACAATTTACAGATCCAC | 2158 |
| Db | 123984 | TTGCAAAACCAATAAATACGCCACCAAGCCAGCAGCCCCCAACAATTTACAGATCCAC | 124043 |
| Qy | 2159 | CTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAAATCTGCACCTTAACCTGCAG | 2218 |
| Db | 124044 | CTCCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAAATCTGCACCTTAACCTGCAG | 124103 |
| Qy | 2219 | GCTTACAGAAAGCAATTTCTGACGTCACCACTGCTTTGTCCTTCAAGGAAAATGTC | 2278 |
| Db | 124104 | GCTTACAGAAAGCAATTTCTGACGTCACCACTGCTTTGTCCTTCAAGGAAAATGTC | 124163 |
| Qy | 2279 | AGGTTGCACAGTCAAAATCTCACAAGAGACCGTTCTTACAGGAAAAGCTTTGACATGGAG | 2338 |
| Db | 124164 | AGGTTGCACAGTCAAAATCTCACAAGAGACCGTTCTTACAGGAAAAGCTTTGACATGGAG | 124223 |
| Qy | 2339 | GAGAAACTCTGTGTCTGTCTGTCCCATGGTGCCGAAAGACHTTGGGCAAAATCTTTGTCTG | 2398 |
| Db | 124224 | GAGAAACTCTGTGTCTGTCTGTCCCATGGTGCCGAAAGACHTTGGGCAAAATCTTTGTCTG | 124283 |
| Qy | 2399 | TGCAAAACCTGATCAGTTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTCAA | 2458 |
| Db | 124284 | TGCAAAACCTGATCAGTTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTCAA | 124343 |
| Qy | 2459 | GTGGCTCCAGAGGCGCAAGATTTTATCCCAAAATGGAGGGAATCCAAATTTGTTATAA | 2518 |
| Db | 124344 | GTGGCTCCAGAGGCGCAAGATTTTATCCCAAAATGGAGGGAATCCAAATTTGTTATAA | 124403 |
| Qy | 2519 | CTGATGAAGAGTGGGTCCCGAAGAGACAGAGACAGACATTTTGAATCCGACCCGACG | 2578 |
| Db | 124404 | CTGATGAAGAGTGGGTCCCGAAGAGACAGAGACAGACATTTTGAATCCGACCCGACG | 124463 |
| Qy | 2579 | CTGCCAGGAAGCTGCCTTTGATCAGACTCTTAAGGACTGGAAGTCAACCATCATCTC | 2638 |
| Db | 124464 | CTGCCAGGAAGCTGCCTTTGATCAGACTCTTAAGGACTGGAAGTCAACCATCATCTC | 124523 |
| Qy | 2639 | AGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCCCTCAGCTTTGCCCTCATGTCAAACTGA | 2698 |
| Db | 124524 | AGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCCCTCAGCTTTGCCCTCATGTCAAACTGA | 124583 |
| Qy | 2699 | AATAAGTCTTCAATTTCTTCCAGGCATAGCAGTTCCTTTAGGCATACATATCATTTGAT | 2758 |
| Db | 124584 | AATAAGTCTTCAATTTCTTCCAGGCATAGCAGTTCCTTTAGGCATACATATCATTTGAT | 124643 |
| Qy | 2759 | GAACTATTTCGAAAGCCCTTCTAAAAGTTGAAATTCGAAGAAATCGGGAAGAACATGAA | 2818 |
| Db | 124644 | GAACTATTTCGAAAGCCCTTCTAAAAGTTGAAATTCGAAGAAATCGGGAAGAACATGAA | 124703 |
| Qy | 2819 | GGCAGTTTATAAGCCCGTTACCTTTTAAATTCGATGAAATTCGATTTTAGGATGGCTAA | 2878 |

| | | | |
|-----------|---|---|--------|
| Db | 124704 | GGCAGTTTAAAGCCCGTACCTTTTAAATTCATGCATGAAATGCATGTTTAGGATGGCTAA | 124766 |
| Qy | 2879 | AAATCCCAAGGTGCATCGACATTAACCCCACTCATTTAGTAAATGTACCTTGAGTTAAAAAGC | 2938 |
| Db | 124764 | AAATCCCAAGGTGCATCGACATTAACCCCACTCATTTAGTAAATGTACCTTGAGTTAAAAAGC | 124823 |
| Qy | 2939 | CTGAGAAACCAAAACACAGCTAATGCTATGGGGGTATGAAATATGTCAAGTTTAGTGCATT | 2998 |
| Db | 124824 | CTGAGAAACCAAAACACAGCTAATGCTATGGGGGTATGAAATATGTCAAGTTTAGTGCATT | 124883 |
| Qy | 2999 | TAGAAGATTTCACACTGTATTTTGAATATATGGGAGTAAACACACCTTCAAAATTTCA | 3053 |
| Db | 124884 | TAGAAGATTTCACACTGTATTTTGAATATATGGGAGTAAACACACCTTCAAAATTTCA | 124938 |
| RESULT 12 | | | |
| AA | AA47618 | | |
| ID | AAA47618 | standard; cDNA; 2335 BP. | |
| XX | XX | | |
| AC | AAA47618; | | |
| XX | XX | | |
| DT | 08-NOV-2000 | (first entry) | |
| XX | XX | | |
| DE | KCNQ4 | Potassium channel gene. | |
| XX | XX | | |
| KW | KCNQ4; | potassium channel; cardiac arrhythmia; neonatal epilepsy; | |
| KW | deafness; | probes; treatment; therapy; transgenic animal; antibody; | |
| KW | agonist; | antagonist; tinnitus; hearing loss; neonatal deafness; | |
| KW | presbycusis; | affective disorder; Alzheimer's disease; anxiety; ataxia; | |
| KW | cognitive deficits; | compulsive behavior; dementia; depression; | |
| KW | Huntington's disease; | mania; memory impairment; motor disorders; | |
| KW | neurodegenerative disease; | Parkinson's disease; Pick's disease; | |
| KW | psychosis; | schizophrenia; spinal cord damage; stroke; tremor; ds. | |
| XX | XX | | |
| OS | Homo sapiens. | | |
| XX | XX | | |
| FH | Key | Location/Qualifiers | |
| FT | CDS | 83..2170 | |
| FT | FT | /*tag= a | |
| FT | FT | /product= "KCNQ4 Potassium channel polypeptide" | |
| XX | XX | | |
| PN | WO2000044786-A1. | | |
| XX | XX | | |
| PD | 03-AUG-2000. | | |
| XX | XX | | |
| PF | 19-JAN-2000; | 2000WO-DK000024. | |
| XX | XX | | |
| PR | 26-JAN-1999; | 99DK-00000076. | |
| PR | 19-MAY-1999; | 99DK-00000093. | |
| XX | XX | | |
| PA | (NEUR-) NEUROSEARCH AS. | | |
| XX | XX | | |
| PI | Jentsch TJ; | | |
| XX | XX | | |
| DR | WPI; 2000-548813/50. | | |
| DR | P-PSDB; AAB01476. | | |
| XX | XX | | |
| PT | Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful | | |
| PT | e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's | | |
| PT | diseases. | | |
| XX | XX | | |
| PS | Claim 1; Page 43-48; 65pp; English. | | |
| XX | XX | | |
| CC | Mutations in 3 known genes of the KCNQ branch of the potassium channel | | |
| CC | gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy | | |
| CC | and in some cases associated with deafness. KCNQ4 has been mapped to the | | |
| CC | DFNA2 locus for autosomal dominant hearing loss, and a dominant negative | | |
| CC | KCNQ4 mutation that causes deafness in a DFNA2 pedigree has been | | |
| CC | identified. KCNQ4 is the first potassium channel gene underlying non- | | |
| CC | syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ | | |
| CC | channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4 | | |
| CC | protein and the protein itself may be used in the prevention, treatment | | |
| CC | and diagnosis of diseases associated with inappropriate KCNQ4 expression. | | |

QY 1825 TTGGCTTCATTCAGTCCAGTCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1884
 Db 2036 CTGGGCGCGTGCAGTGCCTGTTCGACCCGACATCACCTCCGACTACCAAGCCCT 2095
 QY 1885 GTGGATACCAAGATCTTTGGGTTCCGCACAAA 1918
 Db 2096 GTGGACCAAGGACATCTCCGTCTCCGCACAGA 2129

RESULT 13
 ADE31698
 ID ADE31698 standard; DNA; 2335 BP.
 XX
 AC ADE31698;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 32394 gene #SEQ ID 55.
 XX
 KW Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;
 KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
 KW cardiovascular; disease; ischaemia; aortic bending;
 KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
 KW angina; cardiomyopathy; cardiac death; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003065984-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 29-JAN-2003; 2003WO-US002571.
 XX
 PR 01-FEB-2002; 2002US-0353224P.
 PR 15-MAR-2002; 2002US-0364529P.
 PR 19-APR-2002; 2002US-0373861P.
 PR 29-APR-2002; 2002US-0376287P.
 PR 12-JUN-2002; 2002US-0388080P.
 PR 24-JUN-2002; 2002US-0390977P.
 PR 03-JUL-2002; 2002US-0394130P.
 PR 10-JUL-2002; 2002US-0394797P.
 PR 21-AUG-2002; 2002US-0404904P.
 PR 23-AUG-2002; 2002US-0405450P.
 PR 04-SEP-2002; 2002US-0408070P.
 PR 06-NOV-2002; 2002US-0424300P.
 PR 05-DEC-2002; 2002US-0431042P.
 PR 05-DEC-2002; 2002US-0431079P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
 PI Stagliano N, Perodin J, Rodrigue-Way A;
 XX
 DR WPI; 2003-731468/69.
 DR P-PSDB; ADE31699.
 DR
 XX
 PT Identifying a compound capable of treating a cardiovascular disorder
 PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 1682, 6169 or 6193
 PT polypeptide or nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 55; 328pp; English.
 XX
 CC The invention relates to a method for identifying a compound capable of
 CC treating a cardiovascular disorder. The present invention identifies the
 CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
 CC 43726, 69232, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
 CC 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,
 CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 64624, 84237, 8912,
 CC 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
 CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
 CC 6585 genes in cardiovascular disease states. The methods are useful in

CC diagnosing, preventing and treating cardiovascular disorders, such as
 CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
 CC restenosis, arterial inflammation, vascular wall remodeling, coronary
 CC microembolism, tachycardia, bradycardia, pressure overload, aortic
 CC bending, coronary artery ligation, vascular heart disease, valvular
 CC disease, including but not limited to, valvular degeneration caused by
 CC calcification, rheumatic heart disease, endocarditis, or complications of
 CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
 CC heart failure, sinus node dysfunction, angina, heart failure,
 CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
 CC including but not limited to, pericardial effusion and pericarditis;
 CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
 CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
 CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
 CC cardiovascular developmental disorders. The methods may also be used for
 CC identifying compounds that modulate cardiovascular disorders. Sequences
 CC given in ADE31644-ADE31769 represent the genes and proteins that may be
 CC regulated by a compound of the invention.
 XX
 SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Query Match 16.9%; Score 518; DB 10; Length 2335;
 Best Local Similarity 60.1%; Pred. No. 3.7e-134;
 Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;
 QY 226 TACCGCGCGTGCAGAACTACCTGTATACAGCTCTGGAGAGACCCCGCGCTGGCGTTC 285
 Db 320 TACCGCGCGCTGCAGAACTGGGTCTACAGCTCTGGAGCGGCCCGCGCTGGCGTTC 379
 QY 286 ATCTACACACGCTTTCGTTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 345
 Db 380 GTCTACACACGCTTTCATATATTTTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 439
 QY 346 ACCATCCCTCAGCACACAAATTTGGCTCAAGTTGCTCTTCGATCTCGAGTTCGTCGATG 405
 Db 440 ACTATCCAGGAGCACCCAGGAACTTGCCACAGAGTGTCTCTCTCATCTTGAATTCGTCGATG 499
 QY 406 ATTGTCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 465
 Db 500 ATCGTGTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 559
 QY 466 TATAGAGGATGGCAGGAACTGAGGTTTGTCTCGAAGCCCTTCCTTCCTTCCTTCCTTCCTTC 525
 Db 560 TACCGAGGATGGCAGGATCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 619
 QY 526 ATTGTCTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 585
 Db 620 ATCGTGTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 679
 QY 586 ACGTCTGCATTCAGAACTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 645
 Db 680 ACGTCCGCGCTGGCAGCATGCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 739
 QY 646 AGGGAGGCACTTGGAAATTTACTGGGTTTCAGTGTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 705
 Db 740 CGCGCGGCACTTGGAACTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 799
 QY 706 ACAGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 765
 Db 800 ACCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 859
 QY 766 GAAAGGATGCCATAAAGAGTTTCTACATATGACAGTCTCTCTTCCTTCCTTCCTTCCTTCCTTC 825
 Db 860 GAGAAGGACGCCAACTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 919
 QY 826 ACATTGCAACTATTTGGCTATGGAGACAAACTCCCTTAACCTTCCTTCCTTCCTTCCTTCCTTCCTTC 885
 Db 920 ACATTGCAACTATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 979
 QY 886 TCTCAGGCTTCGACCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 945
 Db 980 GCTGCTGCTTCGCTTACTTGGGATCTCTTTTCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 1039

133 GAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGCGGAAGCCGCTCTTTAC 192
127 GCGGGCTCCGAGGCCCCCAAGCGCGGCAANTTTGAGAACGCCGCGGACGCGGGCGG 186
193 ACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGGGGGGTCAGAACTACTCTGAC 252
187 GGANCCGGGAAGCCCCNANCGCAAGCCCTTACCGCAAGCTGCAAGATTTCTCTAC 246
253 AACGTGCTGGAGAGACCCCGGGTGGCGGTTCACTACCAAGCTTTTCGTTTTCTCCTT 312
247 AACGTGCTAGAGCGCGCCCGGGCTGCGGTTCACTACCAAGCTTACCTGCTTCTCCTG 306
313 GTCTTTGGTCTGATTTGCTGAGTTTCTACCATCCCTGAGCAGCAAAATTGGCC 372
307 GTTTTCTCCTGCTGCTGCTTCTGTTTTCACCATCAAGGAGTACGAGAGCTCT 366
373 TCAAGTTGCCCTTCTGATCCTCGAGTTCTGATGATGTTCTGTTTGGATTTTCATC 432
367 GAGGGGCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTGAGTACTTT 426
433 ATTCGAATCTCGTCTGGGTTGCTGTTGTCGATATAGAGATGCGAAGGAGCTGAGG 492
427 GTGAGGATCTGGGCTGAGGCTGCTGTTGCGGATATCGAGGCTGGAGGGCAGGCTCAAG 486
493 TTTGCTCGAAGCCCTCTGTTGTTATAGATACCATGTTCTTATCGCTTCAATAGCAGTT 552
487 TTTGCGAAGAGCGGTTCTGTTGATGATATCAATGTTGCTGATGCTCACTTCTGCTG 546
553 GTTCTGCAAAAACCTCAGGGTAATATTTTTCACAGCTGCTGCACTCAGAACTCTCGTTTC 612
547 CTGGCTGCTGTTCCAGGGCAATGCTTTTCCACATCTGCGCTTCGGAGCTTCGGGTT 606
613 CTAAGATCTCCGATCGTGGCATGCAACGAGGGGAGGCACTTCGAAATTTACTGGT 672
607 TTGCAAAATCTTGGGATGATCCGATGAGCGAGGGGTGGACCTGGAAGCTCTTGGGA 666
673 TCAGTGGTTTATGCTCAGCAAGAAATTAATCAGAGCTTGGTATCATAGGATTTTGGTT 732
667 TCGTAGTCTAGCTCAGCAAGAGCTGGTACTGCTGCTGATTTGGCTTCTCTGC 726
733 CTATTTTTCGCTCTTCTGCTGCTATCTGGTGGAAAGGATGCGAATAAAGAGTTTCT 792
727 CTATCTCTGGCTCATTTCTGGTGTACTTGGCAGAAAGGGGTGGAATGACCACCTTGAC 786
793 ACATATGAGATGCTCTCTGGTGGGCGCAATTAATGACAACTATTGCTTATGGAGAC 852
787 ACCTACGAGATGCACTCTGGTGGGCTGATCACCTGACCATTTGGCTACGGGAC 846
853 AAAAATCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCTTGGCAT 912
847 AAGTACCTCAGACCTGGAAACGGAGGCTGCTGGCAGCGACCTTTACCTCATTTGGTGC 906
913 TCTTTCTTTGCACTTCTCGCGGCAATCTTGGCTCAGGTTTGGATTAAGATACAGAA 972
907 TCGTTCTTTGCTCTTCGCGCTGCAATTTGGGATCCGGCTTGGCCTGAAAGTCAAGAG 966
973 CAACACCGCCAGAAACACTTTGAGAAAGAGGAAACCCAGCTGCGCAACTCATTCAGTGT 1032
967 CAGATCGGCAAAACACTTTGAGAAACGGCGGAACCTTGGCGAGGCTGATCCAGTCT 1026
1033 GTTTGGCGTGTACGAGCTGAT----- 1056
1027 GCTTGAGATTTCTATGCTACTAACTCTCAGCAGCGACCTGCACTCCACGTTGGAGTAC 1086
1057 ---GAGAAATCTGTTTCCATTGCAACCTGGAGCCACACTTGAAGCCCTTGCACACCTGC 1113
1087 TACGAGCGNACAGTCACTGCTCCCCATGTACAGCTCAAACTCAAACTATGGGCGCTCC 1146
1114 AG-----CCCTACCAAGAAAGAACAGGGGGAAGAGCTCAAGCAGTCAAGAGCTTAAGTTTA 1168
1147 AGACTCATCCACCTCTGAACAGCTGGAGCTGCTGAGGAATCTCAAGAGCAAACTGGA 1206

1169 AGGAGCGAGTGGCGCATGGCTAGCCCCAGGGGGCCAGAGTATTAAAGAGCCGACAAAGCCTCAG 1228
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1229 TAGGTGACAGGAGGTCCCAAGCAGCAGCATCACAGC----- 1265
1267 AAGGGAAGAGGGGTCTCCAGGCCCCAGACGGTCCGCGGTCCCGAGTCCGAGTCAAGAT 1326
1266 --CGAGGCGAGTCCCAACCAAGTGCAGAAAGAGCTGAGCTTCAACAGACCGAACCCGCTTC 1323
1327 CTTGATGACAGCCCGAGCAAGGTGCCAAGAGCTGAGCTTTGGTGACCCGAGCCGACACA 1386
1324 CGGCCCTCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCC 1383
1387 CGCAGGCTTTCCGATCAAGGGTCTGATCCCGGAGCAATTCAGAAAGAACGACCTC 1446
1384 CTTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443
1447 CTTGGGGGAGGACATCGTAGAGGCAACAGAGCTGTAACCTGCGAGTTTGTGACTGAAGAT 1506
1444 CTCACCCCAACCTTAAACTGCTATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCA 1503
1507 CTTACCCCTGGCTCAAGTYAGCATCAGAGCCGTGTGTGTATGCGTTCTTTGSHATCT 1566
1504 AAACGGAAGTTTAAAGAACTTTACGTCATATGATGATGATGATGATGATGATGATGATGAT 1563
1567 AAGCGAAAGTTCAAGAGAGTCTGCGCCCATATGATGATGATGATGATGATGATGATGATGAT 1626
1564 TCTGCTGGTCTATCTGACATGTTGTGTAGAAATTTAAAGCCTTCAAAACAGCTTTGATCAA 1623
1627 TCGGCTGGACACTTGGATATGTTGTCGCAATCAGAGCTGCGAGCTGCGAGAGTGGACCAG 1686
1624 ATTCTTGGAAAAGGGCAAAATCAGATCAGATAAGAGCGCGAGAGAAAATAACAGCAGAA 1683
1687 ATTGTGGGGCGGGCCCCCAACAATAACGATAAGGA---TCGCAACCAAGGCCCGAGCGGA 1743
1684 CATGAGACCAAGACAGATCTCAGTATGCTCGGTGGGTGCTCAGGTGTAAGAAACAGGTA 1743
1744 ACGGAGTGGCCGGAAGACCCAGCATGATGGGACGGCTTGGGAAGGTGGGAAACAGGTC 1803
1744 CAGTCCATAGAAATCCAGCTGGAGTGCCTACTAGACATCTATCAACAG 1791
1804 TTGTCATGAAAGAAAGAGCTCGACTTCTTGGTGGAGCATCTATACAG 1851

RESULT 15
AA26588
ID AA26588 standard; DNA; 2169 BP.
XX AA26588;
AC AA26588;
DT 16-JUN-1999 (first entry)
XX Nucleotide sequence of murine KCN2 (formerly known as (KvLR1)).
DE KCN2 protein; nervous system-specific potassium channel;
KW neuronal excitability; neurotransmitter release; KCN2 modulator; ataxia;
KW myokymia; seizure; Alzheimer's disease; Parkinson's disease;
KW age-associated memory loss; learning deficiency; motor neuron disease;
KW epilepsy; stroke; ss.
XX Mus sp.
OS Mus sp.
FH Key
FT CDS 1..2169
FT /*tag= a
XX WO9907832-A1.
XX 18-FEB-1999.
XX 26-JUN-1998; 98WO-US013276.
XX

PR 12-AUG-1997; 97US-0055599P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Blumar MA, Dworetzky S, Yang W, Levesque PC, Gribkoff VK;
PI Neubauer MG, Little WA;
XX WPI, 1999-190047/16.
DR P-PSDB; AAY01530.
XX
XX New potassium channels, KCNQ2 and KCNQ3 - may be involved in
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia.
XX
XX Claim 7; Fig 10A-D; 64pp; English.
XX
CC The present sequence encodes murine KCNQ2/KVLRI. KCNQ proteins are
CC nervous system-specific potassium channels. In neurons, potassium
CC channels regulate neuronal excitability, action potential shape and
CC firing pattern, and neurotransmitter release. KCNQ modulators may be used
CC to treat disorders such as ataxia, myokymia, seizures, Alzheimer's
CC disease, Parkinson's disease, age-associated memory loss, learning
CC deficiencies, motor neuron diseases, epilepsy, and stroke
XX
SQ Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 U; 0 Other;

Query Match 16.7%; Score 511.6; DB 2; Length 2169;
Best Local Similarity 58.2%; Pred. NO. 2.2e-132;
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;

QY 73 GGCTGCTACTGCTGGGACCCGCGCCACCGCTTGGTGGCGGGGTGGCTGAGG 132
DB 67 GCCTTCTGCTGGGCTGGACCCCGCGCGCCGAGTCCACACGCGCGCGCTACTCATC 126

QY 133 GAGAGCCCGCGGGCAAGCAGCGGGCCCGGATGAGCTGCTGGGAAACCGCTCTCTTAC 192
DB 127 GCGGCTCCGAGGCCCGCCAGCGGGCAGCGTTTGGACAAAGCGCGAGCGGGCGG 186

QY 193 ACGAGTAGCAGAGCTGCGGGGCGGACGTAAGTACCGGGGGTGCAGAACTACCTGTAC 252
DB 187 GGAGCGGGGAAGCCCGAAGCGCAACGCTTCTACCGCAAGCTGCAGAAATTCCTCTAC 246

QY 253 AACGTGCTGGAGAGACCCCGCGCTGGCGCTTCATCTACACGCTTTCGTTTTCTCCTT 312
DB 247 AACGTGCTAGAGCGCCCGCGCTGGCGCTTCATCTACACGCTACGTTGTTCTTTTA 306

QY 313 GTCTTTGGTGTGTAATTTGTCAAGTGTCTTACCATCCCTGAGCACACAAAATTTGCC 372
DB 307 GTCTTCTCCTGCTTGTGCTTCTGTTTCCACCATCAAGGAGTACGAGAAGCTCT 366

QY 373 TCAAGTTCCTCTTGATCCTGAGTTCGTGATGATGTCGTTCTTTGGTTTGGAGTTCAATC 432
DB 367 GAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGGTATTCGGTGTGAGTACTTT 426

QY 433 ATTCAATCTGCTGCGGGTGTGTTGTCGATATAGAGATGCAAGGAAGTCAAGG 492
DB 427 GTGAGATCTGGGCTGAGCTGCTGTTTCCGGTATCGAGGCTGAGGGCAGGCTCAAG 486

QY 493 TTTGCTCGAAAGCCCTCTGTTTATAGATACCAATTTCTTATCGCTTCAATAGCAGTT 552
DB 487 TTTGCCAGGAAGCCGTTCTGTGTGATTGATATCATGTGCTGATTGCTCCATTGCTGTG 546

QY 553 GTTTCTGAAATACTCAGGGTAATAATTTTGGCAGCTCTGCACTCAGAAAGTCTCGTTTC 612
DB 547 CTGGCTGTGTTTCCAGGGCAATGTCTTTGCCACATCTGGGCTTCGGAGCTTGGGGTTC 606

QY 613 CTACAGATCTCCGATGCTGGCATGACCGAAGGGGAGGCACTTGGAAATTAAGTGGT 672
DB 607 TTGCAATCTTGGGATGATCCGTATGACCGAGGGGTGGACCTGGAAGCTCTTGGGA 666

QY 673 TCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTATCATAGGATTTTGGTT 732
DB 667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTACTGCTGTCATTTGGCTTCTCTGCG 726

QY 733 CTTATTTTTCGTTCTTCTTCTATCTCTGTTGAAAGGATGCCAATAAAGAGTTTCT 792
DB 727 CTCATCTGGCCTCAITTTCTGGTGTACTTTGGCAAAAAGGTTGAGATGACCACTTTGAC 786

QY 793 ACATATGCAGATGCTCTCTGGTGGGACCAATTAATTAACAACTATTGGCTATGGAGAC 852
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DB 847 AAGTACCTCAGACCTCGAACCGGAGGCTGCTGGCAGCGACCTTTACCTCTATTTGGTCTC 906

QY 913 TCTTTCTTTCGACCTCTCTGCGGCAATTTTGGCTCAGGTTTTCATTAAGATTAAGAA 972
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QY 1033 GTTTGGGCTAGTTACGCGAGCTGATGAGAAAT----- 1063
DB 1027 GCCTGGAGATCTTATGCTACTTAACCTCTCACGACCGACCTGCACTCCACGTGGCAGTAC 1086

QY 1064 -----CTGTTTCCATTTGCACTTGGAAAGCCACACTTGAAGCCCTTGAC 1107
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QY 1108 ACCTGACGCCCTACCAAGA-----AAGAAACAAGGGAA 1140
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QY 1258 ATCACGCGAGGCGAGTCCCAACAAAGTGACAGAGCTGAGCTTCAACGACCGAACCC 1317
DB 1327 CAGAGTCTTATGACAGCCCGAGCAGAGTCCCAAGAGCTGGAGCTTTGGTGAACGAGC 1386

QY 1318 CGCTTCGGGCGCTCGCTGCGCTCAAAAGTTTCTCAGCCAAAACCAAGTATGATGCTGAC 1377
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QY 1378 ACAGCCCTTGCACCTGATGATGATGATGATAAGAAAGAGTCCAGTGTGATGATCAGTG 1437
DB 1447 C---TCCCTGGGAGGAGACATCGTAGAGGACAAAGAGCTGTAACTGCGAGTTTGTGACT 1503

QY 1438 GAAGACCTCAACCCACCACTTAAACCTGCTATTGAGCTATCAGAAATTTATGAATTTTCAT 1497
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QY 1498 GTTGCAAAACGGAAGTTTAAAGAAACRTTACGTCCATATGATGATAAAGATGTCAATGAA 1557
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QY 1558 CAATATTTCTGCTGCTGATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAACAGCTGTT 1617
DB 1624 CAGTACTCGGCTGGACACTTGGATATGTTGTCCCGCATCAAGAGCCTGCACTCCAGAGTG 1683

QY 1618 GATCAAAATCTTGAAAGGGGCAATCAATCAGATGAAGAGAGCCGAGAGAAATAACA 1677
DB 1684 GACCAAGATTGGGGCGGGCCCAACAAATACGATTAAGGA---TCGCACAAAGGCCCA 1740

QY 1678 GCAGAAATGAGACCAAGAGATCTCAGTATGCTCGGTGGGTGGTCAAGTTGAAAAA 1737
DB 1741 GCGGAAACGGAGCTGCCCGAAGACCCAGCATGATGGAACGGCTTGGGAAGGTGGAGAA 1800

QY 1738 CAGTACAGTCCATAGAAATCCAGCTGAGTGCCTACTAGACATCTATCAACAG 1791

Db 1801 CAGGCTTGTCCATCGAAAGAGCTCGACTTCTTGGTGAGCACTATACACAG 1854

Search completed: April 2, 2005, 23:56:47
Job time : 1556 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 06:38:16 ; Search time 352.267 Seconds
(without alignments)
4166.553 Million cell updates/sec

Title: US-09-810-796-4
Perfect score: 4588
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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued Patents NA -QFWT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US09810796 @CGN 1 1 147 @runat 31032005 141121 18218 -NCFU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
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-FCGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 4588 | 100.0 | 3137 | 4 | US-09-590-304-1 |
| 2 | 4574 | 99.7 | 3074 | 4 | US-09-813-148-1 |
| 3 | 4527.5 | 98.7 | 2772 | 4 | US-09-825-147-1 |
| 4 | 4527.5 | 98.7 | 3111 | 4 | US-09-825-147-3 |
| 5 | 2012 | 43.9 | 2335 | 4 | US-09-492-361-1 |
| 6 | 2003 | 43.7 | 2196 | 4 | US-09-949-016-1823 |
| 7 | 1813 | 39.5 | 2169 | 3 | US-09-105-058C-22 |
| 8 | 1806.5 | 39.4 | 3237 | 3 | US-09-177-650-95 |
| 9 | 1805 | 39.3 | 3287 | 3 | US-09-105-058C-19 |
| 10 | 1800.5 | 39.2 | 3232 | 3 | US-09-177-650-1 |
| 11 | 1769.5 | 38.6 | 2273 | 3 | US-09-177-650-88 |
| 12 | 1611 | 35.1 | 2565 | 3 | US-09-105-058C-26 |

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| 13 | 1611 | 35.1 | 2914 | 3 | US-09-177-650-6 | Sequence 6, Appli |
| 14 | 1575 | 34.3 | 2814 | 3 | US-09-177-650-90 | Sequence 90, Appli |
| 15 | 1207.5 | 26.3 | 900 | 3 | US-09-105-058C-5 | Sequence 5, Appli |
| 16 | 1201.5 | 26.2 | 900 | 3 | US-09-105-058C-3 | Sequence 3, Appli |
| 17 | 1117 | 24.3 | 3181 | 3 | US-09-135-021-1 | Sequence 1, Appli |
| 18 | 1117 | 24.3 | 3181 | 3 | US-09-135-020-1 | Sequence 1, Appli |
| 19 | 1117 | 24.3 | 3181 | 3 | US-09-135-010A-1 | Sequence 1, Appli |
| 20 | 1117 | 24.3 | 3181 | 3 | US-09-444-871-1 | Sequence 1, Appli |
| 21 | 1117 | 24.3 | 3181 | 3 | US-09-597-735-1 | Sequence 1, Appli |
| 22 | 1117 | 24.3 | 3181 | 3 | US-09-444-295-1 | Sequence 1, Appli |
| 23 | 1117 | 24.3 | 3181 | 3 | US-09-597-732-1 | Sequence 1, Appli |
| 24 | 1117 | 24.3 | 3181 | 4 | US-09-597-731-1 | Sequence 1, Appli |
| 25 | 1114.5 | 24.3 | 2028 | 3 | US-09-634-920-1 | Sequence 1, Appli |
| 26 | 1114.5 | 24.3 | 2028 | 4 | US-09-840-125-1 | Sequence 1, Appli |
| 27 | 1104 | 24.1 | 3182 | 3 | US-09-135-021-5 | Sequence 5, Appli |
| 28 | 1094.5 | 23.9 | 2734 | 3 | US-09-135-021-79 | Sequence 79, Appli |
| 29 | 1094.5 | 23.9 | 2821 | 3 | US-09-135-010A-115 | Sequence 115, App |
| 30 | 1094.5 | 23.9 | 2821 | 3 | US-09-597-735-115 | Sequence 115, App |
| 31 | 1094.5 | 23.9 | 2821 | 3 | US-09-597-732-115 | Sequence 115, App |
| 32 | 1094.5 | 23.9 | 2821 | 4 | US-09-597-731-115 | Sequence 32, Appl |
| 33 | 1094.5 | 23.9 | 2924 | 4 | US-09-949-016-32 | Sequence 17, Appl |
| 34 | 1085 | 23.6 | 930 | 3 | US-09-105-058C-17 | Sequence 3215, Ap |
| 35 | 1028 | 22.4 | 2633 | 4 | US-09-949-016-3215 | Sequence 7, Appli |
| 36 | 993.5 | 21.7 | 735 | 3 | US-09-105-058C-7 | Sequence 1, Appli |
| 37 | 901.5 | 19.6 | 896 | 3 | US-09-105-058C-1 | Sequence 303, App |
| 38 | 852 | 18.6 | 582 | 4 | US-09-495-050A-303 | Sequence 305, App |
| 39 | 731 | 15.9 | 575 | 4 | US-09-495-050A-305 | Sequence 13565, A |
| 40 | 702.5 | 15.3 | 58543 | 4 | US-09-949-016-13565 | Sequence 4101, Ap |
| 41 | 506 | 11.0 | 1481 | 4 | US-09-949-016-4101 | Sequence 304, App |
| 42 | 450 | 9.8 | 284 | 4 | US-09-495-050A-304 | Sequence 296, App |
| 43 | 387 | 8.4 | 251 | 4 | US-09-495-050A-296 | Sequence 2971, Ap |
| 44 | 310 | 6.8 | 1080 | 4 | US-09-328-352-2971 | Sequence 3, Appli |
| 45 | 262.5 | 5.7 | 1927 | 3 | US-09-336-643A-3 | |

ALIGNMENTS

RESULT 1
US-09-590-304-1
; Sequence 1, Application US/09590304
; Patent No. 6649371
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHAN
; FILE REFERENCE: 2815-0136P
; CURRENT APPLICATION NUMBER: US/09/590.304
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-09-590-304-1

Alignment Scores:
Pred. No.: 0
Score: 4588.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 3137
Matches: 897
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-810-796-4 (1-897) x US-09-590-304-1 (1-3137)

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Oy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyLeu 40

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| Db | 61 | GACGGCTGCTACTGCTGGGACCCCGCGCCACAGCTCGTGGCGCGCGCGTGGCGCTG | 120 | Db | 1141 | AGTCAGAGCTAAGTTTTAAGGAGCGAGTGCGCTAGCTAGCCCGGCGCGCAGAGTATT | 1200 |
| Qy | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 | Qy | 401 | LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu | 420 |
| Db | 121 | AGGGAGAGCCCGGGGCAACAGCGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT | 180 | Db | 1201 | AAGAGCCGACAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCAGCATCACAGCCGAG | 1260 |
| Qy | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 | Qy | 421 | GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro | 440 |
| Db | 181 | TACAGAGTACGACAGCTGCGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG | 240 | Db | 1261 | GGCACTCCACCAAGCTGCAGAGAGCTGGAGCTTCAACGACCGAAACCGCTCCGGGCC | 1320 |
| Qy | 81 | TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu | 100 | Qy | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 |
| Db | 241 | TACACGCTGCTGGAGAGCCCGCGGCTGGCGCTTCACTACCAAGCTTCGTTTTCTC | 300 | Db | 1321 | TCGCTGGCCTCAAAAGTTCTCAGCCAAACACGATAGATGCTGACACAGCCCTTGCC | 1380 |
| Qy | 101 | LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 | Qy | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 |
| Db | 301 | CTTGCTTTGGTTGCTTGAATTTGTCACTGTTTCTACCATCCCTGAGCACACAAATTG | 360 | Db | 1381 | ACTGATGATGATATATGATGAAAAGAGTCCAGTGTGATGATCATGTCGAAGACCTCAC | 1440 |
| Qy | 121 | AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 | Qy | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 |
| Db | 361 | GCCTCAAGTTGCTCTTGATCTCGAGTTCGTGATGATGTCGCTTTGGTTTGGAGTTC | 420 | Db | 1441 | CCACCACCTTAAACCTGCTCATTGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG | 1500 |
| Qy | 141 | IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu | 160 | Qy | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 |
| Db | 421 | ATCATTGCAATCTGCTGCGGGTTCGTGTTGCTGATATAGAGGATGCAAGGAGACTG | 480 | Db | 1501 | AAGTTTAAAGGAAACATTACGTCATATGATGTAAGAAGTGTCAATTTGAACAATTTCTGCT | 1560 |
| Qy | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 | Qy | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| Db | 481 | AGGTTGCTCGAAGCCCTTCTGTGTATAGATACCATTTGTTTATCGCTTCAATAGCA | 540 | Db | 1561 | GGTCATCTGGACATGTTGTGTAGATTAAAGCCTTCAAAACACGTTGTCATCAAAATTTCTT | 1620 |
| Qy | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 | Qy | 541 | GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu | 560 |
| Db | 541 | GTTGTTCTCGCAAAACTCAGGGTAATAATTTTGGCCAGCTCGCACTCAGAACTCTCCGT | 600 | Db | 1621 | GGAAAAGGGCAATCATCATCAGATAAGAAGCCGAGAGAAATACACAGACACATGAG | 1680 |
| Qy | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu | 220 | Qy | 561 | ThrThrAspAspLeuSerMetLeuGlyArgValValLysValLysGlnValGlnSer | 580 |
| Db | 601 | TTCTTACAGATCTCCGCAATGTCGCGATGAGCGAGGAGGAGGACCTTGGAAATTAATCTG | 660 | Db | 1681 | ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGTTTGAAACACAGGTACAGTCC | 1740 |
| Qy | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu | 240 | Qy | 581 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 600 |
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| Qy | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 | Qy | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer | 620 |
| Db | 721 | GTTCTTATTTTTCGCTTCTCTGCTGCGGCACAAATTAATGACAACTATTGGCTATGGA | 780 | Db | 1801 | GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCCACTTTCAGTGTGAACACATCT | 1860 |
| Qy | 261 | SerThrTyrAlaAspAlaLeuTrpTyrGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 | Qy | 621 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 640 |
| Db | 781 | TCTACATATGACATGCTCTCTGCTGGGCGACAAATTAATGACAACTATTGGCTATGGA | 840 | Db | 1861 | GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGCAACAAACAGTGGCTGC | 1920 |
| Qy | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 | Qy | 641 | LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn | 660 |
| Db | 841 | GACAAACTCCCTTAACCTGGCTGGGAAGATTGCTTCTGAGGCTTTCACATCTCTGGC | 900 | Db | 1921 | TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTTCAGCTTTCATCTGACGCCAAT | 1980 |
| Qy | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 | Qy | 661 | GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln | 680 |
| Db | 901 | ATTCTTCTTCTGACCTCTCTGCGGCACTTCTTGGCTCAGGTTTGCATTTAAAGATACAA | 960 | Db | 1981 | GAGTTCACTGCCAGACTTTCACGCTTAGCCCTACTATGCACAGCTCAAGCAACACAG | 2040 |
| Qy | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaSerLeuIleGln | 340 | Qy | 681 | ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln | 700 |
| Db | 961 | GAACAACACCCGCAAAACACTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTCAG | 1020 | Db | 2041 | GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACATCTGCAACCAA | 2100 |
| Qy | 341 | CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro | 360 | Qy | 701 | IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro | 720 |
| Db | 1021 | TGTGTTTGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTCGAAGCCA | 1080 | Db | 2101 | ATAAATACGCAACCCAGCCAGAGCCCAACACTTTACAGATCCCACTCTCTCCCA | 2160 |
| Qy | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer | 380 | Qy | 721 | AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu | 740 |
| Db | 1081 | CACTTGAAGGCTTGACACCTGAGCCCTACCAAGAAAGAACAAAGGGGAGCATCAAGC | 1140 | Db | 2161 | GCCTCAAGCATCTGCCAGGCGCAAACTCTGCACCCCTAACCTGCGGGCTTACAGAA | 2220 |
| Qy | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 | Qy | 741 | SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln | 760 |
| | | | | Db | 2221 | AGCATTTCTGAGCTCACCACTGCTGTTGCTTCCCTCCAGGAAATGTTTCAGGTTGCACAG | 2280 |

Qy 761 SerAenLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2281 TCAAACTCTCACCAGGACCGTTCTATAGGAGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2341 TTGTCGTCTGTCCTCCATGGTCCGAGGACCTTGGCAAACTCTTGTCTGTGCAAAACCTG 2400
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCCAGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2461 GCGAGCCCAAGATTTTATACCCCAATGGAGGGAATCCAAATTTGTATTAACATGATGAAGAG 2520
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAProGlnProAlaArgGlu 860
Db 2521 GTGGTCCCGAGAGACAGACAGACACTTTTGTATGCGGACCCGACGCTGCCAGGGA 2580
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2581 GCTGCTTTGTCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCCTCATGTCAAACTGAAA 2691

RESULT 2

US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-148-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4574.00 Matches: 895
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 2
Query Match: 99.69% Indels: 0
DB: 4 Gaps: 0

US-09-810-796-4 (1-897) x US-09-813-148-1 (1-3074)

Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
Db 215 ATGAAGGATGTGAGTCCGGCGGGGAGGGTGTGCTGAATCGGACGCGCGAGGGGC 274
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 275 GACGCGCTGCTACTGCTGGGACCCGCGCGGCGGACGCTTGTGGCGGGGGTGGCTG 334

Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 335 AGGAGAGACCCCGCGGGCAAGCAGGGGCGCGGATAGCCTGCTGGGAAGCGCCCTCTCT 394
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 395 TACACGAGTAGCAGAGCTGCCGGCGCAACCTCAAGTACCGCGGGGTGCAGAACTACCTG 454
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 455 TACAACGTCGTGGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTTCGTTTTCTC 514
Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 515 CTTCTCTTTGGTCTTGAATTTTGTCAAGTGTGTTTCTACCATCCCTGAGCAGCAAAAATG 574
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 575 GCCTCAAGTTCCCTCTTGATCCTGGAGTTCTGATGATGATGTCGCTTTTGGTTGGAGTTC 634
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 635 ATCATTGCAATCTGTCGTGGGGTTCGTTGTCGATATAGAGGATGSCAAGGAGACTG 694
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180
Db 695 AGGTTGTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTTATCGCTTCAATAGCA 754
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 755 GTTGTTCGCAAAACTCAGGGTAATATTTTCCAGCTCTGCACTCAGAAAGTCTCCGT 814
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 815 TTCCTACAGATCTCCGCGATGTCGCGATGACCGAAGGGGAGGACCTTGGAATTTACTG 874
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 875 GGTTTCAGTGGTTTATGCTACAGCAAGGAATTAATCAAGCTTGGTATACATAGGATTTTG 934
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 935 GTTCTTATTTTTCGTCCTTCCTTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 994
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 995 TCTACATATGACAGATGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1054
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1055 GACAAAACTCCCTTAACCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1114
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1115 ATTTCTTTTTCGTCCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1174
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1175 GAACAACACCCGAGAAACACTTTTGAGAAAAAGAGAACCCAGCTGCCAACCTCATTCAG 1234
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1235 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACCTGGAAGCA 1294
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1295 CACTTGAAGGCTTGCACACCTGCGCCCTTACCAGAAAGAACCAAGGGAAGCATCAAGC 1354
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1355 AGTCAGAAAGCTAAGTTTTAGGAGCGAGTGGCATGCTAGCCCCCAGGGGCCAGAGTATT 1414

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401 QY LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420
1415 DB AAGAGCCGACAGGCTCAGTAGGTGACAGAGGTCCCAAGCAGCAGCATCACAGCCGAG 1474
421 QY GlySerProThrLysValGlnLysSerThrPheAsnAspArgThrArgPheArgPro 440
1475 DB GCGAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGCGCC 1534
441 QY SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
1535 DB TCGCTGCCGCCCTCAAAAGTTCTCAGCCAAACACCATGTATGATGCTGACACAGCCCTTGGC 1594
461 QY ThrAspAspValTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
1595 DB ACTGATGATGATATGATGAAAGAGTGCAGGAGTGCAGTGTATGATGATGAGGAGACCTCAC 1654
481 QY ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
1655 DB CCACCACTTAAACACTGTATTCGAGCTATCAGAAATTAATTAATTTCAATTTGCAAAACGG 1714
501 QY LysPheLysGluThrLeuArgProTyAspValLysAspValIleGluGlnTySerAla 520
1715 DB AGTTTAAAGAAACATTCAGTCCATATGATGATAAAGATGTCAATTTGAACAAATATCTGCT 1774
521 QY GlyHisLeuAspMetLeuLysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
1775 DB GGTCTATCTGGACATGTTGTAGAAATTAAGAGCCTTCAACACGTTGTGTATCAAAATCTT 1834
541 QY GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
1835 DB GGAAGAGGCAATCACATCAGTAAAGAGCCGAGAGAAATAAACAGCAGAAACATGAG 1894
561 QY ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
1895 DB ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954
581 QY IleGluSerLysLeuAspCysLysLeuAspIleTyGlnGlnValLysArgLysGlySer 600
1955 DB ATAGATCCAGCTGACCTGCTTCTAGACATCTATCAACAGTCTTTCGGAAGGCTCT 2014
601 QY AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
2015 DB GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 2074
621 QY AspTyrcLysSerProValAspLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
2075 DB GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCACAAACAGTGGCTGC 2134
641 QY LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
2135 DB TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTGCAGTTCAATTCGACGCCAAT 2194
661 QY GluPheSerAlaGlnThrPheTyrcAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
2195 DB GAGTTACAGTCCCGACCTTCTACGGGCTTAGCGCTTATGACAGTCAAGCAACACAG 2254
681 QY ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
2255 DB GTGCCAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCACAA 2314
701 QY IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
2315 DB ATAAATACGCCCAAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCTCCCA 2374
721 QY AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
2375 DB GCCATCAAGCATCTGCCAGCCGAGAACTCTGCACCTTAACCTCTGAGGCTTACAGGAA 2434
741 QY SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
2435 DB AGCATTTCTGACGTCACCACTGCTGTTTTCGCTTCCAGAGGAAATGTTTCAGGTTGCACAG 2494
761 QY SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780

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RESULT 3

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US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIORITY FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1

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Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 4 Gaps: 1

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US-09-810-796-4 (1-897) x US-09-825-147-1 (1-2772)

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QY 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20
DB 106 ATGAAGGATGTGAGTCGGCGGCGGAGGTGCTGTAACCTCGGAGCCGCCAGGGGC 165
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaThrLeuGlyGlyGlyGlyLeu 40
DB 166 GACGCTCTACTCTCGGCGGCGGAGGTGCTGTAACCTCGGAGCCGCCAGGGGC 225
QY 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuLysProLeuSer 60

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Db 226 AGGAGAGCGCGCGGAGCAGCGGCGCCGGATGAGCCTCTCTGGGAAAGCGCTCTCT 285
Qy TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTAGCAGAGCTGCCGCGCAACGTCAGTACCGCGCGGTGCAGAACTACCTG 345
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACAACGTCGTGGAGAGACCGCGCGCTGGGGGTTTCATCTACACGCTTTCGTTTTCTC 405
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTGTGCTTTGGTGTCTGATTTGTAGTGTTCCTACCATCCCTGAGCACAAATGT 465
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGCTCTCTGCATCTCGAGTTCTGTGATGATGTCGTCTTTGGTGTTC 525
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 526 ATCATTCGAATCTGTCTCGCGGTTCGTGTTCGATATAGAGGATGCAAGGAAGACTG 585
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 645
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTCTTCTGCAAAACTCAGGGTAATATTTTGCACGCTCTGCACTCAGAAGTCTCCGT 705
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 706 TTCTTACAGATCTCTCGCATGTGCGCATGACCGAAGGGAGGCACTTGGAAATTAATCTG 765
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 766 GTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGATAGGATTTTGT 825
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTTATTTTTCGTTCTTCTCTATCTGTGTGGAAAGAGATGCCAATAAAGAGTTT 885
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGCAGATGCTCTCTGTGGGGCACAAATACATTGCAACTATTGGCTATGGA 945
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 946 GACAAACTCCCTTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCTCTGGC 1005
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTTCTTGTGACTTCTCTCGCGCATCTTGGCTCAGGTTTTCATTAAAGTACAA 1065
Qy 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAACAACACCGCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1125
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1126 TGTGTTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCATTGCAACCTTGAAGCCA 1185
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1186 CACTTGAAGGCTTGCACACCTGACGCTTAC----- 1218
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1219 AATCAGAAGCTAAGTTTTTAAAGAGCGAGTGCATGGCTAGCCCCCAGGGGCGCAGAGTAT 1278
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420

Db 1279 AAGGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCAGCATCACAGCCGAG 1338
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1339 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACAGCCGAAACCGCTTCCGGCCC 1398
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1399 TCGTGCCTCTCAAAAGTTCTCAGCCAAACAGTGTAGATGTGTGATCATCTAGTGGAGACTCACC 1458
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1459 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGATCATCTAGTGGAGACTCACC 1518
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1519 CCACACTTAAACCTGTCATTTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1578
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1579 AAGTTTAAAGGAACATTAACGTCATATGATGTAAAGATGTCAATTGAAACAATTTCTGCT 1638
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1639 GGTCACTCTGGACATGTTGTGTAGAAATTAAGACCTTCAACACGCTGTGTGATCAAAATCTT 1698
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1699 GGAAGAGGCAATACACATCAGATAGAAAGAGCCGAGAGAAATAAACAGCAGAACATGAG 1758
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1759 ACCAGACGATCTCAGTATGCTCGTCTGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1819 ATAGATCCAAAGCTGGACTGCTCTAGACATCTATCAACAGGCTCTTCGGAAAGGCTCT 1878
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1879 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1938
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1939 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCCACAAAAACAGTGGCTGC 1998
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1999 TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTGACAGTTCTTCTGACGCCAAT 2058
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2059 GAGTTCAAGTCCAGACTTCTACGCGCTTAGCCCTACTATGCAGTCAAGCAACACAG 2118
Qy 681 ValProLysSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2119 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCATTTGCAAAACCAA 2178
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2179 ATAAATACGGCACCCCAAGCCAGAGCCCAACAATTTTACAGATCCCACTCTCTCTCCA 2238
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2239 GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCTTAACCTTCAGGCTTACAGGAA 2298
Qy 741 SerLysSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2299 AGCATTTCTGACGTCAACCTGCTGCTTGTTCCTCCAGGAAAAATGTTTCAGGTTGACAG 2358
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2359 TCNAATCTCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAAACTCTG 2418

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QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2419 TTGTCGTCTCTCCATGTTCCGAGGACTTGGGCAAAATCTTTGTCGTGCAAAACCTG 2478
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2479 ATCAGGTCGACCGAGGAACCTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2538
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2539 GCACCCCAAGATTTTACCCCAATAGGAGGAATCCAAATGTTTATAACTGATGAAGAG 2598
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2599 GTGGGTCCGGAAGACAGACAGACACTTTTGTATGCCGCGACCGCCCTGCCAGGGAA 2658
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2659 GCTGCCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2718
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2719 AAGGACGCGGAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2769
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RESULT 4
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 676736el Human Ion Channel Protein and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 4 Gaps: 1

US-09-810-796-4 (1-897) x US-09-825-147-3 (1-3111)
QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
Db 165 ATGAGAGTGTGAGTGTGGCCGGGCGAGGGTGTCTGCTGAACCTCGGACCGCGCGGGGC 224
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrIleuGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGTCTACTGTCTGGGACCCCGCGCGGCACCGCTCGGTGGCGCGCGGTGGCCG 284
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 285 AGGGAGAGCCCGCGCGGCAGACAGGGGGCCCGGATGAGCTGTCTGGGAGAGCCGCTCTCT 344
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QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 345 TACACAGTAGGACGAGCTGCCGGCGCAACGTCAAGTACCGGGGGGTGCAGACTACCTG 404
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 405 TACACAGTGTCTGAGAGACCCCGCGGTGGGGTTCATCTACACGCTTTCGTTTCTC 464
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTGTGCTTTGGTGTGATTTTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATG 524
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTGTCTTGTATCTCGAGTTCGTGATGATGTTGCTCTTTGTTGGATTC 584
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyLeu 160
Db 585 ATCATTCGAATCTGCTCGGGTTCCTGTTTCGATATAGAGGATGGCAAGAAAGACTG 644
QY 161 ArgPheAlaArgProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 645 AGTGTTCGTCGAAAGCCCTTCGTGTATAGATACCATGTTCTTATCGCTTCAATAGCA 704
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeu 200
Db 705 GTTGTTCGCAAAACTCAGGGTAATAATTTTGCACGCTCTGCACCTCAGAAAGTCTCCGT 764
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeu 220
Db 765 TTCTACAGATCCTCCGATGTCGTCGATGGACGAAAGGGGGGACCTTTGGAAATTACTG 824
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 825 GGTTCAGTGTGTTATGCTCACACAGGAATTAATCACAGCTTGTGTACATAGGATTTTG 884
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTATTTTTCGTCCTTTCCTTGTCTATCTGCTGGAAGAGATGCCAATAAAGAGTTT 944
QY 261 SerThrTyrAlaAspAlaLeuTrpTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGAGATGCTCTCTGTTGGGCGACAAATACATTGACAACTATTGGCTATGGA 1004
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAAACTCCCTTAACCTTGGCTGGGAAGATGCTTCTGCAGGCTTTGCACCTCTTGGC 1064
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTTTCGCTTCTGCGCGCATCTTGGCTCAGGTTTGCATTTAAAGTACAA 1124
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaLeuIleGln 340
Db 1125 GAACAACACCCGACAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCGCAACTCATTCAG 1184
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTTGGCGTAGTACGCGAGCTGATGAGAAATCTGTTTCCATTCGAACCTGGAAGCCA 1244
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1245 CACTTGAAGGCTTTGACACCTCGAGCCCTTACC----- 1277
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1278 AATCAGAAAGCTAAGTTTTTAAGAGCGAGTGGCGCATGGCTAGCCCCCAGGGCGCAGATTT 1337
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1338 AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCTCCACAGCACCGACATCACAGCCGAG 1397
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QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
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QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1458 TCGCTGCGGCTCAAAAGTTCTCAGCCCAAAACGAGTATAGATGCTGACACAGCCCTTGGC 1517
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1518 ACTGATGATGATATATGATCAAAAGAGTGCAGTGTGATGTATCAGTGGAGACCTCAC 1577
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1578 CCACACATTAAACCTGTCATTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1637
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1638 AAGTTTAAGGAAACATTAGCTCCATATGATGTAAAGATGTCTTTGAACATATTTCTGCT 1697
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1698 GGTCACTCGACATGTTGTGTAGATTTAAAGCCCTTCAAAACAGCTGTGATCAAAATTCCT 1757
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1758 GGAAAGGGCAAAATCACATCATGATGAAGAGCCGAGAGGAGAAATTAACAGCAGAAATGAG 1817
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1818 ACCACAGACATCTCAGTATGCTCGGTGGGTGTCAGGTTTGAAGTTGAACAGTACAGTCC 1877
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAATCCAGCTGAGCTGCCTACTAGACATCTATCAACAGTCTCTTCGGAAAGGCTCT 1937
QY 601 AlaSerAlaLeuAlaLeuSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCAACCTTTTGAATGTGAACAGACATCT 1997
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGACAAACAGTGGCTGC 2057
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTGCAGTTCATTCGACGCCAAT 2117
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTTCAGTGGCCAGACTTCTACGCGCTTACGCCCTTACTATGACAGTCAAGCAACACAG 2177
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2178 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2237
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2238 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2297
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2298 GCCATCAAGCATCTGCCAGGCGCAAGAACTCTGCAACCCCTAACCCCTGCAAGGCTTACAGAA 2357
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2358 AGCATTTCTGAGCTCACCACTGCTTGTGTGCTCTCAAGGAAATGTTTCAGTGTGCACAG 2417
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2418 TCAAATCTCACCAAGACCGTTCTATGAGAAAGCTTTGACATGGGAGGAGAACTCTG 2477
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
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Db 2478 TTGTCTGTCTGTCCATGGTCCGAAGACTTGGCAAAATCTTTGTCTGTGCAAAACCTGT 2537
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2538 ATCAGTTCGACCGAGGAACCTGAATATACAACTTTTCAGGAGGTGAGTCAAGTGGCTCCAGA 2597
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2598 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG 2657
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2658 GTGGTCCCGAAGACAGACAGACACTTTTGATGCGCCAGCCAGCTGCCAGGGAA 2717
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2718 GCTGCTTTGCATCAGACTCTCTAAGGACTCGAAGGTCCAGATCATCTCAGAGCATTTGT 2777
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2778 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2828

RESULT 5
US-09-492-361-1
; Sequence 1, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492.361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

Alignment Scores:
Pred. No.: 1,91e-195 Length: 2335
Score: 2012.00 Matches: 437
Percent Similarity: 65.45% Conservative: 82
Best Local Similarity: 55.11% Mismatches: 136
Query Match: 43.85% Indels: 138
DB: 4 Gaps: 16

US-09-810-796-4 (1-897) x US-09-492-361-1 (1-2335)
QY 8 ArgGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
Db 127 CGGGGAGCCCCCGCGGAGCTAGTGGCGCTCAGGC----- 165
QY 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeuArgGluSerArgArgGlyLys 47
Db 166 ---CGTCAGAGCGAAACAGGCGGAGCGCGG-----CGGGGGCGG 201
QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
Db 202 CTCGCCGCGCGCTCGGCTCTCGGCGAGCCCTTCGCCGCGGCGCGCCCTCCCTGG 261
QY 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLys 73
Db 262 GCGGGGCTCCGGCTCGGGCTCGGCTCGGCGGCGGCTCTCGGCGGCGGCGGCGGCTA 321
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QY 73 rArgArgValGlnAsnTyrLeuTyrAsnValLeuGluAArgProArgGlyTrpAlaPheIl 93
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 QY 93 eTyrHisAlaPheValPheLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113
 Db 382 CTACACGCTCTTATATTTTGGTGTCTTCAGCTGCTGTGTGTGTGTGTGTGTGTGT 441
 QY 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuLeuValMetIl 133
 Db 442 TATCAGAGGACACGAGAACTTGCACAGAGTGTCTCTCATCTTGGAAITGGTGATGAT 501
 QY 133 eValValPheGlyLeuGluPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 153
 Db 502 CGTGGTTTTCGCTTGGAGTACATCGTCCGGTCTGTGTGTGTGTGTGTGTGTGTGT 561
 QY 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIl 173
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 QY 173 eValLeuIleAlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193
 Db 622 CGTGTTCGTGGCTCGGTGGCGTTCATCGCGCGGTATACCCAGGCGCAACATCTTCGCC 681
 QY 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr 213
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 Db 742 CGCGGCGACCTGAGAGT 801
 QY 233 rAlaTrpTyrIleGlyPheLeuValLeuLeuPheSerSerPheLeuValTyrLeuValGl 253
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 QY 293 rAlaGlyPheAlaLeuLeuGlyLysPhePheAlaLeuProAlaGlyIleLeuGlySe 313
 Db 982 TGT 1041
 QY 313 rGlyPheAlaLeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAs 333
 Db 1042 CGGCTTTGCTGAGGTCCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1101
 QY 333 nProAlaAAsnLeuLeuGlnCysValTrpArgSerTyrAlaAlaAsp---GluLysSe 352
 Db 1102 GCGGCGAGCAGCACTCATCCAGGCTGCTGGCGCTGTACTCCACGATATGAGCGGGC 1161
 QY 352 rValSerIleAlaThrTrp----- 358
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 QY 358 ----- 358
 Db 1222 CCTCTTGTGTGAGCAGTGCACCGGCGCCGCAATGGGGGCTTACCGGCCCTGAGGTGGC 1281
 QY 359 -----LysProHisLeuLysAlaLeuHisTh 367
 Db 1282 GCGGGCGCGGTACCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1341
 QY 367 rCysSerProThrLysLysGluGlnGlyGluAlaSerSerSerGlnLysLeuSerPheTh 387
 Db 1342 GCGGGCGCAGCAGCT 1392
 QY 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405

Db 1393 AGACGCGATCCGATGGGAGCTCCAGCGGGAGCGGTCTCTTCAAAGCAGCAGCTGGC 1452
 QY 405 aSerValGlyAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424
 Db 1453 ACTCTCAACAATGCGCACCTCCCAAGCAGCAGCGGTGGGTGAGGCCACAGCCCGCCAC 1512
 QY 424 rLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLe 444
 Db 1513 CAAGGTGCAAAAGAGCTGGAGCTTCAATGACCGCACCCTTCGCGGATCTCTGAGACT 1572
 QY 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464
 Db 1573 C-----AAACCCCGCACCTCTCTGAGGATGCC---CCCTCAGAGGAAGT 1614
 QY 464 lTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLys 484
 Db 1615 AGCAGAGAGAGAGAGTACACAGTGTGAGCTACGGTGGAGCAGCATCATCCCTGCTGTGAA 1674
 QY 484 sThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGl 504
 Db 1675 GACAGTCATCCGCTCCATCAGGATTTCTCAAGTTCTCTGTGTGGCCMAAAGGAAATTCAGGA 1734
 QY 504 uThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAs 524
 Db 1735 GACACTGCGACCTACGACGTGAAGGACGTCTATTGAGCAGTACTCAGCAGGCCACCTGGA 1794
 QY 524 pMetLeuCysArgLysLeuSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGl 544
 Db 1795 CATGCTGGGCGGATCAAGAGCTCGAACTCGGTGGACCAAAATTTGTGGTGGGGGG-- 1852
 QY 544 nIleThrSerAspLysSerArgGlu-----LysIleThrAlaGluHisGluTh 561
 Db 1853 -----CCCGGGGACAGGAAGCCCGGAGAGGCGCAAGGGGCGCTCCGACCGGAGT 1908
 QY 561 rThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIl 581
 Db 1909 GGTGGATGAATCAGCATGATGGAGCGGTGGTCAAGGTGGAGAGCAGGTGCGTCCAT 1968
 QY 581 eGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAl 601
 Db 1969 CGACACAGCTGACCTGCTGTGGCTTCTATTGCGCTGCTGCGCTCTGCGCACCTC 2028
 QY 601 aSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAs 621
 Db 2029 GGCC-----AGCCTGGCGCGCGTGAAGTGGCGCTGTTCCGCCCGCAGCATCCTCCGA 2082
 QY 621 pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641
 Db 2083 CTACACAGCCCTGTGACCCAGCAGGACATCTCGTCTCCGACAGCAGCGCTCAGC---AT 2139
 QY 641 uSerArgSerThrSerAlaAsnIleSerArgLysLeuGlnPheIleLeuThrProAsnGl 661
 Db 2140 CTCCGCTGCTGTCAGCACCACATGAGCTGAGG----- 2173
 QY 661 uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681
 Db 2173 ----- 2173
 QY 681 lProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIl 701
 Db 2174 -----ACTTCTCAGAGGCGGCGAGCACA----- 2197
 QY 701 eAsnThrAlaProLysProAlaAlaProThrThrLeu-GlnIleProProLeuProA 721
 Db 2198 -CGGCGAGCCCGCGGCTGCGCTGCGACTGCGCTCTGAGCGCTCCGAGCTCTCTCGT 2256
 QY 721 lAlaLysHisLeuProArgProGluThrLeuHis 732
 Db 2257 ACTTGAACCTCACTCCCTCAGCGGGAGAGAGACCAC 2291
 RESULT 6
 US-09-949-016-1823


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; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1823

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Db 1678 CTGCAAACTCGGTGGACCAAAATGTGGTTCGGGGG-----CCCGGGACAGCAAGGCC 1731
Qy 552 ArgGlu-----LysleThrAlaGluHisGluThrThrAspAspLeuSerMetLeu 568
Db 1732 CGGGAGAGGCGCAAGGGCCCTCCACCGGAGGTGGTGAATGAATCAGATGATG 1791
Qy 569 GlyArgValValLysValGlnValGlnSerileGluSerLysLeuAspCysLeu 588
Db 1792 CGACGGTGTCAAGTGGAGAGCAGGTGAGTCCATCGAGCACAAGCTGGACTGCTG 1851
Qy 589 LeuAspIleThrGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSer 608
Db 1852 TTGGCTTCTATTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1905
Qy 609 PheGlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSer 628
Db 1906 GTGAAGTGGCGCTGTTTCGACCCGACATCATCCGACTACACAGCCCTGTGGACAC 1965
Qy 629 LysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsn 648
Db 1966 GAGGACATCTCGTCTCGCACAGCAGCTCAGC---ATCTCCGCTCGGTGAGCAGCAC 2022
Qy 649 IleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyr 668
Db 2023 ATGGACTGAGGG----- 2034
Qy 669 AlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGly 688
Db 2035 -----ACTTCTCAGAGGAGGCG 2052
Qy 689 SerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAla 708
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Qy 709 AlaProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgPr 728
Db 2080 GCTCCGACTGCCCTCTGAGGCTCCGAGCTCCTCGTACTTGAACCTCACTCCCTCAGG 2139
Qy 728 oGluThrLeuHis 732
Db 2140 GGAGAGACACCAC 2152
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RESULT 7

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; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22
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Alignment Scores:
Pred. No.: 4,26e-175 Length: 2169
Score: 1813.00 Matches: 393
Percent Similarity: 65.68% Conservative: 72
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Best Local Similarity: 55.51% Mismatches: 153
Query Match: 39.52% Indels: 90
DB: 3 Gaps: 17
US-09-810-796-4 (1-897) x US-09-105-058C-22 (1-2169)
Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db 100 TCCACACGCGAGCGCGCTACTCATCGCGGCTCCGAGGCCCCCAAG-----CGC 150
Qy 37 GlyGlyLeuArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 151 GGCACGCGTTTGTAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 195
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
Db 196 AAGCCC-----CCGAAGCGCAACGCCCTTCTACCGCAAGCTG 231
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 232 CAGAAATTTCTCTACAAAGTGTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 291
Qy 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db 292 TACGTGTCTCTTTAGTCTTCTCTCTGCTTGTGCTTCTGCTTCTGCTTCTGCT 351
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetIleValValPhe 136
Db 352 TACGAGAAGAGCTCTGAGGGGCGCTCTACATCTTGGANATCGTGACTATCTGGTATTC 411
Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
Db 412 GGTCTTCAGTACTTTGTGAGGATCTGGGCTGCGGCTGCTGCTGCGGTATCGAGGCTG 471
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
Db 472 AGGGGAGGCTCAAGTTTGCAGAGCGGCTTCTGTGTGATTTGATATCATGCTGCTGAT 531
Qy 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 532 GCCTCCATTTGCTGTGCTGGCTGGTTCACAGGGCAATGCTTTGGCCACATCTGCGCT 591
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThr 216
Db 592 CGGAGCTTGGGTTCTTTGCAAACTTTCGGATGATCCGTATGGACCGGAGGCTGGCACC 651
Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
Db 652 TGAAGCTCTTGGGATCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCTGGTAC 711
Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db 712 ATTGGCTTCTCTGCTCATCTCGCTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 771
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276
Db 772 AATGACCATTTGACACCTACGAGATGCACTCTGTGGGTCTGCTGCTGCTGCTGCTGCT 831
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 832 ATTGGCTACGGGGACAAGTACCTCAGACCTGGAAACCGGGAGGCTGCTGGCAGCGCTTT 891
Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 892 ACCCTCATTTGGTCTCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
Qy 317 LeuLysValGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAla 336
Db 952 CTGAAGTCCAAAGAGCAGCATCGGCAAAACACATTTGAGAAACCGCGGAAACCTCGCGCA 1011
Qy 337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 1012 GGTCTGATCCAGTCTGCTGGAGATTCTATGCTACTAACTCTTCACGACCGCCTGCAC 1071
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177 AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
178 GCTTCCATTGGGTCCTGGCGCGCGCTCCAGGGCAACCTTTGGCACAATCTGGCGTC 718
197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThr 216
719 CGAGAGCTTGGCTTCTTCAGATTCTGGGATGATCGCATGGACCGCGGGAGGACAC 778
217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTrpTyr 236
779 TGAAGCTGCTGGCTCTGTCTATGCCACACAGAGAGCTGGTCACTGCTCGTATC 838
237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
839 ATCGGCTCTCTTGTCTATCTCGCTGCTCTGTGTGTCTGTGTGTGTGTGTGTGTGT 898
257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276
899 AACGACCACTTGTACACCTACCGGATGACATCTCTGTGTGGGCTGATCAGCTGACCA 958
277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
959 ATTGGCTACGGGGACAGTACCTGAGACCTGGAAACGCGAGGCTCTTGGCGCAACCTTC 1018
297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
1019 ACCCTCATCGGTGCTCTCTTCTCGCTGCTCTCGAGCATCTTGGGCTTGGGTTGGC 1078
317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgAsnProAlaAla 336
1079 CTGAGGTTTCAGGACGACGACGAGGAGGACATTTGAGAGAGGCGGAAACCGCGAGCA 1138
337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349
1139 GGCCTGATCCAGTCGGCTGGAGATTACGCCAACCACTCTCGCGCAGACCTGCGAC 1198
350 -----GluLysSerValSerIleAlaThrTrpLys----- 359
1199 TCACGTGGCAGTACTACGAGGAGGAGGTACCGTGCCTATGACAGTTGCAAACTCAA 1258
360 -----ProHisLeuLysAlaLeuHisThrCysSerProThr 371
1259 ACCTACGGGCTCCAGACTTATCCCGCTGTAACACAGCTGGAGCTCTGAGGAACCTC 1318
372 LysLysGluGlnGlyGluAla----- 378
1319 AAGAGTAAATCTGGACTCGCTTTCAGGAAGGACCCCGCGGAGCGCTCTCCAAGTAA 1378
379 -----SerSerSerGlnLysLeu 384
1379 GGCAGCCCTGCAGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1438
385 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 404
1439 AGTTTGAAGATGTGTCTCTTCTCAGCCCGGAGGCTGGCTGCCAAGGGAAGGGG 1495
405 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlySer 422
1496 TCCCGCGAGCCCGAGTGTGAGCGGTCCAGCGCGCGAGCCGAGGCTCGAGGACAGC 1555
423 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 442
1556 CCCAGCAAGTGTCAGAGCTGAGCTTTCGGGACCGGAGCGCGGAGCGGAGGCTTTC 1615
443 ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp 462
1616 CGATCAAGGGTCCCGCTACCGGAGAACTCAGAA-----GAGCAAGGCTTCCCGGAG 1672
463 AspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro 482
1673 GACATTGTGATGACAGAGCTGCTCCCTGCGAGTTTGTGACCGGAGGACCTGACCCGCG 1732
483 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 502

1733 CTCAAAGTCAGCATCAGAGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1792
503 LysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHis 522
1793 AAGGAGAGCTCGGCGCTTACGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1852
523 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 542
1853 CTGGACATCTGTCTCGAATTAAAGCTGTGAGTCCAGAGTGGACCCAGATCTGTGGGCG 1912
543 GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlnThrThr 562
1913 GGCCAGCGCATCAGGAC-----AAGGACCGCACCAAGCGCGCGCGGAGCGGAGTGC 1969
563 AspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlu 582
1970 GAGGACCCAGCATGATGGAGCGCTCGGGAGGTGGAGAGCAGAGTCTGTTCATGGAG 2029
583 SerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer 602
2030 AAGAAGCTGGACTTCTGTGTGAATACTATCATGCAG-----CGATGGGC----- 2074
603 AlaLeuAlaLeuAlaSerPheGlnIleProPheGluCys----- 616
2075 -----ATCCCCCGACAGACCGAGCGCTACTTTGGGGCC 2110
617 -----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 633
2111 AAGAGCGGAGCGCGCGCGCTTACACAGCGCGGAGACAGCGCGGAG----- 2161
634 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 653
2162 CATGTCAGACGACGCGCTGCTTGTCAAGATGCTGCTGCCAGAGTCTCCAGCGC----- 2218
654 GlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThr 673
2218 ----- 2218
674 MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAla 693
2218 ----- 2218
694 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrLeu 713
2219 -----CAGAAGAACTTCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2257
714 GlnIleProPro-----ProLeuProAlaIleLysHis 724
2258 CAGTGTCCGCTCCACTCTGCGCAGCCACAGAGCCACCGCGC-----CCAGGCGCAGG 2316
725 LeuProArg-----ProGluThr-----LeuHis-----ProAsnProAlaGlyLeuGln 740
2317 CTCCCGCGTGGGACCAACGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2376
740 uSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaG 760
2377 GTCGCTGCGCTTACCGCGCGGCGGCAACCGCGCGCATGTGAGTCTCTGCGGAGGAGGA 2436
760 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGly 778
2437 CACCGCGGTGAGGCGCGCGCGGAGGAACTCTGGGAGACG-----GA 2481
778 uThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValG 798
2482 CAGCTCCAGTCCAAAGGAGAACTGTGCTCTCAACAGCTGCTACGCGCGCGGCTT 2541
798 nAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerG 818
2542 CAGCATCTCCAGTCCAAAGGAGAACTGTGCTCTCAACAGCTGCTACGCGCGCGGCT 2601
818 ySerArgGlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAs 838

Db 2602 GCCTGTGCCAAAGTCAGGCCCTACATTGGCGGAGGAGTCAGAC-----ACCGA 2652
Qy 838 pGluGluVal-----GlyPro-----GluGluThrG1 847
Db 2653 CTCGACCTCTGTACCCGCGTGGGCCCCCGCCAGCTCGGCCACCGCGAGGGTCCCTT 2712
Qy 847 uThrAspThrPheAspAlaA1aProGlnProAlaArgGluAlaA1aPheAlaSerAspSe 867
Db 2713 TGGTACCTGGGTGGCGCGCGGCCCGCCAGGAAGTGAAGCGCGCTGGGC----- 2764
Qy 867 rLeuArgThrGlyArgSerArgSerSerGlnSerileCysLysAlaGly 883
Db 2765 ----CAGTGGAGCCCGCGCGCCCTCTCTCAGCACGGTGCCTCCGAGT 2809

RESULT 9

US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; SOFTWARE: Patent In Ver. 2.1
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 5,98e-174 | Length: | 3287 |
| Score: | 1805.00 | Matches: | 414 |
| Percent Similarity: | 59.13% | Conservative: | 101 |
| Best Local Similarity: | 47.53% | Mismatches: | 188 |
| Query Match: | 39.34% | Indels: | 169 |
| DB: | 3 | Gaps: | 21 |

US-09-810-796-4 (1-897) x US-09-105-058C-19 (1-3287)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db 160 TCCACCCGGGACGGGCGCTGTGATCGCGGCTCCGAGGCCGCCAAG-----CGC 210
Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 211 GGCAGATCCTCAGCAAACTCGCGCGGCGCGCGCGCC-----GGG 255
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
Db 256 AAGCCC-----CCCAAGCGCAACGCCCTTACCGCAAGCTG 291
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 292 CAGAATTTCTCTACAACTGTGAGCGCGCGCGCGCTGGCGCTTCATCTACACGCC 351
Qy 97 PheValPheLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlu 116
Db 352 TACGTGTTCTCTCGGTGTTCTCTCGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 411
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPhe 136
Db 412 TATGAGAAGAGCTCGGAGGGGGCCCTCTACATCTCTGGAAATCGTGAATCTGTGTGT 471

Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysCysArgTyrArgGlyTyr 156
Db 472 GGCCTGGAGTACTTCGTGGCGGATCTGGGCCGAGGCTGCTGTCGGGTACCGTGGCTGG 531
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
Db 532 AGGGGGGGCTCAAGTTGGCCGAAACCGCTTCTGTGTGATGTGACATCATGGTGTCTATC 591
Qy 177 AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 592 GCCTCCATTGGGTGCTGGCCCGCGCTCCAGGGCAACGCTTCTTGGCACATCTGGGCTC 651
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThr 216
Db 652 CGGAGCCTGCGCTTCTCGAGATTCTCGGATGATCGCATGGACCGCGCGGAGGACACC 711
Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
Db 712 TGGAAAGTGTGGGCTCTGTGGTCTATGCCACAGAGAGAGTGGTCACTGCTGTGTGAC 771
Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db 772 ATCGGCTTCTTCTCTCATCTCGCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 831
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThr 276
Db 832 AACGACCACCTTTGACACCTACCGGATGCACTCTGTGGGGCCTGATCAGCTGTACACC 891
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 892 ATTGGCTACGGGGACAAGTACCCACAGACCTGGGAACCGGACGGCTCTTGGCGCAACCTTC 951
Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 952 ACCCTCATCGGTGCTCTTCTTCTGCGCTGCTGCGAGCATCTTGGGGTCTGGGTTCGCC 1011
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
Db 1012 CTGAAGGTTTCAGGAGCAGCAGCAGGAGACACTTTGAGAAGAGGCGGAGCCCGGAGCA 1071
Qy 337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 1072 GGCCTGATCCAGTCGGGCTGGAGATTTTACGCCACCAACCTCTCGCGCACAGACCTGCAC 1131
Qy 350 -----GluLysSerValSerIleAlaThrTrpLys----- 359
Db 1132 TCCACGTGGCAGTACTACGAGGAACGTCACCGTCCCATGTACAGTTCCGAAACTCAA 1191
Qy 360 -----ProHisLysAlaLeuHisThrCysSerProThr 371
Db 1192 ACCTACGGGGCTCCAGACTTATCCCGCGCTGAACCCAGCTGGAGCTCTGAGAAACCTC 1251
Qy 372 LysLysGluGlnGlyGluAla----- 378
Db 1252 AAGAGTAATCTGAGCTCGCTTTTCAGGAAGACCCCGCGCGAGCCCTCTCCAGGTAAA 1311
Qy 379 -----SerSerSerGlnLysLeu 384
Db 1312 GGCAGCCGTCACAGGGCCCTCTGTGTGATGTCGCCCGGACGCTCTAGCCAGAGGTC 1371
Qy 385 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 404
Db 1372 AGTTTGAAGATCGTGTCTCTCCAGCCCCCGAGCGGTGGCTGCTGCAAGGGGAAGGG 1428
Qy 405 AlaserValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlyLysSer 422
Db 1429 TCCCGGAGGCCACAGACTGTGAGCGGTGTCACCCAGCGCCGACAGAGCTCGAGACAGC 1488
Qy 423 ProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgProSerLeu 442
Db 1489 CCCAGCAAGGTGCCAAGAGCTGAGGCTTCGGGAGCCCGCAGCCCGGAGCCCGAGCTTTC 1548

| | | | |
|----|------|--|------|
| Qy | 277 | IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe | 296 |
| Db | 959 | ATTGGCTACGGGACAGTAGTACCCACAGCTGGAAACGCAGGCTCTTGGCGCAACCTTC | 1018 |
| Qy | 297 | AlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla | 316 |
| Db | 1019 | ACCTCATCGGTGTCCTCTTCGCGCTGCTGCAGGCATCTTGGGGTCTGGGTTTGCC | 1078 |
| Qy | 317 | LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla | 336 |

[illegible]

DD T199 TCCACGTGGCAGTAC TACGAGCGATCGGTCACCGTGTCCCA TGTACAGTTCGCATACATCATTA T230

| | | | |
|----|------|---|------|
| Qy | 360 | PHHSHHLLYSAIARALAHSHINIRCYSSSRPPIRIR | 371 |
| | | | |
| | | | |
| | | | |
| | | | |
| Db | 1259 | ACCTACGGGGCTCCAGACTTATCCCCCCCTGAACGCTGGAGCTGCTGAGGAACCTC | 1318 |
| | | | |
| Qy | 372 | LYSLYSGLUGLNGLYGLUALA | 378 |
| | | | |
| | | | |
| | | | |
| Db | 1319 | AAGAGTAAATCTGGACTCGCTTTTCAGGAAGGACCCCGCGGAGCGCTCTCCAAGTAA | 1378 |

| QY | 379 | 1379 | 1438 |
|----|---|------|--------------------------|
| Db | GGCAGCCCGTCAGAGGGCCCCCTGTGTGATGTCGCCCGGACGCTCTAGCCAGAGGTC | | SeiSeiSeiGlnGlySerLeu381 |

D_b

1439 AGTTTGAAGATCGTGTC---TTCTCAGCCCCGAGCGTGGCTGCCAAGGGGAAGGGG 14955

43
105
1496
Db

Db

| | | |
|------|--|------|
| 1556 | CCACGACGAGGTGCCCAAGAGCTGGAGCTTCGGGGACCGCAGCCGGGACGCCAGGCTTTC | 1615 |
|------|--|------|

D_b 1616 CGATCAAGGGTCCCGGCTACGCGCAACTCAGAA---GAAGCAAGCCTCCCCGGAGAG 1672

Db
1673 GACATTGGGATGACAAGAGCTGCCCTTGGAGTTTGTGACCGAGGACTGACCCCGGC 1732

Db

1733 CTCAAAGTCAGCATCAGAGCCGTTGTGTGTCATGCGGTTCTGGTGTCCAGCGGAAGTTC

Db
1793 AAGGAGGACCTGGGGCCCTACGACGTCATGGACGTCATCGAGCAGTACTCAGCGGGCCAC 1852

Db
1853 CTGGACATGCTGCCCGAATTAAAGAGCTGCAGTCCAGATGGGACCAAGATCGTGGGGCGG 1912

1913 GGCCAGCGATCAGGAC---AAGGACCGCACCAAGGGCCGGCCGAGCGGAGCTGCCC 1969

DB 1970 GAGGACCCAGCATGTGGGACGGCTCGGGAAGGTGGAGCAGGCTTGTCATGGAG 2029

Db 892 ACCCTCATTTGGTCTCGTCTTTCTTCTCGGGTGGCATTTTGGGATCCGGCTTTGCC 951
Qy 317 LeuylsValGlnGluGlnHiArgGlnlyHisPheGluylsArgArgAsnProAlaAla 336
Db 952 CTGAAGTCTCAAGAGCAGCATCGGCAAAACACATTTTGAGAAACGGCGGAACCCCTGCGGCA 1011
Qy 337 AsnLeuileGlnCysValTrrArgSerTyAlaAlaAasp----- 349
Db 1012 GGTCTGATCCAGTCTGCTGGAGATTCATGCTACTAACTCTCAACGACCGACCTGAC 1071
Qy 350 -----GluylsSerValSerIleAlaThrTrpLys----- 359
Db 1072 TCCAGTGGCAGTACTAGACGCGACAGTCACTGTCCTCCATGTACAGTCTCAAACTCAA 1131
Qy 360 -----ProHisLeuylsAlaLeuHisThrCysSerProThr 371
Db 1132 ACCTATGGGGCTCCAGACTCATCCACTCTGAACCAAGCTGGAGCTGCTGAGGAATCTC 1191
Qy 372 LysLysGluGlnGlyGluAlaSerSerSerGlnLysLeuSerPheLysGluArgValArg 391
Db 1192 AAGACAAATCTGGA-----CTCACCTTCAGGAAGGAGCCACAG 1230
Qy 392 -----MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGly 408
Db 1231 CCAGAGCCATCACCAAGCCCCGAGGATGCTGCCAAGGGAAGGGGTCTCCCCAGGCC 1290
Qy 409 Asp-----ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysVal 426
Db 1291 CAGACGGTCCGGCGTCCCGCAGTCCGATCAGAGTCTTTGATGACAGCCCGAGCAAGGTG 1350
Qy 427 GlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer 446
Db 1351 CCCAAGAGCTGGAGCTTTGGTGACCGCGACCGCACACCGCCAGGCTTTCGGCATCAAGGGT 1410
Qy 447 SerGlnProLysProValIleAlaAspAlaAspThrAlaLeuGlyThrAspValTyAsp 466
Db 1411 GCTGCATCCCGCAGAAATTCAGAAGAACAGCCCTCCCTGGGAGGACATCGTAGAGAC 1470
Qy 467 GluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrVal 486
Db 1471 AACAGAGCTGTAACTGCGAGTTTGTGACTGAAGATCTTACCCCTGGCGCTCAAGTYAGC 1530
Qy 487 IleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeu 506
Db 1531 ATCAGAGCGGTGTGTATGCGGTCTTGTATCTAAGCGCAAGATTCANAGAGAGTCTG 1590
Qy 507 ArgProTyAspValLysAspValIleGluGlnTySerAlaGlyHisLeuAspMetLeu 526
Db 1591 CGCCCATATGATGTATGAGCTCATCGACAGTACTCGGCTGGACACTTGGATATGTTG 1650
Qy 527 CysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThr 546
Db 1651 TCCCGCATCAAGAGCTGCAGACCAAGAGTGACCAAGATTGTGGGCGGGGCCCAACAATA 1710
Qy 547 SerAspLysLysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSer 566
Db 1711 ACGGAT---AAGGATCGCAACCAAGCGCCAGCGGAACGGAGCTGCCCGAAGACCCACG 1767
Qy 567 MetLeuGlyArgValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 586
Db 1768 ATATGGAGCGCTTGGAGAGGTGGAGAAACAGGCTTGTCTCATGGAAAGAGAGCTGCAC 1827
Qy 587 CysLeuLeuAspIleTyrglnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeu 606
Db 1828 TTCTTGTGGATCATATACAG-----AGAATGGGCATCCAAACACGACGACAGACAG 1881
Qy 607 AlaSerPheGlnIleProProPheGluCysGluGlnThrSerAspTyrglnSerProVal 626
Db 1882 GCCTATTTTGGGCGCAAG-----GAGGCTGAGCGCGCACCCACCTTACACAGCCCGCAG 1935
Qy 627 AspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys-----LeuSerArg 643
Db 1936 GACAGCCGTGAC-----CATGCAGAACAGATGGCTGTATCATTAAGATCTCGC 1986

Qy 644 SerThrSerAlaAsnIleSerArgGly-----LeuGln 654
Db 1987 TCCACCAAGCTCTACGG--GCCAGAGGAACACTACGACGACACCCCGACCATCCCCCTGCC 2044
Qy 655 PheIleLeuThrProAsnGluPheSerAlaGlnThr----- 666
Db 2045 AGTGTCTCTCCCTCCACCTCGTGGCGGCGAGACCCAGCCGCGCATCCCTCCCTGTGG 2104
Qy 667 -----PheTyrglnAlaLeuSerProThrMetHisSerGlnAlaThrGlnVal 681
Db 2105 GAGACCATGGCTCACTGTAGCATCCACCACTCCCTGCACACGAGCGGTGCTGTCTG 2164
Qy 682 ProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIle 701
Db 2165 CCT-----ACGTTGGGGCAACAGACGACGACGACGATCCAGATTCTTGA 2203
Qy 702 Asn---ThrAlaProLysProAlaAlaProThrThrLeu 713
Db 2204 GGCTGGAGGGCACCCCGCTGCAGGCCCTCTGAGGCTG 2242

RESULT 12

US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360

GENERAL INFORMATION:

; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052

; CURRENT APPLICATION NUMBER: US/09105,058C

; CURRENT FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 60/055,599

; PRIOR FILING DATE: 1997-08-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26

; LENGTH: 2565

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-105-058C-26

Alignment Scores:

Pred. No.: 3e-154 Length: 2565
Score: 1611.00 Matches: 392
Percent Similarity: 55.43% Conservative: 108
Best Local Similarity: 43.46% Mismatches: 244
Query Match: 35.11% Indels: 158
DB: 3 Gaps: 28

US-09-810-796-4 (1-897) x US-09-105-058C-26 (1-2565)

Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAaArgGlyAspGly 22
Db 91 GACCTGGAGCAA-----GTCACCTTGGCGTGGGGCGGAGCCGCAACAGACGGG 141
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
Db 142 ACCCTGTCTGTG-----GAGGGCGGGCGGCGGACGAGGGG 177
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyrg 61
Db 178 CAGCGGAGGACCCCGCAGGGC-----ATCGGGCTCTCTGGCCCAAGACCCCGCTGAGCCGC 231
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrgArgValGlnAsnTyrgLeuTyrg 81
Db 232 CCAGTCAAG-----AGAAACACGCCCAAGTACCGCGCATCCAAACATTTGATCTAC 282


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Db      2263 ---CGAATCTCCCGCGCAG-----AGACGTAGCATC 2292
Qy      774 AspMetGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLys 793
Db      2293 ACGGAGACAGTGCACACACCTGTGCTCTG-----2322
Qy      794 SerLeuSerValGlnAsnLeuLeuArgSerThrGluGluLeuAsnIleGlnLeuSerGly 813
Db      2323 ---ATGTCGGTCAACAC-----GAGGAGCTGGAGAGGTCTCCAAGTGGC 2364
Qy      814 SerGluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTyr 829
Db      2365 TTCACATCTCCAGCAGACAGATGATTATGTGTCGCCCCCAATGGGGGTGCGAGCTGG 2424
Qy      830 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 849
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Qy      850 ThrPhe 851
Db      2476 CCCTTC 2481

RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.

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Score: 1611.00 Matches: 392
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Best Local Similarity: 43.46% Mismatches: 244
Query Match: 35.11% Indels: 158
DB: 3 Gaps: 28

US-09-810-796-4 (1-897) x US-09-177-650-6 (1-2914)
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Db      163 GACGTGGAGCAA-----GTCACCTTGGCGTCGGGGCGGAGCGACAAAGACGGG 213
Qy      23 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlu 42
Db      214 ACCCTGTGCTG-----GAGGGCGGGCGGCGCAGCAGGGG 249
Qy      43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db      250 CAGCGGAGGACCCCGCAGGGC-----ATCGGGCTCTTGGCCAAAGACCCCGCTGAGCCGC 303
Qy      62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
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Qy      82 AsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
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Qy      102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
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Qy      142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeuArg 161
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Qy      162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db      595 TTTGCCAGGAAGCCCTGTGTCATGTGACATCTTTGTGCTGATTGCTCTGTGCGCATG 654
Qy      182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db      655 GTTCTGTGGGAACCAAGGCAATGTTCTGGCCACCTCC---CTGCGAAGCTGCGCTTC 711
Qy      202 LeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrPheLeuLeuGly 221
Db      712 CTGAGATCTTGGCATCTGCGATGCGGATGACCGAGAGGTGACCTGGAAGCTTCTGGGC 771
Qy      222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
Db      772 TCAGCCATCTGTGCCACAGCAAAAGAACTCATCAGGCTGGTACATCGGTTTCTGTACA 831
Qy      242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla-----256
Db      832 CTCATCTCTTTCTTCAATTTCTGTCTACCTGTGAGAAAGACGTCCTCAGAGGTGGATGCA 891
Qy      257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyThr 271
Db      892 CAGGAGAGGAGATGAAAGAGGAGTTTGACACCTATGACATGCCCTGTGTGGGGCGCTG 951
Qy      272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrPheLeuVal 291
Db      952 ATCACACTGGCCACCATTTGCTATGGACACACACCCAAACGCTGGGAGGCGCTGTG 1011
Qy      292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeu 311

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Qy 614 PheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeu-SerG1 633
Db 2194 GCCGAAGGGGAGAGAAAGACACAAAGGTAAGTCTCT--GATTTGAAACCATCATCTGCG 2250
Qy 633 ySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLe 653
Db 2251 AACTACTCAGAGACAGAGGCGCCCTGACCTCTTACAGCTTCCACCGAGTCCCATCGAC 2310
Qy 653 uGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProTh 673
Db 2311 AGAGTTGGCCCTTACGGG-----TTTTTGGCATGATCCT-- 2346
Qy 673 rMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAl 693
Db 2347 -----GTGAACCTGACCGAGGGGACCCAGCTTCTACAAAGGC 2384
Qy 693 aThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLe 713
Db 2395 TCAGCTAACCTTCCCTCC-----TCGGGAATGATACATATGC 2420
Qy 713 uGlnIleProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisPr 733
Db 2421 AGAGAGCCCAAGTCTGCTGCCATCTTGACTCTTCTGGACTCATGTGTGAGCTACCAC-- 2478
Qy 733 oAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLy 753
Db 2479 -----TCCCA 2483
Qy 753 sGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPh 773
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Qy 773 eAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLy 793
Db 2541 CACTAGGACAGTGATACACCTCTGTCCCTC----- 2571
Qy 793 sSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerG1 813
Db 2572 -----ATGTCCCTCAATCAC-----GAGGAACGGAGCGGTCTCCAAGTGG 2612
Qy 813 ySerGluSerSerGlySerArgGlySerGlnAspPheThrPro-----LysTr 829
Db 2613 CTTGACGATCTCACAGACAGATGATGATTGTCGCCCAAGTGGGGGATCGAGCTG 2672
Qy 829 pArgGluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAs 849
Db 2673 GATGGGGGAAAGCGGTACTGCTGGCTGAA-----GGAGAACGGACACGGACACAGA 2723
Qy 849 pThrPhe 851
Db 2724 CCCCTTC 2730

RESULT 15
US-09-105-058C-5
; Sequence 5, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blumar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
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; LENGTH: 900
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5

Alignment Scores:
Pred. No.: 1,08e-113 Length: 900
Score: 1207.50 Matches: 227
Percent Similarity: 83.88% Conservative: 28
Best Local Similarity: 74.67% Mismatches: 40
Query Match: 26.32% Indels: 9
DB: 3 Gaps: 2

US-09-810-796-4 (1-897) x US-09-105-058C-5 (1-900)
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Db 13 GGGAAAGCCC-----CCGAAGCGCAACGCCCTTCTACCGCAAG 48
Qy 76 ValGlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHis 95
Db 49 CTGCAGAAATTTCTCTCAACAGCTGTAGAGCGGCCCGCGCTGGCGTTCTATCCAC 108
Qy 96 AlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
Db 109 GCCTACGTTGTTCTTTAGTCTTCTCTGCTTCTTCTGTTCTTCCACCATCAAG 168
Qy 116 GluHisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValVal 135
Db 169 GAGTACGAGAGAGAGCTCTGAGGGGGCCCTCTACATCTTGGAAATCGTGACTATCGTGTA 228
Qy 136 PheGlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysCysArgTyrArgGly 155
Db 229 TTCGGTGTGAGTACTTTTGAGGATCTGGCTCGAGCTGCTGTGCGGTATCGAGGC 288
Qy 156 TrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 175
Db 289 TGGAGGGGAGGCTCAAGTTTCCAGGAGCGGTTCTGTGTGATTGATATCATCGTGTGCTG 348
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Qy 196 LeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGly 215
Db 409 CTTCCGAGCTTGGCTTCTTGCAATCTTGGGATGATCGGTATGGACCGAGGGGTGGC 468
Qy 216 ThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrp 235
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Qy 236 TyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAsp 255
Db 529 TACATTGGCTTCTCTGCTCATCTCTGCTCATCTTCTGGTGTACTTTGGCAGAAAAGGGT 588
Qy 256 AlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThr 275
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Qy 296 PheAlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPhe 315
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Qy 316 AlaLeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAla 335
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: April 3, 2005, 06:10:16 ; Search time 9703.68 Seconds
(without alignments)
4479.159 Million cell updates/sec

Title: US-09-810-796-4

Perfect score: 4588

Sequence: 1 MKDVESGGRVLLNSAARG.....SICKAGESTDALSLPHVKLK 897

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: gb.ro.*
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13: gb.un.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 4588 | 100.0 | 3137 | 6 AR430568 | AR430568 Sequence |
| 3 | 4588 | 100.0 | 3137 | 6 AX056817 | AX056817 Sequence |
| 4 | 4588 | 100.0 | 3137 | 9 AF202977 | AF202977 Homo sapi |

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| 9 | 4527.5 | 98.7 | 2772 | 6 | AR565635 | Sequence |
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| 12 | 4527.5 | 98.7 | 3111 | 6 | AX268476 | Sequence |
| 13 | 4407 | 96.1 | 3718 | 6 | BD275572 | Novel Hum |
| 14 | 4389 | 95.7 | 2832 | 9 | AF263835 | Homo sapi |
| 15 | 4288 | 93.5 | 3108 | 10 | AF263836 | Mus muscu |
| 16 | 2613 | 57.0 | 1552 | 6 | CO720576 | Sequence |
| 17 | 2012 | 43.9 | 2335 | 6 | AX032994 | Sequence |
| 18 | 2012 | 43.9 | 2335 | 6 | AX456863 | Sequence |
| 19 | 2012 | 43.9 | 2335 | 9 | AF105202 | Homo sapi |
| 20 | 1971 | 43.0 | 1508 | 9 | BC050689 | Homo sapi |
| 21 | 1832.5 | 39.9 | 4165 | 10 | AF087453 | Rattus no |
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| 23 | 1815 | 39.6 | 2613 | 10 | AF490773 | Homo sapien |
| 24 | 1813 | 39.5 | 2169 | 6 | AR213255 | Mus muscu |
| 25 | 1813 | 39.5 | 2169 | 6 | BD074166 | Sequence |
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| 31 | 1806.5 | 39.4 | 3237 | 6 | BD086411 | KCNQ2 and |
| 32 | 1805 | 39.3 | 3287 | 6 | AR213254 | Sequence |
| 33 | 1805 | 39.3 | 3287 | 6 | BD074165 | KCNQ2 and |
| 34 | 1800.5 | 39.2 | 3232 | 6 | AR216854 | Sequence |
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| 36 | 1792.5 | 39.1 | 3232 | 9 | AF033348 | Homo sapi |
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| 38 | 1786 | 38.9 | 2750 | 9 | AF110020 | Homo sapi |
| 39 | 1784.5 | 38.9 | 3029 | 6 | A94974 | Sequence 1 |
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| 42 | 1781 | 38.8 | 2935 | 10 | AB000494 | Sequence |
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| 45 | 1749 | 38.1 | 2899 | 10 | AB000496 | Mus muscu |

ALIGNMENTS

RESULT 1
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LOCUS AX322509 2694 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0192526.
ACCESSION AX322509
VERSION AX322509.1 GI:18093555
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and Gribkoff,V.K.
TITLE Human kcnq5 potassium channel, methods and compositions thereof
JOURNAL Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 2.22e-298 Length: 2694
Score: 4588.00 Matches: 897
Percent Similarity: 100.00% Conservative: 0

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| Best Local Similarity: 100.00% | Mismatches: 0 |
| Query Match: 100.00% | Indels: 0 |
| DB: 6 | Gaps: 0 |
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| DB | 1 ATGAAGGATGTGGAGTCGGCGGGGCAAGGTGCTGTGAACCTCGGAGCGCGCAGGGGC 60 |
| QY | 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40 |
| DB | 61 GACGGCTGCTACTCTGGCACCCGCGCGCCACGCTTGTGTGGCGGGCGGTGGCCCTG 120 |
| QY | 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60 |
| DB | 121 AGGAGAGCGCGCGGGGAGCAGGGGGCGCGGATGAGCCTGCTGGGGAAGCGCGCTCT 180 |
| QY | 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80 |
| DB | 181 TACACGAGTAGCAGAGCTGCGCGGCAACGTCAGTAGTACCGCGGGTGCAGAACTACCTG 240 |
| QY | 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100 |
| DB | 241 TACAACGCTGTGAGAGACCCCGCGCTGGCGCTTCATCTACCAGCTTTCGTTTCTC 300 |
| QY | 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120 |
| DB | 301 CTGTGCTTTGGTTGCTTGTATTTTGTTCAGTGTGTTTCTACCATCCCTGAGCACACAAATTG 360 |
| QY | 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140 |
| DB | 361 GCCTCAAGTTGCTCTTGTATCTCGAGTTGCTGATGATGTCGCTTGTGGTGGAGTTC 420 |
| QY | 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160 |
| DB | 421 ATCAATTCGAATCTGGTCTGGGGTGTCTGTGTGATATAGAGGATGCGCAGGAAGACTG 480 |
| QY | 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180 |
| DB | 481 AGGTTTGCTCGAAAGCCCTTCTGTATTAGATACCATTTGTTATCGCTTCAATAGCA 540 |
| QY | 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200 |
| DB | 541 GTTGTCTTCGCAAAACCTCAGGGAATATATTTTGCACGCTGCTGCTCAGAACTCCGT 600 |
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| DB | 661 GGTTCACTGTTTATGCTCAGCAAGGAATTAATCACAGCTGGTACATAGGATTTTG 720 |
| QY | 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260 |
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| QY | 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280 |
| DB | 781 TCTACATATGAGATGCTCTCTGTTGGGGCAAAATTAATTAATTTGGCTATGGA 840 |
| QY | 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300 |
| DB | 841 GACAAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTCTGAGGCTTTGCACTCCCTTGGC 900 |
| QY | 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320 |
| DB | 901 ATTTCTTCTTGTGACATCTCTGCGGCATCTTCTGGCTCAGGTTTGTGATTAAGATACAA 960 |
| QY | 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340 |
| DB | 961 GAACAAACCGCCAGAAACACTTTGAGAAAGAGGAACCCAGCTGCCAACCTCATTCAG 1020 |


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LOCUS AR430568 3137 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6649371.
ACCESSION AR430568
VERSION AR430568.1 GI:40191384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3137)
AUTHORS Jentsch,T.J.
TITLE Potassium channel KCNQ5 and sequences encoding the same
JOURNAL Patent: US 6649371-A 1 18-NOV-2003;
FEATURES
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-810-796-4 (1-897) x AR430568 (1-3137)

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Db 61 GACGCGCTGCTACTGCTGGGCACCGCGCGGCCACGCTCGGTGGCGCGCGGTGGCGCTG 120
QY 41 ArgGluSerArgArgGlyLysGlnGlyValaArgMetSerLeuLeuGlyLysProLeuSer 60
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 VERSION AX056817.1 GI:12309758
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 SOURCE Homo sapiens
 ORGANISM Homo sapiens
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 Jentsch, T.J.
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 Patent: WO 0077035-A 1 21-DEC-2000;
 NEUROSEARCH A/S (DK)
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Alignment Scores:
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Score: 4588.00 Matches: 897
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-810-796-4 (1-897) x AX056817 (1-3137)

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Db 1201 AAGAGCCGCAAGCCCTCAGTAGTGACAGGAGGTCCCCAAGCACCCGACATCACAGCCGAG 1260
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1261 GGCAGTCCCCACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCGCTTCCGGGCC 1320
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1321 TCGCTGCGCCTCAAAAGTTTCTCAGCCAAACCCAGTGATAGTGCATGACACAGCCCTTGGC 1380
Qy 461 ThrAspAspValTyraAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1381 ACTGATGATATATATGATGAAAGATGCGAGTGTGATGATCATCAGTGAAGACCTCACC 1440
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1441 CCACCACTTAAACCTGCTATTGAGCTATCAGAAATATGAAATTTTCAATGTTCAAAACCG 1500
Qy 501 LysPheLysGluThrLeuArgProTyraAspValLysAspValIleGluGlnTyraSerAla 520

Db 1501 AAGTTTAAGGAAACATTTACGTCCTATATGATGTAAAGATGTCAATTGAACAATATTCTGCT 1560
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1561 GGTCACTCGGACATGTTGTGTAGAAATTAAGAGCCCTTCAACACAGCTGTTGATCAAAATCTTT 1620
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1621 GGAAAGAGGCAATACATCAGATAAGAGAGCCGAGAGAAATTAACAGCAGAAATGAG 1680
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1681 ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrlleGlnGlnValLeuArgLysGlySer 600
Db 1741 ATAGAATCCAAGCTGGACTGCTCTACTACATCTATCAACAGGTCCTTCGGAAGGCTCT 1800
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATGCCACCTTTTGAATGTGAACAGACATCT 1860
Qy 621 AspTyrlleGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCCGCAACAAACAGTGGCTGC 1920
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
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Qy 661 GluPheSerAlaGlnThrPheTyraAlaLeuSerProThrMetHisSerGlnIleThrGln 680
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Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
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Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2101 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2161 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACTTAACTTCCCTGCAAGGCTTACAGAA 2220
Qy 741 SerIleSerAspValThrThrCysLeuValAlaLaserLysGluAsnValGlnValAlaGln 760
Db 2221 AGCATTTCTGAGTCAACCACTGCTGCTTGTTCCTTCAAGGAAATGTTTCAGGTTGCACAG 2280
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
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Qy 821 GlySerGlnAspPheTyrlleProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2461 GGCAGCAAGATTTTTTACCCCAATGGAGGGAATCCAAATTTGTTTATAACTGATGAAGAG 2520
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2521 GTGGGTCCCGAAGACAGACAGACACTTTTGTATGCGCGCACCCGACCCCTCCCGGGAA 2580
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2581 GCTGCTTTGCTCAGACTCTCTAAGGACTGGAAGGTCAGCATCATCTCAGAGCATTTGT 2640

| | | | | | | | |
|---|--|--|-----------------|----|------|---|------|
| QY | 881 | LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisVallysLeuLys | 897 | Db | 755 | GTGTTTCTGCAAAACCTCAGGGTAATATTTTCCACAGTCTGCACCTCAGAAGTCTCGT | 814 |
| Db | 2641 | AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCACAACTGAAA | 2691 | QY | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTpLysLeuLeu | 220 |
| RESULT 5 | | | | Db | 815 | TTCTTACAGATCCTCCGCATGGTGGCATGGACCAAGGGAGGACCTTGGAAATTACTG | 874 |
| LOCUS | AR393778 | Sequence 1 from patent US 6617131. | PAT 18-DEC-2003 | QY | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaIleTyrIleGlyPheLeu | 240 |
| DEFINITION | AR393778 | Sequence 1 from patent US 6617131. | | Db | 875 | GTTTCAAGTGGTTATGCTCAGCAAGGAATTAATACAGCTTGATACATAGGATTTTG | 934 |
| ACCESSION | AR393778 | GI:40120748 | | QY | 241 | ValLeuIlePheSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| VERSION | AR393778.1 | | | Db | 935 | GTTCTATTTTTCGCTTCTCTCTATCTGGTGGAAAGGATGCCAAATAAGAGTTT | 994 |
| KEYWORDS | Unknown. | | | QY | 261 | SerThrTyrAlaAspAlaLeuTyrTpGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 |
| SOURCE | Unknown. | | | Db | 995 | TCTACATATGCAAGATGCTCTCTGGTGGGCACAAATTACATTGACAACTATTGGCTATGGA | 1054 |
| ORGANISM | Unclassified. | | | QY | 281 | AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
| REFERENCE | 1 (bases 1 to 3074) | | | Db | 1055 | GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCATCTCCTTGGC | 1114 |
| AUTHORS | Steinmeyer, K., Lerche, C., Scherer, C., Seeböhm, G. and Busch, A.E. | | | QY | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| TITLE | Nucleic acid molecule encoding the potassium channel protein, KCNQ5 | | | Db | 1115 | ATTCTCTTCTTGGCACTTCTCCCGGCATCTTGGCTCAGGTTTGGATTAAAGTACAA | 1174 |
| JOURNAL | Patent: US 6617131-A 1 09-SEP-2003; | | | QY | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuLeuGln | 340 |
| FEATURES | Location/Qualifiers | | | Db | 1175 | GAACACACCGCCAGAAACACATTTTGAGAAAGAGAACCCAGCTGCCAACCTCATTCAG | 1234 |
| 1..3074 | /organism="unknown" | | | QY | 341 | CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro | 360 |
| /mol_type="genomic DNA" | | | | Db | 1235 | TGTGTTTGGCGTAGTTACCGCAGCTGATGAGAAATCTGTTTCCATTGCCACCTTGGAGCCA | 1294 |
| ORIGIN | | | | QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer | 380 |
| Alignment Scores: | 2.34e-297 | Length: 3074 | | Db | 1295 | CACCTGAGAGCCCTTGACACCTTGACAGCCCTTACCAGAAAGAACAGGGGAAGCATCAACG | 1354 |
| Pred. No.: | 4574.00 | Matches: 895 | | QY | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 |
| Score: | 99.78% | Conservative: 0 | | Db | 1355 | AGTCAGAAAGCTAAAGTTTAAAGGAGCGAGTGGCATGGTAGCCCAAGGAGGAGGATTT | 1414 |
| Percent Similarity: | 99.78% | Mismatches: 2 | | QY | 401 | LysSerArgGlnAlaSerValGlyArgArgSerProSerThrAspIleThrAlaGlu | 420 |
| Best Local Similarity: | 99.78% | Indels: 0 | | Db | 1415 | AAGAGCCGACAGCCTCAGTAGTGACAGGAGTCCCAGAGCCACGACATCACAGCCGAG | 1474 |
| Query Match: | 99.69% | Gaps: 0 | | QY | 421 | GlySerProThrLysValGlnLysSerTyrPheAsnAspArgThrArgPheArgPro | 440 |
| DB: | 6 | | | Db | 1475 | GGCAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGCGCC | 1534 |
| US-09-810-796-4 (1-897) x AR393778 (1-3074) | | | | QY | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 |
| QY | 1 | MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly | 20 | Db | 1535 | TCGCTGGCGCTCAAAAGTTCTCAGCCAAACACGATAGATGCTGCACACAGCCCTTGGC | 1594 |
| Db | 215 | ATGAGAGATGTGAGTTCGGCGGGGCGGAGGTGCTGCTGAACCTCGGACGCGCCAGGGGC | 274 | QY | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 |
| QY | 21 | AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu | 40 | Db | 1595 | ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGTATCATGAGTGGAGACCTCAC | 1654 |
| Db | 275 | GACGGCTGCTACTGCTGGCACCCGCGGCGCACCTTGGTGGCGGCGCGGTGGCCTG | 334 | QY | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 |
| QY | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 | Db | 1655 | CCACCATTAACACTGCTATTCGAGCTATCAGAAATTAAGAAATTTTCAATTTGTCAAACGG | 1714 |
| Db | 335 | AGGAGAGCCCGCGGGCAGAGCGGGGCGGATGAGCTGCTGGGAAGCCGCTCTCT | 394 | QY | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 |
| QY | 61 | TyrThrSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 | Db | 1715 | AAGTTTAAAGAAACATTACGTCCTATGATGATAAAGATGTCAATTAACATAATTTCTGCT | 1774 |
| Db | 395 | TACACGAGTAGCAGAGCTCCGCGCGCACGTCACAGTACCGCGCGGTGCAGAACTACCTG | 454 | QY | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| QY | 81 | TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu | 100 | Db | 1775 | GGTCATCTGGAATCTGTTAGTAATTAAGAGCCCTTCAACACCGTGTGTGATCAAAATCTT | 1834 |
| Db | 455 | TACAACTGCTGGAGAGACCCGCGGCTGGCGGTTCATCTACACGCTTTCGTTTCTCTC | 514 | QY | 541 | GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu | 560 |
| QY | 101 | LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 | Db | 1835 | GGAAAGGGCAATCATCATCATGATTAAGAGCCGAGAGAAAAATAACAGCAGACATGAG | 1894 |
| Db | 515 | CTTGCTTGTGTTGTTGATTTTGTCAAGTGTCTTCTACCATCCCTGAGCACACAAATTTG | 574 | | | | |
| QY | 121 | AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 | | | | |
| Db | 575 | GCCTCAAGTTCCTCTTGATCCTCGAGTTCGTGATGATTTGTCGTTTGGAGTTTC | 634 | | | | |
| QY | 141 | IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu | 160 | | | | |
| Db | 635 | ATCATTCGAACTGGTCTGCGGGTTCGTTGTCGATATAGAGATGCCAAGGAAGACTG | 694 | | | | |
| QY | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 | | | | |
| Db | 695 | AGGTTTGTCTGAAACCCCTCTGTTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA | 754 | | | | |
| QY | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 | | | | |

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|----|------|---|------|
| QY | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu | 240 |
| DB | 875 | GGTTTCAGTGGTTTATGCTCACAGCAGGAATTAATCACAGCTTGGTACATAGGATTTTG | 934 |
| QY | 241 | ValLeuIlePheSerSerPheLeuValTyrIleuValGluLysAspAlaAsnLysGluPhe | 260 |
| DB | 935 | GTTCCTATTTTTCCTCTTCCTGCTATCTGCTGGAAAGGATGCAATAAAGAGTTT | 994 |
| QY | 261 | SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 |
| DB | 995 | TCTACATATGAGATGCTCTCTGTTGGGGCAATATACATGACAACTATTGGCTATGGA | 1054 |
| QY | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
| DB | 1055 | GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGAGGCTTTGCACTCTTGGC | 1114 |
| QY | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| DB | 1115 | ATTTCCTTTCTTGGCACTTCCCTGCCGCCATTCTTGCTCAGGTTTTCATTTAAAGTACA | 1174 |
| QY | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln | 340 |
| DB | 1175 | GAAACACCCGCGAGAACACTTTGAGAAAGAGAACCCAGCTGCGCAACTCATTCAG | 1234 |
| QY | 341 | CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro | 360 |
| DB | 1235 | TGTGTTTGGCGTAGTTACGACGTGATGAGAAATCTGTTTCATTTGCAACTGGAAGCCA | 1294 |
| QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaLysSer | 380 |
| DB | 1295 | CACCTGAAGCCCTTGACACCTGCGACCTTACCAAGAAAGAACAGGGGAGCATCAAGC | 1354 |
| QY | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 |
| DB | 1355 | AGTCAGAACTAAGTTTAAAGAGCGAGTGCATGGCTAGTCCCGAGGGCGCAGAGTATT | 1414 |
| QY | 401 | LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu | 420 |
| DB | 1415 | AAGAGCGGCAAGCCCTCAGTAGTGACAGAGGTCCCCAAGCACCGACATCACAGCCGAG | 1474 |
| QY | 421 | GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro | 440 |
| DB | 1475 | GGCAGTCCCACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC | 1534 |
| QY | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 |
| DB | 1535 | TCGCTGCGCCTCAAAAGTTCTCAGCCAAACACCAAGTATGATGCTGACACAGCCCTTGGC | 1594 |
| QY | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 |
| DB | 1595 | ACTGATGATGATATGATGAAAAGGATGCCAGTGTGATGATCAGTGGAAAGACCTCACC | 1654 |
| QY | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 |
| DB | 1655 | CCACCACTTAAACTGTCAITTCGAGCTATCAGAAATATGAAATTTTATGTTGCAAAACGG | 1714 |
| QY | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 |
| DB | 1715 | AAGTTTAAAGAAACATTACGTCCATATGATGATAAGATGCTTGAACAATATTCTGCT | 1774 |
| QY | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| DB | 1775 | GGTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAAAACAGCTGTGATCAAAATCTT | 1834 |
| QY | 541 | GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu | 560 |
| DB | 1835 | GGAAAAGGCGAAATCACATCAGATAAGAGCCGAGAGAAATAACAGCAGAACATGAG | 1894 |
| QY | 561 | ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer | 580 |
| DB | 1895 | ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAGAACAGGTACAGTCC | 1954 |

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|----|------|---|------|
| QY | 581 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 600 |
| DB | 1955 | ATAGAAATCCAAGCTGGAGCTGCTACTAGACATCTATCAACAGGCTCTTCGAAAGGCTCT | 2014 |
| QY | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGlnThrSer | 620 |
| DB | 2015 | GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT | 2074 |
| QY | 621 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 640 |
| DB | 2075 | GACTATCAAGACCCCTGTGATAGCAAGATCTTCGGGTCCGCACAAAACAGTGGCTGC | 2134 |
| QY | 641 | LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn | 660 |
| DB | 2135 | TTATCCAGATCAACTAGTGGCAACATCTCGAGAGCCCTGCAGTTTCAATCTCACGCCAAAT | 2194 |
| QY | 661 | GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln | 680 |
| DB | 2195 | GAGTTTCAGTGGCCGACATTTCTACCGCTTACCCCTACTATGACAGTCAAGCAACACAG | 2254 |
| QY | 681 | ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln | 700 |
| DB | 2255 | GTGCCAATTTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAACCAA | 2314 |
| QY | 701 | IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProProLeuPro | 720 |
| DB | 2315 | ATAAATACGGCACCCCAAGCCAGCAGCCCAACACTTTTACAGATCCACCTCTCTCCA | 2374 |
| QY | 721 | AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu | 740 |
| DB | 2375 | GCATCAAGCATCTGCGCAGCCAGCAAACTCTGCAACCTTAACCTGCAGCTTACAGGAA | 2434 |
| QY | 741 | SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln | 760 |
| DB | 2435 | AGCATTTCTGACGCTCACCACTGCTTGTGCTCCCAAGGAAATGTTTTCAGGTTCACAG | 2494 |
| QY | 761 | SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu | 780 |
| DB | 2495 | TCAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG | 2554 |
| QY | 781 | LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu | 800 |
| DB | 2555 | TTGCTGCTGCTCCCATGGTGGCAAGGACTTGGCAAAATCTTTGTCTGTGCAAAACCTG | 2614 |
| QY | 801 | IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg | 820 |
| DB | 2615 | ATCAGGTGCAACCGAGGAACCTGAATATACAACTTTTTCAGGGAGTGAATGAGTCCAGA | 2674 |
| QY | 821 | GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu | 840 |
| DB | 2675 | GGCAGCCAGATTTTACCCTCAATGAGGGAATCCAAATTTGTTTATTAATGATGAAGAG | 2734 |
| QY | 841 | ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu | 860 |
| DB | 2735 | GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCCTGCCAGGAA | 2794 |
| QY | 861 | AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys | 880 |
| DB | 2795 | GCTGCTTTGATCAGACTCTCTAAGGACTTGAAGGTCAAGATCATCTCAGAGCATTTGT | 2854 |
| QY | 881 | LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys | 897 |
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RESULT 7
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SOURCE
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ORGANISM

AX456864
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SOURCE
Homo sapiens
ORGANISM

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Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
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Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
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Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
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Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTriPlysLeuLeu 220
Db 815 TTCTTACAGATCTCCGATGTCGCGATGGACCGAGGGAGGCACCTTGGAAATTAATCTG 874
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrIleGlyPheLeu 240
Db 875 GGTTTCAGTGTATTATGCTCACAGCAGGAATTAATCACAGCTTGTGTACATAGGATTTTG 934
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 935 GTTCTTATTTTTCGTCTTTCCTGTATCTGTGGTGAAGAGATGCCAATAAAGAGTTT 994
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 995 TCTACATATGAGATGCTCTCTGTTGGGCGACAAATTAATGACAACTATTGGCTATGGA 1054
Qy 281 AspLysThrProLeuThrTriPlysGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
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Db 1775 GGTCACTTCGACATGTTGTGTAGAAATTAAGAGCTTCAACACAGCTGTGTGATCAAAATCTCT 1834
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Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
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Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
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| | | | | | | | | |
|---|--|--|------|--------|------|--|------|--|
| QY | 821 | GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu | 840 | Db | 466 | GCCTCAAGTTGCCTCTTGATCTCGAGTTCGTGATGATGTCGTCTTTGGTGGAGTTC | 525 | |
| Db | 2675 | GGCAGCCAGATTTTACCCCAATGGAGGAATCCAAATGTTTATTAACATGATGAAGAG | 2734 | QY | 141 | IleIleArgIleTyrSerAlaGlyCysCysCysArgTyrArgGlyTyrGlnGlyArgLeu | 160 | |
| QY | 841 | ValGlyProGluGluThrGluThrAspThrPheAspAlaProGlnProAlaArgGlu | 860 | Db | 526 | ATCATTCGAATCTGTGCTGCGGGTGTCTGTGTGATATAGAGATGGCAAGAACTG | 585 | |
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| QY | 861 | AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys | 880 | Db | 586 | AGGTTTGTCTCGAAAGCCCTTCTGTATATAGATACCATTTGTTCTTATCGCTTCAATAGCA | 645 | |
| Db | 2795 | GCTGCTTTTGCATCAGACTCTCTAAGACTGGAAGTTCAGATCATCTCAGAGCAITTTGT | 2854 | QY | 181 | ValValSerAlaLysThrGlnGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 | |
| QY | 881 | LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys | 897 | Db | 646 | GTGTGTTTCTGCAAAACTCAGGGTAATATTTTGGCCAGCTCTGCACCTCAGAGTCTCCGT | 705 | |
| Db | 2855 | AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA | 2905 | QY | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu | 220 | |
| Db | 2855 | AAGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA | 2905 | Db | 706 | TTCTTACAGATCTCTCGCATGCTGCGCATGGACCGAAGGGGAGGCATCTTGGAAATTAAGT | 765 | |
| RESULT 9 | | | | | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu | 240 | |
| LOCUS | AR565635 | 2772 bp | DNA | linear | 766 | GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATAGGATTTTGT | 825 | |
| DEFINITION | Sequence 1 from patent US 6767736. | | | | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 | |
| ACCESSION | AR565635 | | | | 826 | GTCTTATTTTTCGTCCTTCTCTCTGTCATCTGCTGGTGGAAAGGATGCCAATAAAGAGTTT | 885 | |
| VERSION | AR565635.1 | GI:53981668 | | | 261 | SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 | |
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| ORGANISM | Unknown. | | | | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 | |
| REFERENCE | 1 (bases 1 to 2772) | | | | 946 | GACAAACTCCCTTAACTTGGCTGGGAAAGATTCCTTCTGAGGCTTTCGACTCTCTTGGC | 1005 | |
| AUTHORS | Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambronicz, B. and Sands, A.T. | | | | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 | |
| TITLE | Human ion channel protein and polynucleotides encoding the same | | | | 1006 | ATTCTTCTTTCGACTCTCTGCGGCAATCTTGGCTCAGGTTTTCATTAAGATACAA | 1065 | |
| JOURNAL | Patent: US 6767736-A 1 27-JUL-2004; | | | | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln | 340 | |
| FEATURES | Location/Qualifiers | | | | 1066 | GAACAACACCGCCAGAAACACTTTTGAAGAAAGAAAGAACCCAGCTGCCAACCTCATTCAG | 1125 | |
| source | 1. .2772 | | | | 341 | CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro | 360 | |
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| | /mol_type="genomic DNA" | | | | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer | 380 | |
| Alignment Scores: | 2.67e-294 | Length: | 2772 | | 1186 | CACTTGAAGGCTTGCACACTGCGAGCCCTTACC----- | 1218 | |
| Pred. No.: | 4527.50 | Matches: | 887 | | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 | |
| Score: | 99.00% | Conservative: | 1 | | : | : | : | |
| Percent Similarity: | 99.00% | Mismatches: | 0 | | 1219 | AATCAGAAAGCTTAAGTTTTAAGGACGAGTGGCATGGCTAGCCCCAGGGGCCAGAGTATT | 1278 | |
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| Query Match: | 98.68% | Gaps: | 1 | | 1279 | ARGAGCCGACAGCCTCAGTAGGTGACAGGAGGTCCCAAGACCCGACATCACAGCCGAG | 1338 | |
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| QY | 1 | MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly | 20 | QY | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 | |
| Db | 106 | ATGAAGATGTGGATCGGCGCGGCGAGGCTGCTGTAACCTCGGACGCCGCGAGGCG | 165 | Db | 1399 | TGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAAGTATAGATAGTGTGATGATCAGTGGAAAGCTTGGC | 1458 | |
| QY | 21 | AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu | 40 | QY | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 | |
| Db | 166 | GACGGCTGTACTGCTGGGACCCGCGCGGACCGCTCGGTGGCGGCGGCTGGCCTG | 225 | Db | 1459 | ACTGATGATGATATGATGAAAAGGATGCCAGTGTGATGATCAGTGGAAAGACTCACC | 1518 | |
| QY | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 | QY | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 | |
| Db | 226 | AGGAGAGCCCGCGGCGCAGCAGGCGCGCGGATGAGCTGCTGGGGAAGCGCTCTCT | 285 | QY | 1519 | CCACCACCTTAAACCTGTCATTCAGCTATCAGAAATTTATGAAATTTTCATGTTTGCAAAACGG | 1578 | |
| QY | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 | Db | | | | |
| Db | 286 | TACACGATAGCAGAGTCCGCGCAACGTCGAAGTACCGCGGCGGTCGAGAACTACCTG | 345 | QY | | | | |
| QY | 81 | TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu | 100 | Db | | | | |
| Db | 346 | TACACGTCGTCGAGAGACCCCGCGGCTGGCGCTTCATCACCACGCTTCTCGTTTCTC | 405 | QY | | | | |
| QY | 101 | LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 | Db | | | | |
| Db | 406 | CTTGCTTTGGTTGCTTGTATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 465 | QY | | | | |
| QY | 121 | AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 | Db | | | | |


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QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
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QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1999 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGCCCTGCAGTTCATTCTCAGCGCAAT 2058
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RESULT 10
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LOCUS Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu, Y., Kieke, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B.,
Zambrowicz, B. and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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1. .2772
/organism="Homo sapiens"
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ORIGIN
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Best Local Similarity: 98.89% Mismatches: 0
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US-09-810-796-4 (1-897) x AX268474 (1-2772)
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| QY | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 | QY | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| DB | 586 | AGGTTGCTCGAAAGCCCTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA | 645 | DB | 1639 | GGTCATCTGGACATCTGTTGTAGAAATTAAGAAGCTTCAAAACAGCTGTGATCAAAATCTT | 1698 |
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| QY | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 | QY | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer | 620 |
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| DB | 1126 | TGTGTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCATTTGCACCTGGGAAGCA | 1185 | DB | 2179 | ATAAATACGGACCCCAAGCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA | 2238 |
| QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysGluGlnGlyGluAlaSerSer | 380 | QY | 721 | AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu | 740 |
| DB | 1186 | CACCTTGAGGCCCTGCACACCTGCAGCCCTACC----- | 1218 | DB | 2239 | GCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTCAACCTCGAGCTTACAGAA | 2298 |
| QY | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 | QY | 741 | SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln | 760 |
| DB | 1219 | AATCAGAAGCTAAGTTTAAAGGACGAGTCCGATGGCTAGCCCCCAGGGGCCAGATAT | 1278 | DB | 2299 | AGCATTTCTCAGCTCACCATCTGCTTGTGCTTCCAGGAAATGTTCAAGTTCACAG | 2358 |
| QY | 401 | LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu | 420 | QY | 761 | SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu | 780 |
| DB | 1279 | AAGAGCCGACNAGCTCAGTAGGTGACAGAGGTCGCCAAGCACCCGACATCACAGCCGAG | 1338 | DB | 2359 | TCAATCTCACCAAGGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG | 2418 |
| QY | 421 | GlySerProThrLysValGlnLysSerTprSerPheAsnAspArgThrArgPheArgPro | 440 | QY | 781 | LeuSerValCysProMetValProLysAspLeuGlyLysSerLysSerValGlnAsnLeu | 800 |
| DB | 1339 | GGCAGTCCACAAAGTGCAGAGAGTGGAGCTTCAACAGCCAGCCCGCTTCCGCCCC | 1398 | DB | 2419 | TTGTGTCTCTCCCATCTGGTCCGAGAGACTTGGGGAATCTTGTCTGTGCAAACTCTG | 2478 |
| QY | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 | QY | 801 | IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg | 820 |
| DB | 1399 | TCGCTGCCCTCAAAAGTTCTCAGCCAAACACCATGATAGATGCTGACACAGCCCTTGGC | 1458 | DB | 2479 | ATCAGTCCACCGAGGAACATCAATATACAACTTTTTCAGGAGTCAAGTGGCTCCAGA | 2538 |
| QY | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 | QY | 821 | GlySerGlnAspPheTyrProLysTprArgGluSerLysLeuPheIleThrAspGluGlu | 840 |
| DB | 1459 | ACTGATGATGATATGATGATAAAGGATGCCAGTGTGATGATCAGTGGAGACCTCACC | 1518 | DB | 2539 | GGCAGCCCAAGATTTTATCCCAATGGAGGAAATCCAAATTTGTTTATACTGATGAGAG | 2598 |
| QY | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 | QY | 841 | ValGlyProGluGluThrGluThrAspThrPheAspAlaLapProGlnProAlaArgGlu | 860 |
| DB | 1519 | CCACCACATAAACCTGTCATTCGAGCTATCAGATTAATTAATTTTCATGTTGCAAAACGG | 1578 | DB | 2599 | GTTGGTCCGAGAGACAGACAGACACACTTTTTCATGTCGCCAGCCGACCTGCCAGGGAA | 2658 |
| QY | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 | QY | 861 | AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys | 880 |
| DB | 1579 | AGTTTAAAGAAACATTACGTCCATATGATGATAAAGATGTCATTGAACAAATATCTGCT | 1638 | DB | 2659 | GCTGCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT | 2718 |
| | | | | QY | 881 | LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys | 897 |

|||||
Db 2719 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2769
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AR565636 LOCUS AR565636 3111 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 3 from patent US 6767736.
ACCESSION AR565636
VERSION AR565636.1 GI:53981669
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3111)
AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehis,M.C., Friedrich,G.,
Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 3 27-JUL-2004;
FEATURES
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ORIGIN
Alignment Scores:
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Best Local Similarity: 98.89% Mismatches: 0
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US-09-810-796-4 (1-897) x AR565636 (1-3111)
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Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGTACTCTGGGACACCGCGCGCCAGCTCGGTGGCGGGCGGTGGCCTG 284
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 285 AGGGAGAGCCCGCGGGGAGCAGCGGGCGCGGATGAGCCGTCTGGGGAAGCCGCTCTCT 344
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 345 TACACGATGACCGAGAGTGGCGGGCGAACGTCAGTACCGCGGGGTGCAGACTACCTG 404
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 405 TACAACGTGTGGAGAGACCCCGCGGTGGCGGTTTCATCTACCAAGCTTTCGTTTTCTC 464
Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTGTGTTTGGTGTCTGATTTGTTCAGTGTTCCTACCATCCCTCGAGCACACAAAATTG 524
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTGGCTCTGATCTCGAGTTCGTGATGATGTGCTTTGGTTGGAGTTC 584
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrPglGlnGlyArgLeu 160
Db 585 ATCATTCGAATCTGCTCGCGGTGTCTGTTCGATATAGAGGATGCAAGGAAGACTG 644
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180
Db 645 AGGTTTGTTCGAAGCCCTTCTGTGTATAGATACCATTTGTTTCATCGCTCAATAGCA 704
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
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Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 765 TTCCTACAGATCCTCCGATGGTCGATGACCGAGGGAGGCACCTTGGAAATTAATCTG 824
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Db 1398 GGCACTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGCCC 1457
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
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Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1698 GGTCACTTGGACATGTTGTGTAGATTAATAAGCCCTTCAACACCGTGTGTGATCAAAATCTCT 1757
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
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| | | | |
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| QY | 561 | ThrThrAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer | 580 |
| DB | 1818 | ACCACAGACGATCTCAGTATGCTCGGTGGGTCAAGGTTGAAACACAGGTACAGTCC | 1877 |
| QY | 581 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 600 |
| DB | 1878 | ATAGAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT | 1937 |
| QY | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer | 620 |
| DB | 1938 | GCTTCAGCCCTCGCTTTCGGCTTCATTCAGATCCACCTTTTGAATGTGACAGACATCT | 1997 |
| QY | 621 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAenSerGlyCys | 640 |
| DB | 1998 | GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGACACAAACAGTGGCTGC | 2057 |
| QY | 641 | LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn | 660 |
| DB | 2058 | TTATCCAGATCAACTAGTGCCACATCTCGAGAGGCTTCGACATCTTCTGACCCCAAT | 2117 |
| QY | 661 | GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln | 680 |
| DB | 2118 | GAGTTCAGTCCCGACACTTTCACGGCTTAGCCCTACTATGCACAGTCAAGCAACACAG | 2177 |
| QY | 681 | ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln | 700 |
| DB | 2178 | GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAACCA | 2237 |
| QY | 701 | IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProLeuPro | 720 |
| DB | 2238 | ATAAATACGGCACCACCAAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCA | 2297 |
| QY | 721 | AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu | 740 |
| DB | 2298 | GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTTAACCTTCGAGGCTTACAGAA | 2357 |
| QY | 741 | SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln | 760 |
| DB | 2358 | AGCAATTTCTGACGTCAACCTCGCTTGTTCCTTCAGGAAATATGTTTCAGGTTGCACAG | 2417 |
| QY | 761 | SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu | 780 |
| DB | 2418 | TCAATCTCACCAAGGACCGTCTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG | 2477 |
| QY | 781 | LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu | 800 |
| DB | 2478 | TTGTCTGTCTCTCCATGTCGCCAAGGACTTGGGCAAAATCTTTGTCTGTGCANAACTCTG | 2537 |
| QY | 801 | IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg | 820 |
| DB | 2538 | ATCAGGTGACCGAGGAACTGAATATACACTTTCAGGAGTCAAGTCAAGTGGCTCCAGA | 2597 |
| QY | 821 | GlySerGlnAspPheTyrProLysTyrArgLysSerLysLeuPheIleThrAspGluGlu | 840 |
| DB | 2598 | GGCAGCAAGATTTTATCCCAATGAGGGAATCCAAATTTGTTTAACTGATGAAGAG | 2657 |
| QY | 841 | ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu | 860 |
| DB | 2658 | GTGGGTCCCGAAGACACAGACACACTTTTGTATGCCGACCGCAGCTGCCAGGAA | 2717 |
| QY | 861 | AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys | 880 |
| DB | 2718 | GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTCAGACATTTGT | 2777 |
| QY | 881 | LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys | 897 |
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| LOCUS | AX268476 | 3111 bp | DNA linear PAT 29-OCT-2001 |
| DEFINITION | Sequence 3 from Patent WO0175108. | | |
| ACCESSION | AX268476 | | |

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| VERSION | AX268476.1 | GI:16541653 |
| KEYWORDS | Homo sapiens (human) | |
| SOURCE | Homo sapiens | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | |
| REFERENCE | Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B., Zambrowicz, B. and Sands, A.T. | |
| AUTHORS | Human ion channel protein and polynucleotides encoding the same | |
| TITLE | Patent: WO 0175108-A 3 11-OCT-2001; | |
| JOURNAL | Lexicon Genetics Incorporated (US) | |
| FEATURES | Location/Qualifiers | |
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| DB | 165 | ATGAAGGATGTGGAGTGGGGCCGGGCGGTGCTGTAATCGGCAGCCCGAGGGC 224 |
| QY | 21 | AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40 |
| DB | 225 | GACGGCTGTACTGTGTGGSCACCCCGCGCGGCACCTCGGTGGCGCGCGTGGCCTG 284 |
| QY | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60 |
| DB | 285 | AGGAGAGCGCGCGGGCAAGCAGGGGGGCCGGATGAGCTGCTGGGGAAGCGCTCTCT 344 |
| QY | 61 | TyrThrSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80 |
| DB | 345 | TACACGAGTAGCCAGACTGCCCGCGCAACGTCAAGTACCGCGGTGCAGAACTACCTG 404 |
| QY | 81 | TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100 |
| DB | 405 | TACAACTGTGGAGAGACCCCGCGCTGGCGCTTATCTACCACCGCTTTCGTTTCTC 464 |
| QY | 101 | LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120 |
| DB | 465 | CTTGTCTTGGTTCCTTGTATTTGTCAAGTGTTCAGTGTTCCTACCATCCTGAGCACAAAATTG 524 |
| QY | 121 | AlaSerSerCysLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPhe 140 |
| DB | 525 | GCTCAAGTTCCTCTTGATCCTGGAGTTCGTGATGATTGTCGTCTTTGGTTCGAGTTC 584 |
| QY | 141 | IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160 |
| DB | 585 | ATCATTCGAATCTGGTCTGCGGGTTCCTGTTGTCATATAGAGGATGGCAAGGAAGCTG 644 |
| QY | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180 |
| DB | 645 | AGGTTTGTTCGAAAGCCCTTCGTGTATAGATACCATTTCTTATCGCTTCAATAGCA 704 |
| QY | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200 |
| DB | 705 | GTTGTTTCTGCAAAAACCTCAGGGTAATATTTTTCACAGCTCTGCACCTCAGAGTCTCGT 764 |
| QY | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220 |
| DB | 765 | TTCTACAGATCTCTCGCATGCTGGCATGGCCGATGGACCGAGGGGACCTTGGAAAATTACTG 824 |

QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
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QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 885 GTTCTTAATTTTTCGCTTTCTGCTCATCTGGTGGAAAGGATGCGCAATAAAGAGTTT 944
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QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
DB 1638 AAGTTTAAGGAAACATTACGTCATATGATGTAAAGATGTCATTGAACAATATTCGCT 1697
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
DB 1698 GGTCACTCGGACATGTTGTAGAAATTAAGAGCTTCAAAACAGCTGTTGATCAAAATTCCT 1757
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
DB 1758 GGAAAGGCGCAATCACATCAGATGAAGAGAGCCGAGAGAAATAACAGCAGAAATGAG 1817
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
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DB 1878 ATAGAATCCAAAGCTGGAGCTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAGAGCTCT 1937
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
DB 1938 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1997
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
DB 1998 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCAACAAACAGTGGCTGC 2057
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
DB 2058 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGGCTTCAGATTCATTTCTGACGCCAAT 2117
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
DB 2118 GAGTTCAGTGGCCAGACTTCTACGCGCTTAGCCCTACTATGCAGTCAAGCAACACAG 2177
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
DB 2178 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCAA 2237
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
DB 2238 ATAAATACGGCACCCCAAGCCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2297
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
DB 2298 GCCATCAAGCATCTGCCAGGCCCAAACTCTGACCCCTAACCCCTGAGGCTTACAGAA 2357
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
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QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
DB 2418 TCAATCTCAACAAAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG 2477
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
DB 2478 TTGTCGTCTGTCCATGGTGGCCAGGACTTGGGCAATCTTTGCTGTGCAAAACCTG 2537
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
DB 2538 ATCAGGTCGACCGAGGAACCTGAATATACAACCTTTTTCAGGAGTGAGTCAAGTGGCTCCAG 2597
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
DB 2598 GGCAGCCCAAGATTTTACCCTCAATGGAGGAAATCCAAATTTTATTAACCTGATGAAGAG 2657
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
DB 2658 GTGGGTCCGAGAGACAGACAGACACTTTTGTGCGCAGCCGACCCGACCTGCCAGGNA 2717
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
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LOCUS BD275572 3718 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Human Voltage-Gated Potassium Channel.
ACCESSION BD275572
VERSION BD275572.1 GI:33085340
KEYWORDS JP 2002543768-A/2.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]

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| QY | 617 | GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln | 636 |
| Db | 1833 | GAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCCGCACAA | 1892 |
| QY | 637 | AsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIle | 656 |
| Db | 1893 | AACAGTGGCTGCTTATCCAGATCAACTAGTGCACAATCTCAGAGGCTCGAGTTCATT | 1952 |
| QY | 657 | LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSer | 676 |
| Db | 1953 | CTGACGCCAAATGAGTTCAGTCCCCAGACTTTCTACGGCTTAGCCCTACTATGCACAGT | 2012 |
| QY | 677 | GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThr | 696 |
| Db | 2013 | CAAGCAACACACAGGTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACC | 2072 |
| QY | 697 | IleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro | 716 |
| Db | 2073 | ATTGCAACCAANTAAATACGCACCCAGCCAGCCAGCCCAACCACTTTACAGATCCCA | 2132 |
| QY | 717 | ProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAla | 736 |
| Db | 2133 | CCTCCTCTCCAGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAAACCTGCA | 2192 |
| QY | 737 | GlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerIysGluAsnVal | 756 |
| Db | 2193 | GGCTTACAGGAAGCATTTCTGACGTCCACCTCCTGTTGTCCTCCAAAGGAAATGTT | 2252 |
| QY | 757 | GlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGly | 776 |
| Db | 2253 | CAGTTGCACAGTCAAAATCTACCAAGACCGTTCTATGAGGAAGCTTTGACATGGGA | 2312 |
| QY | 777 | GlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSer | 796 |
| Db | 2313 | GGAGAAACTCTGTTCTGCTGTCCTCCATGGTGGCCGAGGACTTGGGCAATCTTTGTCT | 2372 |
| QY | 797 | ValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSer | 816 |
| Db | 2373 | GTGCAAAACCTGATCAGGTGCGACCGAGGAACCTGAATATACAACTTTCAGGAGTGA | 2432 |
| QY | 817 | SerGlySerArgGlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIle | 836 |
| Db | 2433 | AGTGCTTCAGAGGAGCCAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATA | 2492 |
| QY | 837 | ThrAspGluGluValGlyProGluThrGluThrAspThrPheAspAlaAlaProGln | 856 |
| Db | 2493 | ACTGATGAAGAGGTGGTCCCGAAGAGACAGACAGACACTTTTGTATGTCGCGCACCGCAG | 2552 |
| QY | 857 | ProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSer | 876 |
| Db | 2553 | CCTGCCAGGGAAGCTGCCTTTGTCATCAGACTCTCTAAGGACTTGAAGGTCAGCATCATCT | 2612 |
| QY | 877 | GlnSerIleCysLysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeu | 896 |
| Db | 2613 | CAGACATTTGTAGCGAGGAGGAAGTACAGATGCCCTCAGCTTGCTTCATGTCAAACTG | 2672 |
| QY | 897 | Lys 897 | |
| Db | 2673 | AAA 2675 | |
| RESULT 14 | | | |
| AF263835 | | | |
| LOCUS | | | |
| DEFINITION | Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA, | 2832 bp | linear |
| ACCESSION | AF263835 | | |
| VERSION | AF263835.1 | | |
| KEYWORDS | GI:81322996 | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |

| | | | |
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| REFERENCE | 1 | (bases 1 to 2832) | |
| AUTHORS | | Kniazeva,M. and Han,M. | |
| TITLE | | A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders | |
| JOURNAL | | Unpublished | |
| REFERENCE | 2 | (bases 1 to 2832) | |
| AUTHORS | | Kniazeva,M. and Han,M. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Porter Biociences Bldg., Boulder, CO 80309, USA | |
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| Alignment Scores: | | | |
| Pred. No.: | 5,53e-285 | Length: | 2832 |
| Score: | 4389.00 | Matches: | 856 |
| Percent Similarity: | 99.65% | Conservative: | 2 |
| Best Local Similarity: | 99.42% | Mismatches: | 3 |
| Query Match: | 95.66% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |
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| QY | 57 | LysProLeuSerTyrThrSerSerGlnSerCysArgArgGluValLysTyrArgVal | 76 |
| Db | 61 | AAGCGCTCTCTTACACGAGTAGCAGAGCTGCGCGCGCAACGTCAGTACCGCGGGTG | 120 |
| QY | 77 | GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla | 96 |
| Db | 121 | CAGAACTACCTGTACACGCTGCGAGAGACCCCGCGCGCTGGCGCTTCATCCACACGCT | 180 |
| QY | 97 | PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu | 116 |
| Db | 181 | TTCTGTTTCTCTCTGCTTTGTTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 240 |
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RESULT 15
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 LOCUS Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
 DEFINITION partial cds.

ACCESSION AF263836
 VERSION
 KEYWORDS

SOURCE AF263836.1 GI:8132998
 ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 3108)
 AUTHORS Kniazeva, M. and Han, M.
 TITLE A new gene of the voltage-gated potassium channel KCNQ family,
 KCNQ5, is a candidate gene for retinal disorders

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3108)
 AUTHORS Kniazeva, M. and Han, M.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAY-2000) MCB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA

FEATURES
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ORIGIN

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 DB: 10 Gaps: 0

US-09-810-796-4 (1-897) x AF263836 (1-3108)

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 QY 320 GlnGluGlnHisArgGlnLysHisPheGlyLysArgArgAenProAlaAlaAsnLeuIle 339
 Db 902 CAGGAGCAGCAGCCGCAAGACATTTTGAGAAAAGAGGAACCCAGCTGCCAACCCTCATC 961
 QY 340 GlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLys 359

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 2, 2005, 23:56:51 ; Search time 1122.13 Seconds
(without alignments)
4732.082 Million cell updates/sec

Title: US-09-810-796-4

Perfect score: 4588

Sequence: 1 MKDVESGRVLLNSAARG.....SICKAGESTDALSLPHVKLK 897

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09810796/runat.31032005.141120.18189/app.query.fasta_1.2126
-DB=N Geneseq.16Dec04 -QWTF=fastcap -SUPFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=prc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09810796 @CGN.1.1128 @runat.31032005.141120.18189 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq.16Dec04:

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- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 4588 | 100.0 | 2694 | AA814652 | AA814652 Human CDN |
| 2 | 4588 | 100.0 | 2694 | AAD27192 | AAD27192 Human pot |
| 3 | 4588 | 100.0 | 3137 | AAC85414 | AAC85414 Human KCN |
| 4 | 4584 | 99.9 | 3071 | AA814651 | AA814651 Human CDN |
| 5 | 4574 | 99.7 | 3074 | AH49499 | AH49499 Human KCN |

| | | | | | | |
|----|--------|------|--------|----|----------|--------------------|
| 6 | 4574 | 99.7 | 3074 | 10 | ADB78684 | Adb78684 Human pot |
| 7 | 4527.5 | 98.7 | 2667 | 4 | AA814653 | AA814653 Human CDN |
| 8 | 4527.5 | 98.7 | 2772 | 5 | AAH43633 | Aah43633 Human ion |
| 9 | 4527.5 | 98.7 | 3111 | 5 | AAH43634 | Aah43634 Human ion |
| 10 | 4407 | 96.1 | 3718 | 3 | AAC64371 | Aac64371 Human KCN |
| 11 | 2012 | 43.9 | 2335 | 3 | AA47618 | Aa47618 Kcno4 Pot |
| 12 | 2012 | 43.9 | 2335 | 10 | AD831698 | Ad831698 Human 323 |
| 13 | 1832.5 | 39.9 | 5595 | 13 | ADSI7851 | Adsi7851 Rattus no |
| 14 | 1820.5 | 39.7 | 7407 | 10 | ADB78687 | Adb78687 Human pot |
| 15 | 1819.5 | 39.7 | 7407 | 10 | ADB78685 | Adb78685 Human pot |
| 16 | 1819.5 | 39.7 | 7407 | 10 | ADB78688 | Adb78688 Human pot |
| 17 | 1819.5 | 39.7 | 7407 | 10 | ADB78686 | Adb78686 Human pot |
| 18 | 1819.5 | 39.7 | 7407 | 10 | ADB78683 | Adb78683 Human pot |
| 19 | 1819.5 | 39.7 | 7411 | 10 | ADD29557 | Add29557 Human tum |
| 20 | 1819.5 | 39.7 | 7420 | 11 | ADN38963 | Adn38963 Cancer/an |
| 21 | 1819.5 | 39.7 | 7420 | 11 | ADP65810 | Adp65810 Human mRN |
| 22 | 1819.5 | 39.7 | 7420 | 11 | ADP65731 | Adp65731 Human pot |
| 23 | 1819.5 | 39.7 | 7420 | 12 | ADL06495 | Adl06495 Human tum |
| 24 | 1819.5 | 39.7 | 7863 | 10 | ADJ56529 | Adj56529 Human CDN |
| 25 | 1813 | 39.5 | 2169 | 2 | AAJ26588 | Aax26588 Nucleotid |
| 26 | 1812.5 | 39.5 | 2565 | 2 | AA81548 | Aax81548 Human bra |
| 27 | 1812.5 | 39.5 | 3195 | 5 | AA874831 | Aax74831 DNA encod |
| 28 | 1806.5 | 39.4 | 3237 | 2 | AA857145 | Aax57145 Human mut |
| 29 | 1805 | 39.3 | 3287 | 2 | AAJ26587 | Aax26587 Nucleotid |
| 30 | 1800.5 | 39.2 | 3232 | 2 | AAJ57057 | Aax57057 Human KCN |
| 31 | 1800.5 | 39.2 | 3232 | 10 | AAD58489 | Aad58489 Human pot |
| 32 | 1800.5 | 39.2 | 3232 | 13 | ADSI7844 | Adsi7844 Human KCN |
| 33 | 1797.5 | 39.2 | 7413 | 5 | AA874832 | Aax74832 DNA encod |
| 34 | 1792.5 | 39.1 | 3232 | 5 | AA874830 | Aax74830 DNA encod |
| 35 | 1784.5 | 38.9 | 3029 | 2 | AA81547 | Aax81547 Human bra |
| 36 | 1772.5 | 38.6 | 4512 | 10 | ADJ56528 | Adj56528 Rat cDNA |
| 37 | 1769.5 | 38.6 | 2273 | 2 | AAJ57140 | Aax57140 Mouse KCN |
| 38 | 1667.5 | 36.3 | 125910 | 3 | AA864370 | Aac64370 Human KCN |
| 39 | 1633.5 | 35.6 | 1848 | 12 | ADH51119 | Adh51119 Potassium |
| 40 | 1633.5 | 35.6 | 1848 | 12 | ADM77995 | Adm77995 KCNQ2-15b |
| 41 | 1626.5 | 35.5 | 1878 | 12 | ADH51117 | Adh51117 Potassium |
| 42 | 1626.5 | 35.5 | 1878 | 12 | ADM77993 | Adm77993 KCNQ2-15b |
| 43 | 1614.5 | 35.2 | 1932 | 12 | ADH51115 | Adh51115 Potassium |
| 44 | 1614.5 | 35.2 | 1932 | 12 | ADM77991 | Adm77991 KCNQ2-15b |
| 45 | 1611 | 35.1 | 2565 | 2 | AAJ26596 | Aax26596 Nucleotid |

ALIGNMENTS

RESULT 1

| | |
|----------|--|
| AA814652 | |
| ID | AA814652 standard; cDNA; 2694 BP. |
| XX | |
| AC | AA814652; |
| XX | |
| DT | 18-DEC-2001 (first entry) |
| XX | |
| DE | Human cDNA encoding a voltage gated potassium channel hKVNQ5-1. |
| XX | |
| KW | Human; ss; voltage-gated potassium channel; hKVNQ5-1; nootropic; |
| KW | cerebroprotective; neurotropic; analgesic; vision disorder; |
| KW | central nervous system disorder; epilepsy; migraine; hearing disorder; |
| KW | psychotic disorder; seizure; learning disorder; memory disorder; stroke; |
| KW | pain; gene therapy; splice variant. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 1..2994 |
| FT | /*tag= a |
| FT | /product= "hKVNQ5-1" |
| XX | |
| PN | WO200170759-A1. |
| XX | |
| PD | 27-SEP-2001. |
| XX | |
| PF | 20-MAR-2001; 2001WO-US009328. |
| XX | |

PR 21-MAR-2000; 2000US-0190954P.
XX (ICAG-) ICAGEN INC.
XX Jegla TJ;
XX WPI; 2001-611467/70.
DR P-PSDB; AAU09020.
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximately subunits.
XX Claim 5; Page 62-63; 78pp; English.
XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2694
Score: 4598.00 Matches: 897
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-810-796-4 (1-897) x AAS14652 (1-2694)

QY 121 AlaSerSerCysLeuLeuIleValPheValMetIleValValPheGlyLeuGluPhe 140
DB 361 GCTCAAGTTGGCTCTTGATCTCTGGAGTTCTGATGATGTTGCTGTTGGTTGGAGTTC 420
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTrpArgGlyTrpGlnGlyArgLeu 160
DB 421 ATCATTCGAATCTGGTCTCGGGTTGCTGTCGATATAGAGGATGCGACAGAGACTG 480
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 481 AGGTTTGGCTCGAAAGCCCTCTGTGTATAGATACCATTTGTTCTTATCGCTCAATAGCA 540
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 541 GTTGTTCCTGCAAAACTCAGGGTAATAATTTTGGCCAGCTCTGCACTCAGAAAGTCTCCGT 600
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 601 TTCTACAGATCTCCGCATGGTGGCATGGACCCGAGGGAGGCACCTTGGAAATTTACTG 660
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 661 GGTTCAGTGGTTTATGCTCACCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 720
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaLeuLysGluPhe 260
DB 721 GTTCTTATTTTTCGTTCTTCTCTATCTGTTGGAAGGATGCCAATAAAGAGTTT 780
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 781 TCTACATATGATGATGCTCTCTGTTGGGCAACATTCATTCACACTATTGGCTATGGA 840
QY 281 AsplysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 841 GACAAACTCCCTTAACCTTGGTGGGAAGATTCCTTCTGACGGCTTTCACCTCTTGGC 900
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 901 ATTTCTTTCTTTCACCTTCTCGCGGCAATCTTGGCTCAGGTTTTCATTTAAAGTACAA 960
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaLeuLeuGln 340
DB 961 GAACACACCGCCAGAACACTTTGAGAAAGAGGAACCCAGCTGCCAACCTCATTCAG 1020
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1021 TGTGTTTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTTGCACTGGAAGCCA 1080
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
DB 1081 CACTTGAAGGCTTTGCAACCTCTGAGCCCTTACCCAGAAAGAACCAAGGGAGGATCAAGC 1140
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
DB 1141 AGTCAGAAGCTAACTTTTAAAGAGCGAGTGCATAGCTAGCTAGCCCGGCGGCGAGTATT 1200
QY 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420
DB 1201 AAGAGCCGACCAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1260
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
DB 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCGCTTCGGGCC 1320
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
DB 1321 TCGCTGCGCTCAAAAGTTCTCAGCAAAACGAGTAGATGCTGACACAGCCCTTGGC 1380
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
DB 1381 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

QY 481 ProProLeuLysThrValIleArgAlaIleMetLysPheHisValAlaLysArg 500
Db 1441 CCACCACCTTAAACCTGTCATTCGAGCTATCAGAATTATGAAATTTTCATGTTGCAAAACGG 1500
QY 501 LysPheLysGluThrLeuArgProFyrAspValLysAspValIleGluGlnFyrSerAla 520
Db 1501 AAGTTTAGGAAACGTTACGTCATATGATGTAAAGATGTCATTGAACAATATTCGCT 1560
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1561 GGTCACTCGCATCTGTTGTAGATTAAAGCCCTTCAACACACGCTGTGTGATCAAAATCTT 1620
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1621 GGAAAGGGCAAAATCACATCAGATCAGATGAAGAGCCGAGAGAAATTAACACAGCAATGAG 1680
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleFyrGlnGlnValLeuArgLysGlySer 600
Db 1741 ATAGAGTCCAAAGCTGAGCTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACACAGACATCT 1860
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1861 GACTATCAAGCCCTGTGGTAGCAAGATCTTTCGGGTTCGCACAAAAACAGTGGCTGC 1920
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1921 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCGCTGCAGTTCATTCTGAGCGCAAT 1980
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 1981 GAGTTCAGTGCCACAGCTTCTACCGCTTACCCCTTACTATGCACAGTCACAGCAACACAG 2040
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
Db 2041 GTGCCAATTTAGTCAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCATTTGCCAAACCA 2100
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2101 ATAATACGGCACCCCAAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2160
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2161 GCCATCAAGCATCTGCCCGAGCCAGAAACTCTGCACCCCTTAACCTTGCAGGCTTACAGGA 2220
QY 741 SerIleSerAspValThrThrCysLeuValAlaLaserLysGluAsnValGlnValAlaGln 760
Db 2221 AGCATTTCTGAGTCAACACCTGCTTGTGCTTCAAGGAAATGTTCAAGTTGCACAG 2280
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2281 TCAATCTCAACAGGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2341 TTGTCGTGCTGTCCCATGGTCGAGGACTTGGGCAAAATCTTTGCTGTGTGCAAAACCTG 2400
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 820
Db 2401 ATCAGTTCGACGAGGAACCTGATATACACTTTCAGGGAGTGAGTCAAGTGGCTTCCAGA 2460
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2461 GGCACCAAGATTTTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAG 2520
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 860

Db 2521 GTGGTCCGGAAGAGACAGACAGACACTTTTGTATGCCGACCCAGCCTGCCAGGAA 2580
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2581 GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGTCAAGCATCATCTCAGAGCATTTGT 2640
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691
RESULT 2
RAD27192
ID AAD27192 standard; cDNA; 2694 BP.
XX
AC AAD27192;
XX
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5 cDNA.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
addiction; myokymia; Alzheimer's disease; age-associated memory loss;
learning deficiency; cognitive disorder; motor disease; neuron disease;
neurophysiological disorder; neuropsychological disorder; asthma;
neuron cell death; brain tumour; gene therapy; antisense therapy;
synaptic transmission; electrical excitability; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2694
FT /tag= a
FT /product= "Human KCNQ5 protein"
XX
PN WO200192526-A1.
XX
PD 06-DEC-2001.
XX
PF 24-MAY-2001; 2001WO-US017314.
XX
PR 26-MAY-2000; 2000US-0207389P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Dworetzky SI, Ramanathan CS, Trojnak JT, Boissard CG;
PI Gribkoff VK;
XX
DR WPI; 2002-122069/16.
XX
PT P-PSDB; AAE16599.
XX
PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
it, for diagnosing, treating and identifying modulators useful in
treating neurological, neurophysiological and neuropsychological
diseases.
XX
PS Claim 3; Fig 1; 128pp; English.
XX
XX The invention relates to potassium channel polypeptides referred to as
KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
polypeptides are useful for identifying compounds that modulate their
biological activity. The compounds identified and KCNQ5 polynucleotides
are useful for treating acute and chronic pain, migraine, acute stroke,
dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
depression, bipolar disorders, sleep disorders, eating disorders,
addiction, myokymia, Alzheimer's disease, age-associated memory loss,
learning deficiencies, cognitive disorders and motor neuron diseases. The
nucleic acid molecules of the invention are further useful for treating
neurophysiological, neuropsychological disorders, asthma, neuron cell

CC death and brain tumors. They are also used in gene therapy and antisense
CC therapy. KNO5 polypeptides modulate synaptic transmission and electrical
CC excitability in the brain and are useful for generating antibodies. They
CC are also useful to affinity purify biological effectors from biological
CC materials e.g. disease tissues or cells. The present sequence is human
CC KNO5 cDNA
XX
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

| | | | |
|---|---------|--|------|
| Alignment Scores: | | | |
| Pred. No.: | 0 | Length: | 2694 |
| Score: | 4588.00 | Matches: | 897 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |
| US-09-810-796-4 (1-897) x AAD27192 (1-2694) | | | |
| QY | 1 | MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAargGly | 20 |
| DB | 1 | ATGAAGGATGTGGAGTCCGGCGGGGCGAGGTGCTGCTGAACTCGGCAGCCGCCAGGGGC | 60 |
| QY | 21 | AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu | 40 |
| DB | 61 | GACGGCTGCTACTGCTGGGACCCCGCGGGCCAGCTTGTGGCGCGCGCGTGGCCCTG | 120 |
| QY | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 |
| DB | 121 | AGGGAGAGCGCGGGGCAAGCAGGGGGCCGCGATGAGCTGCTGGGGAAGCCGCTCTCT | 180 |
| QY | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 |
| DB | 181 | TACACAGTAGCAGAGCTGCGCGGCACCGTCAAGTACCGCGGGTGCAGAACTACCTG | 240 |
| QY | 81 | TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu | 100 |
| DB | 241 | TACACGCTGCTGAGAGACCCCGCGCTGGCGCTTCATCTACCAGCTTCGTTTCTCTC | 300 |
| QY | 101 | LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 |
| DB | 301 | CTTGCTTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 360 |
| QY | 121 | AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 |
| DB | 361 | GCTCAAGTTGCTCTTGATCTCTGGATCTCGTATGATTCGCTTGTGGTTGGAGTTC | 420 |
| QY | 141 | IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTrpGlnGlyArgLeu | 160 |
| DB | 421 | ATCATTGGAATCTGGTCTGGCGGTGCTGTGTGTCATATAGAGGATGCGCAAGGAGACTG | 480 |
| QY | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 |
| DB | 481 | AGGTGTCGCGAAGCCCTTCGTGTATAGATACCATTTCTTATCGCTTCATAGCA | 540 |
| QY | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 |
| DB | 541 | GTTGTTTCTGCAAAACTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCTCGT | 600 |
| QY | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu | 220 |
| DB | 601 | TTCCATCAGATCTCCCGCATGGTGGCGATGGACCGAAGGGGAGGCACTTGGAAATCTAG | 660 |
| QY | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu | 240 |
| DB | 661 | GGTTACAGTGTATGCTACACAGGAATTAATCAGCTTGGTACATAGATTTTGT | 720 |
| QY | 241 | ValLeuIlePheSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| DB | 721 | GTTCTTATTTTTCGCTTCTTCTGCTATCTGCTGGTGGAAAGGATGCCAATAAGAGTTT | 780 |
| QY | 261 | SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 |

| | | | |
|----|------|---|------|
| DB | 781 | TCTACATATGCAGATGCTCTCTGTGGGGCACAATTTACATTGACAACTATTGGCTATGGA | 840 |
| QY | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
| DB | 841 | GACAAACTCCCTTAACTTGGCTGGGAAGATTGCTTTCTTGCAAGCTTTCATCTCTTGGC | 900 |
| QY | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| DB | 901 | ATTTCTTTCTTGGCACTTCTCGCGCACTTCTTGGCTCAGGTTTTCATTTAAAGTACAA | 960 |
| QY | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaSerLeuLeuGln | 340 |
| DB | 961 | GAACAACACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTCCCAACCTCATTCAG | 1020 |
| QY | 341 | CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro | 360 |
| DB | 1021 | TGTGTTTGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA | 1080 |
| QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGlnGlnGluAlaSerSer | 380 |
| DB | 1081 | CACCTTGAAGGCTTGCACACCTGCAGCCCTACCAAGAAAGAACAGGGGAAGCATCAAGC | 1140 |
| QY | 381 | SerGlnLysLeuSerPheLysGluArgValAlaArgMetAlaSerProArgGlyGlnSerIle | 400 |
| DB | 1141 | AGTCAGAGCTAAGTTTAAAGGAGCGAGTCGCGATGCTAGCCCGGAGGCGCAGATATT | 1200 |
| QY | 401 | LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu | 420 |
| DB | 1201 | AAAGCGCAGACAGCCTCAGTAGGTGACAGGAGTCCCAGACCCAGACATCACAGCCGAG | 1260 |
| QY | 421 | GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro | 440 |
| DB | 1261 | GGCAGTCCCACCAAGTGCAGAGAGCTGGAGCTTCAACACCGAACCCCGCTTCCGGCCC | 1320 |
| QY | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 |
| DB | 1321 | TCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTAGTAGTGTGACACAGCCCTTGGC | 1380 |
| QY | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 |
| DB | 1381 | ACTGATGATGATATGATGATAAAGGATGCCAGTGTGATGATATCATCAGTGAAGACCTCAC | 1440 |
| QY | 481 | ProProLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 |
| DB | 1441 | CCACCACTTAAACTGTCTCGAGCTATCAGAAATTAAGAAATTCATGTTGCMAAACGG | 1500 |
| QY | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 |
| DB | 1501 | AAGTTTAAAGGAACGTTACGTCCTCATATGATGATAAAGATGTCATTGAACAATATCTGCT | 1560 |
| QY | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| DB | 1561 | GGTCATCTGGACATGTTGTGTAGAAATTAAGACCTTCAACACGCTGTGTGATCAAAATCTT | 1620 |
| QY | 541 | GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu | 560 |
| DB | 1621 | GGAAAGGGCAAAATCACATCAGATAGAGAGCCGAGAGAAATAACAGCAGAACATGAG | 1680 |
| QY | 561 | ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer | 580 |
| DB | 1681 | ACCACAGCATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC | 1740 |
| QY | 581 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 600 |
| DB | 1741 | ATAGAGTCCAGCTGGACTGCTACTAGACATCATCAACAGGTCCTTCCGAAAGGCTCT | 1800 |
| QY | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer | 620 |
| DB | 1801 | GCTTCAGCCCTCGCTTGTGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT | 1860 |
| QY | 621 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 640 |
| DB | 1861 | GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGACAAAAACAGTGGCTGC | 1920 |

101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120 QY
301 CTGTGTTTGGTGTGCTGATTTTCTAGTGTGTTTCTACCATCCTCGAGCACACAAAATTG 360 Db
121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140 QY
361 GCCTCAAGTTCCTTGTATCCTCGAGTTCTGTGATGATTTGTCTGTTTGGAGTTTC 420 Db
141 IleIleArgIleTTPSerAlaGlyCysCysArgTyrArgGlyTyrPgingIleArgLeu 160 QY
421 ATCATTCGAATCTGTCTCGGGTGTCTGTGTGATATAGAGATGAGGATGCAAGGAGACTG 480 Db
161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleLeuIleAlaSerIleAla 180 QY
481 AGGTTTGTCTCGAAAGCCCTTCTGTATTATAGATACCATTTGTTCATTGCTTCAATAGCA 540 Db
181 ValValSerAlaLeuThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200 QY
541 GTTGTTCCTGCAAAACTCAGGGTAATATTTTGGCAGCTCTGCACCTCAGAAGTCTCGGT 600 Db
201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220 QY
601 TTCCTACAGATCCTCCGATGTCGCATGGACCGAGGGAGGCACCTTGGAAATTTACTG 660 Db
221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240 QY
661 GGTTCAAGTGTATTGCTCACAGCAAGGAATTAATCACAGCTTGTGATAGGATTTTGTG 720 Db
241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260 QY
721 GTTCTATTTTTCGTTCTTCTTCTGTTATCTGGTGGAAAGGATGCAATAAAGAGTTT 780 Db
261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280 QY
781 TCTACATATGAGATCTCTCTGTTGGGACACAAATTACATTGACAACTATTGGCTATGGA 840 Db
281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300 QY
841 GACAAACTCCCTTAATCTGCTGGTGGAGATTTGCTTTCTGCAGGCTTTGCATCTCTGGC 900 Db
301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320 QY
901 ATTTCTTCTTTCGACTCTCTGCGGCAATCTTGGCTCAGGTTTGCATTTAAAGTACAA 960 Db
321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340 QY
961 GAACAAACCGCCAGAAACACTTGGAGAAAGAGAGAACCCAGCTGCCAACTCATTCAG 1020 Db
341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360 QY
1021 TGTGTTTGGCTAGTTAGCGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAGCCA 1080 Db
361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380 QY
1081 CACTTGAAGCCCTTGCAACCTCGAGCCCTTACCAGAAAGAACAGGGAGCATCAAC 1140 Db
381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400 QY
1141 AGTCAGAAAGCTAAGTTTAAAGGAGCGAGTCCGATGCTAGCCCGAGGGGCCAGAGTATT 1200 Db
401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420 QY
1201 AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGAGGTCCCAAGACCCGACATCAAGCCGAG 1260 Db
421 GlySerProThrLysValGlnLysSerTyrPheAsnAspArgThrArgPheArgPro 440 QY
1261 GGCAGTCCCAAGTTCAGAAAGCTGGAGCTTCAACGCCGACCCCGCTTCCGCGCC 1320 Db
441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460 QY
1321 TCGTGGCCCTCAAAAGTTCTCAGCCAAACCAAGTATGATGATGCTGACAGCCCTTGGC 1380 Db
461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480 QY

1381 ACTGATGATATATGATGAAAAAGGATCCAGTGTGATGTATCAGTGAAGACCTACC 1440 Db
481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500 QY
1441 CCACCACCTTAAACATGTTCATTCGAGCTATCAGAAATTAGAAATTTCACTGTCGAAAACGG 1500 Db
501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520 QY
1501 AAGTTTAAAGAAACATTAGCTCCATATGATGTAAAGATGTCAATTGAACAATATCTGCT 1560 Db
521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540 QY
1561 GGTCACTCGACATGTTGTAGAAATTAAAGCCCTCAAAACACGTTGTGATCAAAATCTT 1620 Db
541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560 QY
1621 GGAAGAGGGCAATACATCAGATAGAGAGCCGAGAGAAATTAACAGCAGACATGAG 1680 Db
561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580 QY
1681 ACCACAGACGATCTCAGTATGCTCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740 Db
581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600 QY
1741 ATAGAATCCAAGCTGGACTGCTTACTAGACATCTATCAACAGGTCCTTCGAAAGGCTCT 1800 Db
601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620 QY
1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860 Db
621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640 QY
1861 GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGCAAAACAGTGGCTGC 1920 Db
641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660 QY
1921 TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTCGAGTTTCATCTGACGCCAAAT 1980 Db
661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680 QY
1981 GAGTTTCAGTCCCAAGACTTCTACGGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040 Db
681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700 QY
2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCCACCAACACCATTTGCAACCAA 2100 Db
701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720 QY
2101 ATAAATACGGCACCAAGCCAGCAGCCCAACACTTACAGATCCCACTCTCTCTCCCA 2160 Db
721 AlaIleLysHisLeuProArgProGluThrIleHisProAsnProAlaGlyLeuGlnGlu 740 QY
2161 GCCATCAAGCATCTGCCCGAGCCAGAACTCTGACCCCTTAACCTGCGAGGCTTACAGAA 2220 Db
741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760 QY
2221 AGCATTTCTGACATCAACACTGCTTGTTCCTTCCAGGAAATGTTCAGTTGCAACAG 2280 Db
761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 780 QY
2281 TCAATCTCACAAGGACCGTTCTATAGGAAAAAGCTTTGACATGGGAGGAGAACTCTG 2340 Db
781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800 QY
2341 TTGCTGTCTGTCTCCATGTCGCCGAGGACTTGGCAATCTTTGTCTGTGCAAAACCTG 2400 Db
801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820 QY
2401 ATCAGTTCAGCCAGGAACTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2460 Db
821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840 QY

Db 2461 GGCACCCAGATTTTACCCCAATGGAGGAATCCAAATTTGTTATTAACGTGATGAAGAG 2520
 QY 841 ValGlyProGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
 Db 2521 GTGGGTCCGGAAGACAGACAGACACACTTTTGATGCGCACCGCAGCCTGCCAGGGA 2580
 QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
 Db 2581 CQTGCTTTGTCATCAGATCTCTCTAAGGACTGGAAGTCACGATCATCTCAGAGCATTTGT 2640
 QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLeuLeuLys 897
 Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCTATGTCAAACTGAAA 2691

RESULT 4

AA514651
 ID AA514651 standard; cDNA; 3071 BP.
 XX AC AA514651;
 XX DT 18-DEC-2001 (first entry)
 XX DE Human cDNA for voltage gated potassium channel hKCNQ5.
 XX KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
 KW pain; gene therapy.
 XX OS Homo sapiens.
 XX WO200170759-A1.
 XX FN 27-SEP-2001.
 XX PD 20-MAR-2001; 2001WO-US0093328.
 XX PR 21-MAR-2000; 2000US-0190954P.
 XX PA (ICAG-) ICAGEN INC.
 XX PI Jegla TJ;
 XX WPI; 2001-611467/70.
 XX DR Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ approximately a- subunits.

PS Claim 5; Page 61-62; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-
 CC subunit of a KCNQ potassium channel, with a subsequence having 65%
 CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
 CC and forms a KCNQ potassium channel having the characteristic of voltage-
 CC gating with at least an additional KCNQ alpha-subunit. Also included in
 CC the scope of the invention are the nucleic acids encoding hKCNQ5
 CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
 CC vectors encoding them, antibodies against them, the use of 3-dimensional
 CC computer modelling to identify molecules that bind to a KCNQ containing
 CC potassium channel and modulate ion flux through the channel. The KCNQ
 CC polypeptide is useful for identifying a compound that increases or
 CC decreases ion flux through a potassium channel expressed in an eukaryotic
 CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
 CC used in gene therapy) is useful as a pharmaceutical agent for treating
 CC diseases involving abnormal ion flux, such as disorders of the central
 CC nervous system, such as epilepsy, migraines, hearing and vision problems,
 CC psychotic disorders, seizures, learning and memory disorders, stroke and
 CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
 CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
 CC computer databases to find variants of the sequence which are associated
 CC with disease states, is useful for screening mutations of KCNQ5. The

CC present sequence is a representative cDNA for hKCNQ5
 XX Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 3071
 Score: 4584.00 Matches: 896
 Percent Similarity: 99.89% Conservative: 0
 Best Local Similarity: 99.89% Mismatches: 1
 Query Match: 99.91% Indels: 0
 DB: 4 Gaps: 0
 US-09-810-796-4 (1-897) x AA514651 (1-3071)

QY 1 MetLysAspValGluSerGlyArgValLeuLeuAanSerAlaAlaAlaArgGly 20
 Db 10 ATGAAGGATGTGGAGTCGGGCGGCGGAGGTGCTGCTGAACCTGGCAGCGCCAGGGGC 69
 QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 Db 70 GACGGCTGTCTACTGCTGGGCACCGCGCGCCACGCTTGGTGGCGGGCGGTGGCGCTG 129
 QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 Db 130 AGGAGAGCCCGCGGCGGCAAGCAGGGGCGCGGATGAGCTGCTGGGAAGCCGCTCTCT 189
 QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
 Db 190 TACACGAGTACCCAGAGCTGCGCGCGCAACGTCAAGTACCGCGGGTGCAGAACTACCTG 249
 QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
 Db 250 TACAACGTGCTGGAGAGACCCCGCGGTGGCGGTTCATCTACCAAGCTTTCGTTTTTCTC 309
 QY 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
 Db 310 CTGTGCTTTGGTTGCTGTGATTTTGTGAGTGTTTCTACCATCCCTGAGACACAAATATG 369
 QY 121 AlaSerSerCysLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140
 Db 370 GCCTCAAGTTGCTCTTGATCCTGGAGTTGCTGATGATTGCTCTTTGGTTGGAGTTC 429
 QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
 Db 430 ATCATTCGAATCTGGTCTGCGGGTGTGTTGTGATATAGAGGATGCAAGGAGACTG 489
 QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
 Db 490 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATGTTCTTATCGCTTCAATAGCA 549
 QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
 Db 550 GTTGTCTCTGCAAAACTCAGGGTAATATTTTTGCCACGTCTGCACTCAGAAGTCTCCGT 609
 QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTrpLysLeuLeu 220
 Db 610 TTCCTACAGATCTCTCGCATGTCGCGATGACCCAGGGGAGGACACTTGGAAATTTACTG 669
 QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu 240
 Db 670 GGTTCAGTGGTTTATGTCTACAGCAAGGAATTAATACAGCTTGGTATAGGATTTTGT 729
 QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
 Db 730 GTTCTTATTTTTTCGTTCTTCTTCTGCTATCTGTTGGAAAGGATGCCAATAAGAGTTT 789
 QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
 Db 790 TCTACATATGAGATGCTCTCTGTTGGGGCAACAATTAATTCACAACTATTGGCTATGGA 849
 QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
 Db 850 GACAAAACCTCCCTAACTTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCTCTG 909

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|----|------|---|------|
| QY | 301 | IleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| Db | 910 | ATTTCCTTTCTTGGCTTCCTGCGGCTATCTTGGCTCAGTTTGGCTTAAAGTACAA | 969 |
| QY | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuLysGln | 340 |
| Db | 970 | GAACAACACCCGCGAAGAACCTTTTGAGAAAAGAGAACCCGCTGCGCAACCTCAITTCAG | 1029 |
| QY | 341 | CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro | 360 |
| Db | 1030 | TGTGTTTGGCGTAGTTCGCGAGCTGAGGAAATCTGTTCCATTCGCAACCTGGAAGCCA | 1089 |
| QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer | 380 |
| Db | 1090 | CACITGAAGGCTTGCACACCTGCAGCCCTACCAAGAAAGAACCAAGGGGAGCATCAAGC | 1149 |
| QY | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 |
| Db | 1150 | AGTCAGAAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCGAGGGCCAGATATT | 1209 |
| QY | 401 | LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu | 420 |
| Db | 1210 | AGAGCCGACAGCCCTCAGTAGTGCAGAGGAGTCCCAAGCACCACCATCACAGCCGAG | 1269 |
| QY | 421 | GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro | 440 |
| Db | 1270 | GGCAGTCCCAACCAAGTGCAGAAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC | 1329 |
| QY | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 |
| Db | 1330 | TCGCTGCGGCTCAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGCACAGCCCTTGGC | 1389 |
| QY | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 |
| Db | 1390 | ACTGATGATGATATATGATGAAAAGAGTGCAGAGTGTGATGATCATAGTGGAGACCTACC | 1449 |
| QY | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 |
| Db | 1450 | CCACCACTTAAACTGTCTATCGAGCTATCAGAAATATGAAATTTCAATTTGTCAAAACGG | 1509 |
| QY | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 |
| Db | 1510 | AAGTTTAAAGAAACRTTACGTCCATATGATGATAAAGATGTCAATTGAACAATATTCTGCT | 1569 |
| QY | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| Db | 1570 | GGTCATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAACACCGTGTTCATCAATTTCTT | 1629 |
| QY | 541 | GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu | 560 |
| Db | 1630 | GGAAAGGGCAATACATCAGATAGAGAGCGGAGAGAAATAACAGCAGAACATGAG | 1689 |
| QY | 561 | ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer | 580 |
| Db | 1690 | ACCACACACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAACAGGTACAGTCC | 1749 |
| QY | 581 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 600 |
| Db | 1750 | ATAGAATCCAGCTGGAGTCCCTACTAGACATTTATCAACAGTCTCTCGAAAGCTCT | 1809 |
| QY | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer | 620 |
| Db | 1810 | GCCTCAGCCCTCGCTTGGCTTTCATCCAGTTCCTCCACTTTTGAATGTGAACAGACATCT | 1869 |
| QY | 621 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 640 |
| Db | 1870 | GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGGCACAAAACAGTGGCTGC | 1929 |
| QY | 641 | LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn | 660 |
| Db | 1930 | TTATCCAGATCACTAGTGCCACATCTCCGAGAGGCTGCAGTTTCATTTCTGACGCCAAAT | 1989 |

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|----|------|---|------|
| QY | 661 | GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln | 680 |
| Db | 1990 | GAGTTTCAGTGGCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG | 2049 |
| QY | 681 | ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln | 700 |
| Db | 2050 | GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTCGCAACCAA | 2109 |
| QY | 701 | IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro | 720 |
| Db | 2110 | ATAAATACGGCACCCCAAGCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA | 2169 |
| QY | 721 | AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu | 740 |
| Db | 2170 | GCATCAACATCTGCCAGGCGCAGAACTCTGCACCTTAACCTGCGAGCTTACAGGAA | 2229 |
| QY | 741 | SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln | 760 |
| Db | 2230 | AGCATTTCTGAGCTCACCCCTGCTTGTGCTTCAAGGAAAATGTTTCAGGTTGCACAG | 2289 |
| QY | 761 | SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu | 780 |
| Db | 2290 | TCAATCTCACCAGGACCGTCTTATGAGGAAAAGCTTTGACATGGAGGAGAAACTCTG | 2349 |
| QY | 781 | LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu | 800 |
| Db | 2350 | TTGCTGCTGTGCTCCCTGCGGAGGAGTGGGCAAAATCTTTGCTGTGCAAAACCTG | 2409 |
| QY | 801 | IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg | 820 |
| Db | 2410 | ATCAGGTCGAGCCGAGGAACATGATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCAGA | 2469 |
| QY | 821 | GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu | 840 |
| Db | 2470 | GGCAGCCACAGATTTTACCCTCAATGGAGGAATCCAAATTTGTTATACTGATGAAGAG | 2529 |
| QY | 841 | ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu | 860 |
| Db | 2530 | GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCCACCGCCTGCCAGGAA | 2589 |
| QY | 861 | AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys | 880 |
| Db | 2590 | GCTGCTTTGCTGCTCAGACTCTTAAGGACTGGAAGGTACGATCATCTCAGAGCATTTGT | 2649 |
| QY | 881 | LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys | 897 |
| Db | 2650 | AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGGCTTGCCTCATGTCAAACTGAAA | 2700 |

RESULT 5

AAH49499 standard; DNA; 3074 BP.

AC AAH49499;

DT 11-DEC-2001 (first entry)

XX Human KNO5 DNA.

XX KNO5; potassium channel protein; human; neurological; cardiovascular;

XX anticonvulsant; excitability modulator; membrane potential; neuron;

XX voltage-dependent KNO5 potassium channel; cardiomyocyte; epilepsy;

XX screening; central nervous system disease; cardiovascular disease; ds.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 110..2908

XX /*tag= a

XX /product= "KNO5"

XX DE10013732-Al.

XX 27-SEP-2001.

QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
DB 1775 GGTATCTGGACATGTTGTGTAGAAATTAAAGCCTTCAACACGCTGTTGATCAAAATCTT 1834
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGlnLysIleThrAlaGluHisGlu 560
DB 1835 GGAAAGGCGCAATCACATCAGATAGAAAGAGCGAGAGAAATAACAGCAGAACATGAG 1894
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
DB 1895 ACCACAGACGATCTCAGTATGCTCGTGGGTGTCAAGTTGAAACACAGGTACAGTCC 1954
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrglnGlnValLeuArgLysGlySer 600
DB 1955 ATAGAAATCCAAAGCTGAGCTGCTACTACATCATCAACAGGTCTCTCGAAAGGCTCT 2014
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
DB 2015 GCCTCAGCCCTCGCTTTCGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
QY 621 AspTyrglnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
DB 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGGCACAAACAGTGGCTGC 2134
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
DB 2135 TTATCCAGATCAACTAGTGCACATCTCGAGAGCGCTGCAGTTCATTCGACGCCAAT 2194
QY 661 GluPheSerAlaGlnThrPheTyrrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
DB 2195 GAGTTCAGTCCGACACTTTCAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleAlaThrAsnThrIleAlaAsnGln 700
DB 2255 GTGCCAATTAGTCAMAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCATTCGAAACCAA 2314
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
DB 2315 ATAAATACGCGACCCCAAGCGCAGCGCCCAACACTTTACAGATCCACCTCTCTCCCA 2374
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
DB 2375 GCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAA 2434
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
DB 2435 AGCATTTCTGACGTCAACCTGCTGTGTGCTCCAGAGAAATGTTTCAGTTGCACAG 2494
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
DB 2495 TCAAACTCCAAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAAACTCTG 2554
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
DB 2555 TTGTCTGTCTGCTCCATGGTGGCGAAGACTTGGCGAAATCTTTGTGTGTGCAAAACCTG 2614
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerArg 820
DB 2615 ATCAGGTGCGACCGAGGAACCTGAATATACAACTTCAGGAGTGAATGAGTGCCTCCAGA 2674
QY 821 GlySerGlnAspPheTyrrProLysThrArgLysSerLysLeuPheIleThrAspGluGlu 840
DB 2675 GGCAGCCAAAGATTTTATCCCAATGAGGGAATCCAAATTTGTTATTAATGATGAAGAG 2734
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
DB 2735 GTGGGTCCCGAAGAGACAGACAGACACTTTGATCCCGCAGCCGAGCTCCGAGGAA 2794
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
DB 2795 GCTGCTTTGTCATCAGATCTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2854

QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
DB 2855 AAGCGAGGAGAGATGACAGATGCGCTCAGCTTGCTCATGTCAAACTGAAA 2905
RESULT 6
ADB78684
ID ADB78684 standard; cDNA; 3074 BP.
XX
AC ADB78684;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human potassium channel subunit mutant cDNA SEQ ID NO:55.
XX
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrctic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephroretropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
OS Synthetic.
OS Homo sapiens.
XX WO2003008574-A1.
XX
XX 30-JAN-2003.
XX
XX 08-JUL-2002; 2002WO-AU000910.
XX
XX 18-JUL-2001; 2001AU-00006452.
XX 05-MAR-2002; 2002AU-00009910.
XX 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
XX (WALL/) WALLACE R W.
XX
XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
XX Berkovic SF, Scheffer IE;
XX WPI; 2003-239332/23.
XX
XX Identifying predisposition to an ion channel dysfunction, such as
XX periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
XX schizophrenia, anxiety and depression, by detecting encoding-gene
XX mutation events.
XX
XX Claim 6; SEQ ID NO 55; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyrctic,
XX antiarrhythmic, analgesic, nephroretropic, antidiabetic, and
XX neuroleptic, tranquiliser, antidepressant, antiparkinsonian,
XX ophthalmological activity. A polynucleotide of the invention acts as an
XX ion channel agonist, or ion channel antagonist. The methods, isolated
XX nucleic acids, polypeptides, antibody, selective agonist, antagonist or
XX modulator of an ion channel, cells and genetically modified non-human
XX animal, are useful for the diagnosis and treatment of epilepsy and/or a
XX disorder associated with ion channel dysfunction, such as hyper- or hypo-
XX kalemic periodic paralysis, myotonias, malignant hyperthermia,
XX myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
XX disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
XX depression, phobic obsessive symptoms, neuropathic pain, inflammatory
XX pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
XX Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
XX fibrosis, congenital stationary night blindness and total colour
XX blindness. The present sequence represents a mutant cDNA of the
XX invention. The sequence data for this patent is not represented in the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3074
Score: 4574.00 Matches: 895
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 2
Query Match: 99.69% Indels: 0
DB: 10 Gaps: 0

US-09-810-796-4 (1-897) x ADB78684 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAasnSerAlaAlaAlaArgGly 20
DB 215 ATGAAGGATGTGGAGTCGGCGCGGGCAGGGTGTCTGCTGAATCTGGCAGCCGCGGGGC 274
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 275 GACGGCTGTACTGTGGGCACCCCGCGGCCACGCTTGGTGGCGGGCGGTGGCCGTG 334
QY 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 335 AGGGAGAGCCCGCGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGAAGCCGCTCTCT 394
QY 61 TyrThrSerSerGlnSerCysArgArgAenValLysTyrArgValGlnAasnTyrLeu 80
DB 395 TACACGAGTAGCCAGAGTGC CGCGGCCAACGTCAGAGTACCGCGCGGTGCAGAACTACCTG 454
QY 81 TyrAenValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
DB 455 TACAACGTGTGGAGAGACCCCGCGCGTGGGGTTCATCTACACGCTTTCGTTTTTCCTC 514
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 515 CTGTGCTTTGGTGTCTGATTTTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATTG 574
QY 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheCysLeuGluPhe 140
DB 575 GCCTCAAGTGTCTTGCATCTGGAGTTCTGTGATGATGTCTGCTTTGGTTTGGAGTTC 634
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 635 ATCAATCGAATCTGTCTGCGGGTGTCTGTCTGATATAGAGGATGGCAAGAGACTG 694
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 695 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTTATCGCTTCATAGCA 754
QY 181 ValValSerAlaLysThrGlnGlyAenIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 755 GTTGTCTCTGCAAAACTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAACTCTCGGT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTrpLysLeuLeu 220
DB 815 TTCTTACAGATCCTCCGATGTGGCATGGAGCCGAGGGAGGCACCTTGGAAATTTACTG 874
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 875 GGTTCAGTGTATTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTACATAGGATTTTG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAasnLysGluPhe 260
DB 935 GTTCTATTATTTTTCGTTCTTCTGTCTATCTGTGGTGGAAAGGATGTCCTAATAAGAGTTT 994
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 995 TCTCATATGCAAGTGTCTCTGTGGTGGGCACAATTTACATTACAACTATTGGCTATGGA 1054
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 1055 GACAAAACCTCCCTAACTTGGCTGGGAGAGATTGCTTTCTGACAGGCTTTGCACTCTCTGGC 1114

QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1115 ATTTCTTTTTCGACATTCCTCGCGCATTTCTTGCTCAGGTTTTCATTTAAAGATACAA 1174
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAasnLeuIleGln 340
DB 1175 GAACAAACACCGCCAGAAACACTTTGAGAAAGAGAGAACCCAGCTGCCACCTCATTCAG 1234
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1294
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
DB 1295 CACTTGAAGGGCTTGCACACCTGCAGCCCTACCAAGAAAGAACCAAGGGGAAGCATCAAGC 1354
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
DB 1355 AGTCAGAGCTTAAGTTTTAAGAGCGAGTGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
DB 1415 AAGACCCGACAAAGCCTCAGTAGTGACAGGAGTCCCAAGCACCGACATCACAGCCGAG 1474
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAasnAspArgThrArgPheArgPro 440
DB 1475 GGCAGTCCACCAAGTAGTCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC 1534
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
DB 1535 TCGCTGCCCTTCAAAAGTTCTCAGCCAAACACGATGATAGTGTGACACAGCCCTTGGC 1594
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
DB 1595 ACTGATGATGTATATGATGAAAAGGATGCCAGTGTGATGTATCAGTGGAGACCTCACC 1654
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
DB 1655 CCACCACTTAAACTGTCTATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTCAAAACGG 1714
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
DB 1715 AAGTTTAAGGAACACTTACGTCATATGATGTAAAGATGTCAATTTGAACATATTCGCT 1774
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
DB 1775 GGTCACTCGACATGTTGTTGTGTAGAAATTAAGAGCTTCAACACAGCTGTGATCAAAATCTT 1834
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
DB 1835 GGAAAAGGGCAAAATCACATCAGTAAGAGAGCCGAGAGAAATAACACAGCAACATGAG 1894
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
DB 1895 ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAACACAGGTACAGTCC 1954
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
DB 1955 ATAGAATCCAAGCTGGACTGCTCTTACACATCTATCAACAGGTCCTTCGGAAGGCTCT 2014
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
DB 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCAACCTTTTGAATGTGAACAGACATCT 2074
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAasnSerGlyCys 640
DB 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGGTTCGCAACAAAACAGTGGCTGC 2134
QY 641 LeuSerArgSerThrSerAlaAasnIleSerArgGlyLeuGlnPheIleLeuThrProAasn 660
DB 2135 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGGCCTGCAGTTCATTTCTGACGCCAAT 2194
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680

Db 2195 GAGTTTCAGTCCGACAGCTTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2254
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2255 GTGCCAATTAGTCAAGAGGATGGCTCAGCAGTGGCAGCCACCAACACATGTGCACCAA 2314
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2315 ATAATACGGCACCCCAAGCCAGCCCAACAATTTACAGATCCCACTCTCTCTCCA 2374
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2375 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGACACCCCTAACCTTGACAGGCTTACAGAA 2434
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2435 AGCATTTCTGACGTCACCACTGCTTGTGCTCCCAAGGAAATGTTACAGTTGCACAG 2494
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrIleu 780
Db 2495 TCAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2554
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2555 TTGTCGTCTGTCCCATGTCGCGAGGACTTGGGCAATCTTGTCTGTGCAAAACCTG 2614
Qy 801 IleArgSerThrGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820
Db 2615 ATCAGTGCAGCCAGGAACTGAATATACAACTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2674
Qy 821 GlySerGlnAspPheTyrrProLysThrArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2675 GGCAGCCAGATTTTACCCCAATGAGGAGGAAATCAAATGTTTATTAATGATGAAGAG 2734
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2735 GTGGTCCCGAGAGACAGACAGACACACTTTTGTATGTCGCGCACCGACGCTGCCAGGAA 2794
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2795 GCTGCTCTTGCATCAGACTCTTAAGGACTGGAAGTCCAGATCATCTCAGAGCATTTGT 2854
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2855 AAGCAGGAGAAAGTACAGTGCCTTCAGCTTGCTTCATGTCAAACTGAAA 2905
RESULT 7
AAS14653
ID AAS14653 standard; cDNA; 2667 BP.
XX AAS14653;
XX AC AAS14653;
XX DT 18-DEC-2001 (first entry)
XX DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.
XX KW Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;
KW cerebroprotective; neurotropic; analgesic; vision disorder;
KW central nervous system disorder; epilepsy; migraine; hearing disorder;
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW pain; gene therapy; splice variant.
XX OS Homo sapiens.
XX FH Location/Qualifiers
FT CDS 1..2967
FT /tag= a
FT /product= "hKCNQ5-2"
XX PN WO200170759-A1.
XX PP 27-SEP-2001.

XX PF 20-MAR-2001; 2001WO-US009328.
XX PR 21-MAR-2000; 2000US-0190954P.
XX PA (ICAG-) ICAGEN INC.
XX PI Jegla TJ;
XX WI WIPI; 2001-611467/70.
DR P-PSDB; AAU09021.
XX PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
PT identifying a compound modulating ion flux in eukaryotic cell or cell
PT membrane expressing the protein, comprises KCNQ approximatelya- subunits.
XX Claim 5; Page 63-64; 78pp; English.
XX The invention relates to an isolated polypeptide comprising an alpha-
CC subunit of a KCNQ potassium channel, with a subsequence having 65%
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
CC and forms a KCNQ potassium channel having the characteristic of voltage-
CC gating with at least an additional KCNQ alpha-subunit. Also included in
CC the scope of the invention are the nucleic acids encoding hKCNQ5
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
CC vectors encoding them, antibodies against them, the use of 3-dimensional
CC computer modelling to identify molecules that bind to a KCNQ containing
CC potassium channel and modulate ion flux through the channel. The KCNQ
CC polypeptide is useful for identifying a compound that increases or
CC decreases ion flux through a potassium channel expressed in an eukaryotic
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
CC used in gene therapy) is useful as a pharmaceutical agent for treating
CC diseases involving abnormal ion flux, such as disorders of the central
CC nervous system, such as epilepsy, migraines, hearing and vision problems,
CC psychotic disorders, seizures, learning and memory disorders, stroke and
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
CC computer databases to find variants of the sequence which are associated
CC with disease states, is useful for screening mutations of KCNQ5. The
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 2667
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservatives: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 4 Gaps: 1
US-09-810-796-4 (1-897) x AAS14653 (1-2667)
Qy 1 MetLysAspValGluSerGlyArgValLeuLeuLeuSerAlaAlaArgGly 20
Db 1 ATGAAGGATGTGGAGTCGGCGCGGAGGCTGCTGTAACCTCGGAGCGCGGAGGCG 60
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 61 GACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGGAGAGCCCGCGGCGCAAGCAGCGGGCGCGGATGAGCTGTGCTGGGAGACCGCTCTCT 180
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCAGAGCTGCGCGCAACGTCAAGTACCGCGGCGGCTGCAACTACTCTG 240
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACAACGTGCTGAGAGAGACCCCGCGGCTGGGCTTCTATCTACACGCTTTCGTTTTCTC 300

QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrIysLeu 120
Db 301 CTGTCCTTGGTGTCTGATTTTGTAGGTTTCTTACCATCCCTGAGCACAAATTTG 360
QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCTCAAGTTGCTCTTGATCTGGAGTTCGTGATGATTTGCTCTTGGTTTGGAGTTC 420
QY 141 IleIleArgIleTrpSerAlaGlyCysCysCysArgTyArgIleTrpIleGlyArgLeu 160
Db 421 ATCATTCCGAATCTGCTCTGCGGTTCTGTTTCGATATAGAGGATGGCAAGAGACTG 480
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla 180
Db 481 AGGTTTGCTCGAAAGCCCTTCTGTGTATAGATACATTTGTTCTTATCGCTTCAATAGCA 540
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTCTTCTGCAAAACTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAGTCTCCGT 600
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpIysLeuLeu 220
Db 601 TTCTTACAGATCTCTCGCATGTGCGCATGGACCGAAGGGAGGCACCTTGGAATTTACTG 660
QY 221 GlySerValValTyAlaHisSerIysGluLeuIleThrAlaTrpTyIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTACATAGGATTTTGT 720
QY 241 ValLeuIlePheSerSerPheLeuValTyLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTATTTTTCCTCTCTCTCTATCTGTGTTGGAAAGGATGCCATNANAAGTTT 780
QY 261 SerThrTyAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyGly 280
Db 781 TCTACATATGCAGATGCTCTCTGTGGGGCACAAATTACATTGACAACTATTGGCTATGGA 840
QY 281 AspyIysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAACTCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCTCTGGC 900
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 901 ATTTCTTTCTTTGCACTTCTGCGCGCATCTTGGCTCAGGTTTTCATTAANAAGTACAA 960
QY 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GAAACAACCCGACAGAAACACTTTCAGAAAAAGAGAACCCAGCTGCGCAACCTCATTAG 1020
QY 341 CysValTrpArgSerTyAlaAlaAspGluLysSerValSerIleAlaThrTrpIysPro 360
Db 1021 TGTGTTTGGCGPAGTTACGAGCTGATGAGAAATCTGTTTCATTGCAACCTGGAAGCCA 1080
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1081 CACTTGAAGGCTTGCACACCTGCAGCCCTTACC----- 1113
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1114 AATCAGAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGCCAGAGTATT 1173
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1174 AAGAGCCACCAAGCCCTCAGTAGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1233
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspAtqThrArgPheArgPro 440
Db 1234 GCGAGTCCCAACCAAGTGCAGNAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1294 TCGCTGCGCCTCAAAAGTTCTCAGGCCAAAACCCAGTGTAGATGCTGCACAGCCCTTGGC 1353
QY 461 ThrAspAspValTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480

Db 1354 ACTGATGATGATATATGATGAAAAAGGATGCCAGTGTGATGTATCATGATGGAAGACCTTCACC 1413
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1414 CCACACCTTAAACCTGTCTATTCGAGCTATCAGANTATGAATTTTCATGTTGCAAAACGG 1473
QY 501 LysPheLysGluThrLeuArgProTyArgValLysAspValIleGluGlnTySerAla 520
Db 1474 AAGTTTAAAGGAAACGTTACGTCATATGATGTAAGATGTCTATTGAAACAAATTTCTGCT 1533
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1534 GGTCACTCGGACATGTTGTGTAGATTAAGAGCCTTCAACACAGGTGTGATCAAAATCTT 1593
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1594 GGAAGAGGCAAAATCACATCAGATNAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1653
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1654 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTTCAAGGTTGAAAAACAGGTACAGTCC 1713
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyGlnGlnValIleLeuArgLysGlySer 600
Db 1714 ATAGAGTCCAAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1773
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1774 GCCTCAGCCCTCGCTTGTGCTTCAATCCAGATCCACCTTTTGATGTGAACAGACATCT 1833
QY 621 AspTyGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1834 GACTATCAAGCCCTGTGCATAGCAAGATCTTTCGGGTTCGACACAAAAACAGTGGCTGC 1893
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1894 TTATCCAGATCAACTAGTAGCCCAACATCTCGAGAGGCCCTGCAGTTCATTCTGCAGCCAAAT 1953
QY 661 GluPheSerAlaGlnThrPheTyAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 1954 GAGTTAGTCCGACGATCTTCTACGGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACAA 2073
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2074 ATAAATACGGCACCCCAAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2133
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2134 GCGATCAAGCATCTGCCCGAGCCAGAAACTCTGCACCTTAACCTTCGAGGCTTACAGNA 2193
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2194 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCCAAGGAAAAATGTTTCAGGTTGCACAG 2253
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2254 TCAATCTCAACCAAGGACCGTTCTATAGGAAAAAGCTTTGACATGGGAGGAGAACTCTG 2313
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2314 TTGTCGTCTCTGCCATGCTGCCAGAGACTTGGCAAAATCTTGTCTGTGCAAAACCTG 2373
QY 801 IleArgSerThrGluLeuLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2374 ATCAGGTCGACCGAGGAACCTGAATATACAACTTTTCAGGAGTGTGAGTCAAGTGGCTCCAGA 2433
QY 821 GlySerGlnAspPheTyProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840

Db 1066 GAAACACACCGCAGAAACATTTTGAGAAAGAGAGAAACCCAGCTGCACCACTCATTCAG 1125
Qy CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTriPlysPro 360
Db 1126 TGTGTTGGCTAGTTAGCAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGNAGCCA 1185
Qy HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGluAlaSerSer 380
Db 1186 CACTTGAAGGCGTTGCACACCTGCAGCCCTACC-----1218
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1219 AATCAGAAGCTAAGTTTTAAGAGCGAGTGCGCATGGCTAGCCCCAGGGGCCAGAGTATT 1278
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1279 AAGAGCCGACAGCCCTCAGTAGTCACAGAGGTCCTCCCAAGCACCAGACATCACAGCCGAG 1338
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1339 GGCAGTCCGCCCAACAAAGTCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC 1398
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1399 TCGCTGCCGCTCAAAAGTTCTCAGCCAAACAGGTGATAGTGTGACACAGCCCTTGGC 1458
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1459 ACTGATGATATATGATGAAAGAGATGCCAGTGTGATGATCATCAGTGGAGACCTCACC 1518
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1519 CCACCATTAAACTGTCTATTCGAGCTATCAGAATTATCAAAATTTTCATGTTGCAAAACGG 1578
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1579 AAGTTTAAAGGAAACATTACGTCATATGATGATAAAGATGTCATTGAAACAATATTCGCT 1638
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1639 GGTCACTCGCATGCTGTGTAGATTTAAAGCCITCAACACGCTGTGTGATCAAAATCTT 1698
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1699 GGAAAGGCGCAATCACATCATGATAAGAGAGCCGAGAGAAATAACACAGCAGAACATCAG 1758
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1759 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1819 ATAGATCCAGCTGAGCTGCTACTAGACATCTATCAACAGGCTCTTCGGNAGGCTCT 1878
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1879 GCCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCACTTTTGAATGTGAACACAGACATCT 1938
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1939 GACTATCAAGCCCTGTGTAGTAAAGATCTTTCCGGTTCGCAACAAACAGTGGCTGC 1998
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1999 TTATCCAGATCAACTAGTGCCAAACATCTCAGAGGCGCTGCAGTTCATTTGAGGCCAAT 2058
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2059 GAGTTTCAGTCCGACACTTCTACGCGCTTAGCCCTTACTATGACAGTCAAGTCAACACAG 2118
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700

Db 2119 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2178
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2179 ATAAATACGGCACCCAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2238
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2239 GCCATCAAGCATCTGCCCAGGCCAGAACTCTGCACCCCTAAACCTTCAGGCTTACAGGA 2298
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2299 AGCATTTCTGACGTCAACCACTGCTTGTGGCTCCCAAGGAAATGTTTCAGGTTGCACAG 2358
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2359 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2418
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2419 TTGCTGTCTCTCCCATGTGCGGAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2478
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 820
Db 2479 ATCAGTCCAGCCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2538
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2539 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATCAAGAG 2598
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2599 GTGGTCCGAGAGACAGACACACTTTTGTATGCCGACCGCAGCCCTGCCAGGGAA 2658
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2659 GCTGCCCTTGCATCAGACTCTCTAAGGACTCGAAGTCCAGATCATCTCTCAGAGCATTTGT 2718
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2719 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAA 2769
RESULT 9
AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
XX
XX
AC AAH43634;
DT 21-JAN-2002 (first entry)
DE Human ion-channel forming protein coding sequence.
DE Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
KW
XX Homo sapiens.
XX
XX Key Location/Qualifiers
CDS 59..2831
FT /*tag= a
FT /product= "Human ion-channel forming protein"
XX
XX WO200175108-A1.
XX
XX PD 11-OCT-2001.
XX
XX PF 03-APR-2001; 2001WO-US010875.
XX
XX PR 03-APR-2000; 2000US-0194255P.
XX
XX PA (LEXI-) LEXICON GENETICS INC.
XX
XX HU Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;


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Db 1698 GGTCACTGGACATGTTGTGAGAAATTAAAGCCCTTCAACACAGCGTTGATCAAAATCTT 1757
Qy GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1758 GGAAGAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAAAGCAGAGAACATCAG 1817
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1818 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGAGTCAAGGTTGAAAAACAGTACAGTCC 1877
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAAATCAAGCTGAGTCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1937
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTGGCTTCAATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1997
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGATAGCAAGAAATCTTTCGGGTTCGACAAAAACAGTGGCTGC 2057
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTTGCAGTTCTATCTGACGCCAAT 2117
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTCAAGTCCCACTTCTACGCGCTAGCCCTACTATGCACAGTCAAGCAACACAG 2177
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
Db 2178 GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGGCAGCCACCAACACCAATTCGAAACCA 2237
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2238 ATAAATCGGACCCACAGCCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2297
Qy 721 AlalIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2298 GCCATCAAGCATCTCCCGAGCCAGAAACTCTGCACCCCTAACCTTGCAGGCTTACAGAA 2357
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2358 AGCATTTCTGAGCTCACCACCTGCTCTGTGCTCCTCAAGGAAATGTTTCAGGTTGCACAG 2417
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2418 TCAATCTCACCAGAGCCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2477
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2478 TTGTCGTCTGTCCCATGTCGCGAAGGACITGGGCAAAATCTTGTCTGTGCAAAACCTG 2537
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 820
Db 2538 ATCAGTCGACCGAGAGAACTGAATATACAACTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2597
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2598 GGCACCCCAAGATTTTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAG 2657
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnPheProAlaArgGlu 860
Db 2658 GTGGTCCCGAAGACAGACACACACTTTTGTATGCGCACCGACGCTGCCAGGAA 2717
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2718 GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAAGTATCTCAGAGCAATTTGT 2777
Qy 881 LysAlaGlyLeuSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
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Db 2778 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2828
RESULT 10
AAC64371
ID AAC64371 standard; cDNA; 3718 BP.
XX
AC AAC64371;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
Stargardt-like macular dystrophy; cone-rod macular dystrophy;
Salla disease; ophthalmological; auditory; central nervous system;
cardioactive; anticonvulsant; gastrointestinal; muscular active;
age-related macular degeneration; macular degeneration; deafness;
epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
gastrointestinal disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009587.
XX
PR 14-APR-1999; 99US-0129274P.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
XX
DR WPI; 2000-647417/62.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
inhibitors and activators which can treat e.g. Stargardt-like macular
dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS Claim 3; Fig 2; 99pb; English.
XX
CC The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
which is a voltage-gated potassium channel protein. Human KCNQ5 has
ophthalmological, auditory, central nervous system (CNS), cardioactive,
anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
identifying activators or inhibitors of KCNQ5 protein. These activators
and inhibitors are useful for treating Stargardt-like macular dystrophy,
cone-rod dystrophy, Salla disease, age-related macular degeneration,
other forms of macular degeneration, deafness, epilepsy, and different
forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
chromosome 6q
XX
SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 0 Length: 3718
Score: 4407.00 Matches: 860
Percent Similarity: 99.88% Conservat: 0
Best Local Similarity: 99.88% Mismatches: 1
Query Match: 96.05% Indels: 0
DB: 3 Gaps: 0
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US-09-810-796-4 (1-897) x AAC64371 (1-3718)

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Qy 37 GlyGlyGlyLeuArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 93 GCGCGTGGCTCTGAGGAGAGCGCCGGGGCAAGCAGGGGGCCGATGAGCTGTCTGGG 152
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
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|----|------|---|------|
| Db | 153 | AAGCGGCTCTTTACACAGTAGCCAGAGCTGCGCGCAAGTCAAGTACCGGGGGGTG | 212 |
| Qy | 77 | GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAla | 96 |
| Db | 213 | CAGAACTACCTGTACAAAGTGTGGAGAGACCCCGCGCTGGCGTTTCAITACACAGCT | 272 |
| Qy | 97 | PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu | 116 |
| Db | 273 | TTGGTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCTCGAG | 332 |
| Qy | 117 | HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPhe | 136 |
| Db | 333 | CACACAAAATGGCGCTCAAGTTGCGTCTTGATCCTGGAGTTCGTGATGANTTGTGCTTT | 392 |
| Qy | 137 | GlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrp | 156 |
| Db | 393 | GGTTTGGAGTTCATCATTCGAATCTGCTGCGGGTTCGTGTTGTCATATAGAGATGG | 452 |
| Qy | 157 | GlnGlyArgIleArgPheAlaArgLysProPheCysValIleAspThrIleValleuIle | 176 |
| Db | 453 | CAAGGAAGACTGAGGTTTGTGCGAAGCCCTCTGTGTATATAGATACCATGTTGTTTATC | 512 |
| Qy | 177 | AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu | 196 |
| Db | 513 | GCITTCANTAGCAGTTGTTTCTGCANAACTCAGGTAATATTTTGGCAGCTCGACATC | 572 |
| Qy | 197 | ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr | 216 |
| Db | 573 | AGAAAGTCTCGGTTTCCTACAGATCCTCGCATGGTGGCATGGACCGAAGGGAGGCACT | 632 |
| Qy | 217 | TrpLysIleLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTptTyr | 236 |
| Db | 633 | TGGAAATTTACTGGGTTTCAGTGGTTTATGTCTCAGACNAGGAATTAATCAGCTTGGTAC | 692 |
| Qy | 237 | IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla | 256 |
| Db | 693 | ATAGGATTTTTGGTTCTTATTTTTTTCGCTTTCTCTGCTATCTGTGGAAAAGGATGCC | 752 |
| Qy | 257 | AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr | 276 |
| Db | 753 | AATAAAGAGTTTCTACATATGCAATGCAATGCTCTCTGGTGGGGCAAAATTAATTTGACA | 812 |
| Qy | 277 | IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe | 296 |
| Db | 813 | ATTGGCTATGAGACAAACCTCCCTTAACCTGGCTGGGAAGATGCTTTCTCGACGCTTT | 872 |
| Qy | 297 | AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla | 316 |
| Db | 873 | GCACCTCCTTGGCAATTTCTTTCTTTGGCAATCTCTCTGCGCGCAATCTTGCTCAGGTTTGCA | 932 |
| Qy | 317 | LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla | 336 |
| Db | 933 | TTTAAAGTACAAAGAACACACCGCCAGAAACACTTTTGAGAAAAGAAAGAACAGCTGCC | 992 |
| Qy | 337 | AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAla | 356 |
| Db | 993 | AACTCTCATTTAGTGTGTTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATGCA | 1052 |
| Qy | 357 | ThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGly | 376 |
| Db | 1053 | ACCTGGAAAGCCACACTTGAGGCGCTTGACACCTGCGACCTACCAAGAAAGAACAGGG | 1112 |
| Qy | 377 | GluAlaSerSerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArg | 396 |
| Db | 1113 | GAAGCATCAAGCAGTCAGAAAGTAAAGTTTTTAAAGAGCGAGTGCCTAGCTAGCTAGC | 1172 |
| Qy | 397 | GlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAsp | 416 |
| Db | 1173 | GGCCAGAGATTTAAGAGCCGACAGCCTCAGTAGTACAGAGAGTCCCCAGACCCGAC | 1232 |
| Qy | 417 | IleThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThr | 436 |

[illegible]

QY 797 ValGlnAenLeuileAArgSerThrGluGluLeuAenIleGlnLeuSerGlySerGluSer 816
 DB 2373 GTGCAAAACCTGATCAGGTCGACCGAGAACTGAATATACAACTTTCAGGCGAGTGAGTCA 2432
 QY 817 SerGlySerArgGlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIle 836
 DB 2433 AGTGCTCCAGAGCGGCGGAGATTTTACCCCAAAATGGAGGAATCCAAATTTGTTATA 2492
 QY 837 ThrAspGluGluValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGln 856
 DB 2493 ACTGATGAAGAGTGGTCCCGAGAGACAGACAGACACTTTTGATGCGCGACCGCAG 2552
 QY 857 ProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSer 876
 DB 2553 COTGCAGGGAAGCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCATCT 2612
 QY 877 GlnSerIleCysLysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeu 896
 DB 2613 CAGACATTTGTAGGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTG 2672
 QY 897 Lys 897
 DB 2673 AAA 2675

RESULT 11

AAAA47618
 ID AAA47618 standard; cDNA; 2335 BP.

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CC Mutations in 3 known genes of the KCNQ branch of the potassium channel
 CC gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy
 CC and in some cases associated with deafness. KCNQ4 has been mapped to the
 CC DFNA2 locus for autosomal dominant hearing loss, and a dominant negative
 CC KCNQ4 mutation that causes deafness in a DFNA2 pedigree has been
 CC identified. KCNQ4 is the first potassium channel gene underlying non-
 CC syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ
 CC channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4
 CC protein and the protein itself may be used in the prevention, treatment
 CC and diagnosis of diseases associated with inappropriate KCNQ4 expression.
 CC The nucleotides may also be used as DNA probes in diagnostic assays (e.g.
 CC polymerase chain reactions (PCR)) to detect and quantify the presence
 CC of similar nucleic acid sequences in samples and to identify mutations
 CC within them, and hence which patients may be in need of restorative
 CC therapy. They may also be used to study the expression and function of
 CC KCNQ4 polypeptides and their role in metabolism, for example through the
 CC production of transgenic animals. The KCNQ4 polypeptides may be used as
 CC antigens in the production of antibodies and to identify modulators
 CC (agonists and antagonists) of KCNQ4 expression and activity. The anti-
 CC KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate
 CC KCNQ4 expression and activity. They may be used in this way to treat
 CC tinnitus, loss of hearing (especially progressive hearing loss, neonatal
 CC deafness and presbycusis (deafness of the elderly)) and disease or
 CC adverse conditions of the central nervous system (CNS) such as affective
 CC disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by
 CC trauma, stroke or neurodegenerative illness, cognitive deficits,
 CC compulsive behavior, dementia, depression, Huntington's disease, mania,
 CC memory impairment, memory disorders and dysfunctions, motion disorders,
 CC motor disorders, neurodegenerative diseases, Parkinson's disease,
 CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,
 CC schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,
 CC antisense nucleic acid molecules may be administered to down regulate
 CC KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing
 CC their expression

XX

SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.58e-158 Length: 2335
 Score: 2012.00 Matches: 437
 Percent Similarity: 65.45% Conservative: 82
 Best Local Similarity: 55.11% Mismatches: 136
 Query Match: 43.85% Indels: 138
 DB: 3 Gaps: 16

US-09-810-796-4 (1-897) x AAA47618 (1-2335)

QY 8 ArgGlyArgValLeuLeuAenSerAlaAlaAlaArgGlyAepGlyLeuLeuLeuGly 27
 DB 127 CGGGGAGCGCCCGCGCGAGCTAGTGGCGCTCAGGSC----- 165
 QY 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 47
 DB 166 ---CGTCAGAGCGACAGCGCGAGCGG-----CGGGGCGG 201
 QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
 DB 202 CTCGCCGCGCGCGCTCGGCTCTCTGGGCGAGCCCTGCGCGCGCGCGCGCTCCCTCG 261
 QY 60 -----SerTyrThrSerSerGlnSerCysArgArgAenValLysTy 73
 DB 262 GCCGGGCTCGGCTCGGCGCTCGGCGCGAGCTCTCTCGGCGCGCGACAGCGCTA 321
 QY 73 rArgArgValGlnAenTyrLeuTyrAenValLeuGluArgProArgGlyTyrAlaPheIle 93
 DB 322 CGCGCGCTCGAGAACTGGGTCTACACGTCTGAGGCGGCGCGCGCTCGGCTTCGT 381
 QY 93 eTyrHisAlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerTh 113
 DB 382 CTACACGCTCTCATATTTTGTGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTCAC 441
 QY 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuPheValMetIle 133

/product= "KCNQ4 Potassium channel polypeptide"

/*tag= a

/product= "KCNQ4 Potassium channel polypeptide"

WO200044786-A1.

03-AUG-2000.

19-JAN-2000; 2000WO-DK000024.

26-JAN-1999; 99DK-00000076.

19-MAY-1999; 99DK-00000693.

(NEUR-) NEUROSEARCH AS.

Jentsch TJ;

WPI; 2000-548813/50.

P-PSDB; AAB01476.

Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful
 e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's
 diseases.

Claim 1; Page 43-48; 65pp; English.

Db 442 TATCAGAGAGCAGCAGAACTTGGCAACGAGTGCTCTCTCATCTTGAATTCGTGATGAT 501
 Qy 133 eValValPheGlyLeuGluPheIleAArgIleTyrSerAlaGlyCysCysArgTy 153
 Db 502 CGTGGTTTCGGCTTGGAGTACATCGTCCGGTCTGTGTCGGGATGCTGTCGCGCTA 561
 Qy 153 rArgGlyTyrGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI 173
 Db 562 CCGAGATGGCAGGTCGCTTCCGCTTGGCAGAAAGCCCTTCTGTCTCATCGACTTCAT 621
 Qy 173 eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193
 Db 622 CGTGTCTGGCTCGGTGGCGGTCATCGCCGGGTACCCAGGCGAATCTTTCGGCAC 681
 Qy 193 rSerAlaLeuArgSerLeuPheGlyLeuGlnIleLeuArgMetValArgMetAspArgAr 213
 Db 682 GTCCGGCTCGCAGCATGCTTCTGTCAGATCTGCGCATGCTGCGCATGGACCGCCG 741
 Qy 213 gGlyGlyThrTyrLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleTh 233
 Db 742 CGCGCGCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAGGAGCTGATCAC 801
 Qy 233 rAlaTyrTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGI 253
 Db 802 CCCCTGGTACATCGGTTCTGTGCTCATCTTCGCTCTCTTCTGCTACCTGGCGCA 861
 Qy 253 uLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleTh 273
 Db 862 GAAGACGCAACTCCGACTTCTCTCTCAGCGCACTCGTCTGTGGTGGGAGCATTCAT 921
 Qy 273 rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlyArgLeuLeuSe 293
 Db 922 ATTGACAACTATCGGTATGTGTGACAGACACCGCACATCGCTGGCGCAGGTCCTGGC 981
 Qy 293 rAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313
 Db 982 TGCTGGCTTCGCTTACTGGCATCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTC 1041
 Qy 313 rGlyPheAlaLeuLysValGlnGluHisArgGlnLysHisPheGluLysArgArgAs 333
 Db 1042 CGGCTTTCGCTTGAAGGTCAGAGAGCAGCAGCGGAGAGACTTCGAGAGCGGAGAT 1101
 Qy 333 nProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp---GluLysSe 352
 Db 1102 GCGCGGAGCACTCATCCAGGCTCGCTGGCGCTGTACTCCACCGATATGAGCGGCGC 1161
 Qy 352 rValSerIleAlaThrTrp----- 358
 Db 1162 CTACCTTGACAGCACCTGGTACTACTATGACAGTATCTCCATCTTCAGAGAGCTGGC 1221
 Qy 358 ----- 358
 Db 1222 CCTCTTTGTTGACAGCTGCAACGGCGCGCAATGGGGCCCTACGGCCCTCGAGGTGGC 1281
 Qy 359 -----LysProHisLeuLysAlaLeuHisTh 367
 Db 1282 GCGGGCGCGGTACCCGAGCAGCACCTCCGCTTACCCGCGCTGTGCCACCTGCGCACCG 1341
 Qy 367 rCysSerProThrLysLysGluGlnGlyAlaSerSerSerGlnLysLeuSerPheLy 387
 Db 1342 GCGGGGAGCAGCACTCTCTGCTGCTGGGAAAGCAGC-----CGGATGGGCAATCA 1392
 Qy 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405
 Db 1393 AGACCGGCTCGCATGGGAGCTCCAGCGCGGAGCGGGTCTCTCCAGCAGCAGCTGGC 1452
 Qy 405 aSerValGlyAspArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424
 Db 1453 ACCTCCAAACATGCCACCTCCCAAGCAGCAGCAGGTGGGTGGGCGCCACCGACCCAC 1512
 Qy 424 rLysValGlnLysSerTrpSerPheAsnAspArgTyrArgPheArgProSerLeuArgLe 444
 Db 1513 CAAGGTGCAAAAGAGCTGGAGCTTCATGACCGCACCCGCTTCGGGCACTCTCTGAGACT 1572

Qy 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464
 Db 1573 C-----AAACCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGGAAGT 1614
 Qy 464 lTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLy 484
 Db 1615 AGCAGAGAGAGAGAGCTACCACTGAGCTCAGGTGGAGCAGCATCATCGCTGCTGTGAA 1674
 Qy 484 sThrValIleArgAlaIleArgIleMetIlePheHisValAlaLysArgLysPheLysGI 504
 Db 1675 GACAGTCATCCCTCCATCAGGATTCCTCAAGTTCCTGGTGGCCAAAGAAATTCAGGA 1734
 Qy 504 uThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAs 524
 Db 1735 GACATGCGACCGTACGAGCTGAGGAGCTCATTGAGCAGTACTCAGCAGGCGACCTGGA 1794
 Qy 524 pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGI 544
 Db 1795 CATGCTGGCGCGATCAAGAGCTGCAAGAGCTGCAAACTCGGTGGACCAAAATTGGTGGTGGGG-- 1852
 Qy 544 nIleThrSerAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluTh 561
 Db 1853 ----CCCGGGGACAGGAGCGCGGAGAAAGCGGCACAGGGCGCTCCGACGCGAGT 1908
 Qy 561 rThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerI 581
 Db 1909 GGTGGATGAATCAGCATGATGAGCGCTGCTCAAGGTGAGAGAGCAGTGCAGTCCAT 1968
 Qy 581 eGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAl 601
 Db 1969 CGAGCAAGCTGAGCTGCTGTGTGGCTTCTATTCGCGCTGCTGCTGCTGCTGCTGCTGCT 2028
 Qy 601 aSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAs 621
 Db 2029 GGCC-----AGCTGGGCGCTGCAAGTGGCGCTTTCGACCCCGACATCACCTCCGA 2082
 Qy 621 pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641
 Db 2083 CTACCAAGCCCTGTGGACCCAGGAGCATCTCCGTCTCGCACAGCAGCGCTCAGC---AT 2139
 Qy 641 uSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGI 661
 Db 2140 CTCCCGCTCGGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2173
 Qy 661 uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681
 Db 2173 ----- 2173
 Qy 681 lProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnI 701
 Db 2174 ----ACTTCTCAGAGGCGAGGCGAGCACA----- 2197
 Qy 701 eAsnThrAlaProLysProAlaAlaProThrThrLeu-GlnIleProProLeuProA 721
 Db 2198 -CGGCGAGCCCGCGGCTGGCGCTCGACTGCGCTCTGAGGCGCTCGGAGCTCTCTCTCGT 2256
 Qy 721 laIleLysHisLeuProArgProGluThrLeuHis 732
 Db 2257 ACTTGAACTCACTCCCTCAGCGGAGAGAGACCCAC 2291
 RESULT 12
 ADE31698
 ID ADE31698 standard; DNA; 2335 BP.
 XX
 AC ADE31698;
 XX 29-JAN-2004 (first entry)
 DT Human 32394 gene #SEQ ID 55.
 DE
 KW Antiarteriosclerotic; cardiant; vasotropic; antiinflammatory;
 thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;

QY 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333
DB 1042 CGGCTTTGCCCTGAGGTCCAGAGCAGCAGCCGCGAAGACACTTCAGAGAGCGAGAT 1101
QY 333 nProAlaAlaAsnLeuLeuGlnCysValTyrArgSerTyrAlaAlaAsp---GluLysSe 352
DB 1102 GCCGGCAGCCAACTCATCAGGTGCTGGCGCTGTACTCCACCGCATATGAGCGGGC 1161
QY 352 rValSerIleAlaThrTrp----- 358
DB 1162 CTACTGTACAGCCACCTGCTACTACTATGACAGTATCCTCCATCCTTTCAGAGAGTGGC 1221
QY 358 ----- 358
DB 1222 CCTCTTTGAGCAGGTGCAACGGGCGCCGCAATGGGGGCGCTACGGCCCTCGAGGTGGC 1281
QY 359 -----LysProHisLeuLysAlaLeuHisTh 367
DB 1282 CGCGGGCGGTACCAGGAGCAGCACCTCCGTTTACCGCGCGTGTGCCACTGCCACCG 1341
QY 367 rCysSerProThrLysLysGluGlnGlyGluAlaSerSerGlnLysLeuSerPheLy 387
DB 1342 GCCGGCAGCACCTCTTCTGCGCTGGGAAAGCAGC-----CGGATGGGCATCAA 1392
QY 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405
DB 1393 AGACCGCATCCGATGGCAGTCCAGCGGAGCGGTCTTCCAGCAGCAGTGGC 1452
QY 405 aserValGlyAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424
DB 1453 ACCTCCAAACATGCCACCTCCCAAGCAGCAGCGAGTGGTGGAGCCAGCAGCCGAC 1512
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DB 1513 CAAGGTGCAAAAGAGCTGAGCTTCAATGACCGCAGCCGCTTCCGGGCACTCTGAGACT 1572
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DB 1573 C-----AAACCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGGAAGT 1614
QY 464 lTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLy 484
DB 1615 AGCAGAGGAGAGAGTACCTACAGTGTGAGTCCAGCGTGGAGCAGCATCATGCTGTGTAA 1674
QY 484 sThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysG1 504
DB 1675 GACAGTCATCCCTCCATCAGATTTCTCAAGTTCTGTGTGGCCAAAGAAATCAAGGA 1734
QY 504 uThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAs 524
DB 1735 GACACTGGACCGTAGGAGCGTGAAGGAGCGTCAATTGAGCAGTACTCAGCAGGCGCACCTGA 1794
QY 524 pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyG1 544
DB 1795 CATGTGGCGCGGATCAAGAGCTGCAACTCGGTGGACCAAAATGTGGGTGGGGG--- 1852
QY 544 nIleThrSerAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluTh 561
DB 1853 -----CCCGGGGACAGAGGCGCGGAGAGGCGGCAAGGGCGCTCCGAGCGGAGGT 1908
QY 561 rThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSerIl 581
DB 1909 GGTGGATGAATCAGCATGAGCGCTGAGTCAAGTGGAGAGCAGGAGTGCATCTCAT 1968
QY 581 eGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAl 601
DB 1969 CGAGCAACAAGCTGACCTCTGTGGGCTTCTATTGCGGCTGCTGCGCTTGGCACCTC 2028
QY 601 aserAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAs 621
DB 2029 GGCC-----AGCCTGGCGCGGTGCAAGTGGCGGTGTTTCGAGCCCGGACATCACCTCGA 2082
QY 621 pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641

DB 2083 CTACCACAGCCCTGTGTGACCAAGGACATCTCCGTCTCCGACAGACGCTCAGC---AT 2139
QY 641 uSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnG1 661
DB 2140 CTCCCGCTCGTCCAGCAGCAACATGGACTGAGGG----- 2173
QY 661 uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681
DB 2173 ----- 2173
QY 681 lProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIl 701
DB 2174 ---ACTTCTCAGAGGAGGAGGAGCACA----- 2197
QY 701 eAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuProA 721
DB 2198 -CGGCAGGCGCGCGCTGGCGCTCCGACTGCCCTCTGAGGCTCGGACTCCTCTCGT 2256
QY 721 laIleLysHisLeuProArgProGluThrLeuHis 732
DB 2257 ACTTGAACCTACTCTCCCTCAGGGGAGAGAGACCAC 2291
RESULT 13
ADSL7851
ID ADS17851 standard; cDNA; 5595 BP.
XX AC ADS17851;
XX 02-DEC-2004 (first entry)
DT Rattus norvegicus KCNQ cDNA #2.
XX DE
XX KW KCNQ; potassium channel; anxiety; insomnia; hyper-excitability disorder;
KW Alzheimer's disease; peripheral neuropathy; neurodegenerative disease;
KW neuroprotective; anticonvulsant; nootropic; tranquiliser; sedative;
KW norway rat; gene; ss.
XX OS Rattus norvegicus.
XX PH Key Location/Qualifiers
XX FT CDS 1553..4111
XX FT /*tag= a
XX FT /product= "KCNQ protein"
XX PN US2004175691-A1.
XX PD 09-SEP-2004.
XX PF 08-APR-2004; 2004US-00820307.
XX PR 03-DEC-1998; 98US-0110804P.
XX PR 03-DEC-1999; 99US-00454868.
XX PA (BROW/) BROWN B S.
XX PA (MCKI/) MCKINNON D.
XX PI Brown BS, McKinnon D;
XX PI WPI; 2004-642119/62.
XX DR P-PSDB; ADS17852.
XX FT
XX PT
XX PT Evaluating compound for utility in treating neurological disease such as
XX PT epilepsy and anxiety, involves contacting compound with cell co-
XX PT expressing KCNQ2 and KCNQ3 that form potassium channel, and measuring
XX PT activity of potassium channel.
XX PS Disclosure; SEQ ID NO 8; 38pp; English.
XX CC The present invention relates to a method of evaluating a compound for
XX CC utility in treating neurological disease. The method involves contacting
XX CC a compound with a cell that co-expresses KCNQ2 and KCNQ3, where the KCNQ2
XX CC and KCNQ3 form a potassium channel and measuring the activity of the

Db
2384 ATTGGCTACGGGACAAGTACCTCAGACCTGGAA CGGAGGCTGTTTAGCGACGCTTT 2443

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617  QY  -----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeu 631
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3479  Db  GGGCCCAAGGAGCCTGAGCGGCACCAACACCTACCAAGCCCGAGGACAGCCGTGAC--- 3535
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632  QY  SerGlySerAlaGlnAsnSerGlyCys-----LeuSerArgSerThrSerAlaAsn 648
        |||
        |||
        |||
3536  Db  -----CATGCACAAGCATGGCTGTATTATTAAAGATTGTCGGCTCCACCAAGCTCT--- 3586
        |||
        |||
        |||
649  QY  IleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyr 668
        |||
        |||
        |||
3587  Db  -----ACGGCCAGAGGAATAC 3604
        |||
        |||
        |||
669  QY  AlaLeuSerProThrMethIleSerGlnAlaThrGlnValProIleSerGlnSerAspGly 688
        |||
        |||
        |||
3605  Db  GCCGCACCCCAAGTCATG----- 3622
        |||
        |||
        |||
689  QY  SerAlaValAlaIleAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAla 708
        |||
        |||
        |||
3623  Db  -----CCCTCTCCGAGTGT 3637
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        |||
        |||
709  QY  AlaPro---ThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArg 727
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3638  Db  CCCCCTACCACTCGTGACGCA-GAGCCACCAAGCGCA-----CGGACCTCCCCCGT 3690
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728  QY  ProGluThr-----LeuHisProAsn-ProAlaGlyLeuGlnGluSerIleSe 743
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3691  Db  GGGAGACCATGGCTCACTGTGTAGCGATCCCAACACCCCTCCGACGAGCGGTCACTGTC 3750
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743  QY  rAspValThrThyCysLeuValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLe 763
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3751  Db  TGCCTACAGTGGGGGCAACAGAGCCAGTACCGAGTCTTCAGGCTGGAGGGACCCCGC 3810
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        |||
        |||
763  QY  uThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 781
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        |||
        |||
3811  Db  CTGCAGGCCCTCTGAGGCAGCCCTCCGGGATAGC-----GACACGTCCCAT 3855
        |||
        |||
        |||
781  QY  uSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeuI 801
        |||
        |||
        |||
3856  Db  CTCATCCCTTCGTGTGGACCAACGAGGAGCTGGAGCGTTCTTTAGCGGTTTCAGTATCTC 3915
        |||
        |||
        |||
801  QY  eArgSerThrGluGluLeuAsn 808
        |||
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        |||
3916  Db  CCAGTCCCAAGCAACCTGAAT 3937
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| | |
|-----------|--|
| RESULT 14 | |
| ADBE78687 | |
| ID | ADBE78687 standard; cDNA; 7407 BP. |
| XX | |
| AC | ADBE78687; |
| XX | |
| DT | 04-DEC-2003 (first entry) |
| XX | |
| DE | Human potassium channel subunit mutant cDNA SEQ ID NO:58. |
| XX | |
| KW | ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic; neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine; antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic; nephrotropic; antidiabetic; ophthalmological; epilepsy; |
| KW | ion channel dysfunction; human. |
| XX | |
| OS | Synthetic. |
| OS | Homo sapiens. |
| XX | |
| PN | WO2003008574-A1. |
| XX | |
| PD | 30-JAN-2003. |
| XX | |
| PF | 08-JUL-2002; 2002WO-AU000910. |
| XX | |
| XX | 18-JUL-2001; 2001AU-00006452. |
| PR | 05-MAR-2002; 2002AU-00000910. |
| PR | 13-MAY-2002; 2002AU-00002292. |
| XX | |

(BION-) BIONOMICS LTD.
(WALL/) WALLACE R. W.

Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
Berkovic SF, Scheffer IE;
WPI; 2003-239332/23.

Identifying predisposition to an ion channel dysfunction, such as
periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
schizophrenia, anxiety and depression, by detecting encoding-gene
mutation events.

Claim 6; SEQ ID NO 58; 106pp; English.

The invention relates to a novel method for identifying a subject
predisposed to a disorder associated with ion channel dysfunction. The
method comprises ascertaining if at least one of the genes encoding ion
channel subunits (ICS) has undergone a mutation event so that a cDNA
derived from the subject has any of 134 nucleotide sequences. The method
of the invention has nootropic, neuroprotective, inotropic, antipyretic,
antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
ophthalmological activity. A polynucleotide of the invention acts as an
ion channel agonist, or ion channel antagonist. The methods, isolated
nucleic acids, polypeptides, antibody, selective agonist, antagonist or
modulator of an ion channel, cells and genetically modified non-human
animal, are useful for the diagnosis and treatment of epilepsy and/or a
disorder associated with ion channel dysfunction, such as hyper- or hypo-
kalaemic periodic paralysis, myotonia, malignant hyperthermia,
myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
depression, phobic obsessive symptoms, neuropathic pain, inflammatory
pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
fibrosis, congenital stationary night blindness and total colour
blindness. The present sequence represents a mutant cDNA of the
invention. The sequence data for this patent is not represented in the
printed specification, but was obtained in electronic format directly
from WIPO at frn.wipo.int/pub/published pat sequences.

```

XX
SQ Sequence 7407 BP; 1354 A; 2330 C; 2355 G; 1368 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4 3e-141 Length: 7407
Matches: 436
Percent Similarity: 1820.50
Best Local Similarity: 56.72% Conservative: 96
Mismatch: 46.48% Mismatches: 230
Query Match: 39.68% Indels: 177
DB: 10 Gaps: 26

US-09-810-796-4 (1-897) x ADB78687 (1-7407)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGly 36
Db 142 TCCACCGGGAGCGGGCGCTCTGATCGCGGCTCCGAGGCCGCCAAG-----CGC 192
Qy 37 GlyGlyGlyLeuArgGlySerArgGlyGlyysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 193 GCGAGCATCTCTCAGCAACCTCGCGGGCGCGCGCGCC-----GGG 237
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
Db 238 AAGGCC-----CCCAAGCGCAACGCCCTTCTACCGCAAGCTG 273
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 274 CAGAAATTCCTTACACGTGCTGGAGCGCGCGCGCTGGCGCTTCATCTACCACGCC 333
Qy 97 PheValPheLeuValPheGlyCysIleuLeuLeuSerValPheSerThrIleProGlu 116
Db 334 TACGTGTTTCCTCGTGGTTTTCTCCGCTCGCGTGTCTGTGTTTTTCCACGATCAAGGAG 393

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Db 2304 GGACAGCGACAGCTCCATCTCCATCCGTCGGTG-----GACCACGAGGAGCTGGAGCG 2357
Qy eGlnLeuSerGlySerGlySerGlySerGlySerGlnAsp-----Ph 825
Db 2358 TTCCTTACCGCGCTTCCAGCATCTCCAGTCCAGGAGACCTGGATCTCTCAACAGCTG 2417
Qy 825 eTyrPro-LysTrpArg-----GluserylLeuPheIleThrAspGluValG 842
Db 2418 CTACGCGCGCTGGCGCTGTGCGCAAGTCAGGCCCTACATTCGCGGAGGAGAGTCAGA 2477
Qy 842 LysProGluThrGluThrAspThrPheAsp----- 852
Db 2478 CACCGACTCCGACCTCTGTACCCGTCGGCGCCCGCCGACGCTCGGCCACCGCGGAGGG 2537
Qy 853 -----AlaAlaProGlnProAlaArgGluAlaPheAlaSerAspS 867
Db 2538 TCCCTTTGGTGACGTGGCGCTGGCGCGGCCAGGAGTGAGCGCGCTGGGC----- 2590
Qy 867 eLeuArgThrGlyArgSerArgSerGlnSerIleCysLeuAlaGly 883
Db 2591 -----CAGTGGACCGCGCGCGCCCTCTCTCAGCACGGTGCCTCCGAGGT 2635

RESULT 15
ADB78685
ID ADB78685 standard; cDNA; 7407 BP.
AC ADB78685;
XX
XX
DT 04-DEC-2003 (first entry)
XX
DE Human potassium channel subunit mutant cDNA SEQ ID NO:56.
XX
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX W02003008574-A1.
XX
XX 30-JAN-2003.
XX
XX 08-JUL-2002; 2002WO-AU000910.
XX
XX 18-JUL-2001; 2001AU-00006452.
XX
XX 05-MAR-2002; 2002AU-00000910.
XX
XX 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
XX (WALL/) WALLACE R W.
XX
XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
XX Berkovic SF, Scheffer IE;
XX WPT; 2003-239332/23.
XX
XX Identifying predisposition to an ion channel dysfunction, such as
XX periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
XX schizophrenia, anxiety and depression, by detecting encoding-gene
XX mutation events.
XX
XX Claim 6; SEQ ID NO 56; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyrretic,
XX antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
```

```
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated or
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemia periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant cDNA of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX SQ Sequence 7407 BP; 1353 A; 2329 C; 2355 G; 1370 T; 0 U; 0 Other;
XX
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Score: 1819.50 Matches: 414
Percent Similarity: 61.09% Conservative: 101
Best Local Similarity: 49.11% Mismatches: 189
Query Match: 39.66% Indels: 140
DB: Gaps: 21

US-09-810-796-4 (1-897) x ADB78685 (1-7407)
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Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
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Search completed: April 3, 2005, 07:24:55

Job time : 1191.13 secs

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GenCore version 5.1.1.6
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Run on: April 3, 2005, 06:46:36 ; Search time 1202.53 Seconds
(without alignments)
4514.709 Million cell updates/sec

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Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 4588 | 100.0 | 2694 | 9 | US-09-810-796-2 |
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| 12 | 2012 | 43.9 | 2335 | 17 | US-10-353-690-55 |
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| 44 | 1226.5 | 26.7 | 1425 | 16 | US-10-116-712-662 |
| 45 | 1207.5 | 26.3 | 900 | 13 | US-10-128-870-5 |

ALIGNMENTS

RESULT 1

US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US2002040000A1
; GENERAL INFORMATION:
; APPLICANT: DORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; PRIORITY FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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QY 681 ValProLeuSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
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RESULT 2

US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)...(2694)

; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Alignment Scores:
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Score: 4588.00 Matches: 897
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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QY 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgValGlnAsnTyrLeu 80
DB 181 TACAGAGTACCGAGAGCTGCGCGCAACGTCAGTACCGCGCGGTGCAGAACTACCTG 240
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 241 TACACGTCGTGGAGAGACCCCGCGGTGGCGGTTCATACCGCTTTCGTTTTTCTC 300
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 301 CTTCGTTTGTGCTTGAATTTTGTCAAGTGTTCATCATCCCTGAGCACAATAATTG 360
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 361 GCCTCAAGTTGCCCTCTTGTATCTCGAGTTCGTGATGATTGTCTGTTTGGTGGAGTTC 420
QY 141 IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 421 ATCAATTCGAATCTCGTCTGCGGTTGTCTGTATAGAGGATGCAAGGAAGACTG 480
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 481 AGGTTTGTGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTATCGCTTCAATAGCA 540
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 541 GTTGTTCGCAAAACTCAGGGTAATATTTTTCACGCTGTGCACTCAGAAGTCTCCGT 600
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 601 TTCTACAGATCTCCCGCATGTGCGCATGACCAAGGGAGGAGGAGGAGGAGGAGGAGG 660
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 720
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 721 GTTCTTATTTTTCGTTCTTCTTGTCTATCTGTTGGAAGAGGATGCAATAAAGAGTTT 780
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 781 TCTACATATGAGATGCTCTCTGTGGGGGCAATTAATTAATTAATTAATTAATTAATTA 840
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 841 GACAAACTCCCTAACTTGGCTGGGAAGATTTGCTTCTGCGAGGCTTTCCTCTCTCTGCG 900

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleIleuGlySerGlyPheAlaLeuLysValGln 320
Db 901 ATTTCTTTCTTTGACATTCCTGCGGCAATCTTGCTGCTGAGTTTGTCAATTAAGTACAA 960
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuLysGln 340
Db 961 GAACAACACCCGACGAAACACTTTGAGNAAGAAGAACCCAGCTGCGCAACCTCATTCAG 1020
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTGGCGTAGTACGACGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCCA 1080
Qy 361 HisIleuLysAlaLeuHisThrCysSerProThrLysLysGlnGlnGlyAlaLaserSer 380
Db 1081 CACTGGAAGGCTTGCACACCTCGACGCTTACCAGAAAGAACAGGGAGACATCAAGC 1140
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1141 AGTCAGAGCTTAAGTTTAAAGAGGAGTGCATGCTAGCCCGAGGGCCAGAGTATT 1200
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1201 AAGAGCCGACAAAGCTCAGTAGTGACAGAGAGTCCCGAACCGACATCACAGCCGAG 1260
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1261 GCGAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1320
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1321 TCGTGGCCCTCAAAAGTTCTCAGCCAAACCCAGTATAGATGCTGACACAGCCCTTGGC 1380
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1381 ACTGATGATGATATGATGAAGAGATGCGAGTGTGATGATGATGATGATGATGATGAT 1440
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1441 CCACCACTTAACCTGCTATTCGAGCTATCAGAAATTAATAATTTTCAATTTGCAAAACGG 1500
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1501 AAGTTTAAGGAACGCTTACGTCATATGATGATAAAGATGTCAATTAAGCAATATTCGCT 1560
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1561 GGTCACTCGGACATGTTGTGTAAGATTAAGCCCTCAACACGCTGTGATCAATTCCT 1620
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1621 GGAAGAGGCAATCACATCATCAAGAGAGCCGAGAGAAATTAACAGCAGAACATGAG 1680
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1741 ATAGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGTCTCTCGGAAGGCTCT 1800
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1801 GCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1861 GACTATCAAGGCTGTGATAGCAAGATCTTTCGGGTTCGACACAAACAGTGGCTGC 1920
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1921 TTATCCAGATCAACTAGTGCAACATCTCGAGAGGCTCGAGTTCATCTGACGCGCAAT 1980
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680

Db 1981 GAGTTTCAGTGCCAGACATTTTCTACGCGCTTAGCCCTACTATGCAGAGTCAAGCAACACAG 2040
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGGAGCCACCAACACCATTTGCNAACCAA 2100
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2101 ATAAATACGACCCCAAGCCAGCAGAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2160
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProHlaGlyLeuGlnGlu 740
Db 2161 GCCATCAAGCATCTGCCAGGCGCAGAACTCTGCACCTTAACCTTCAGCGCTTACAGGAA 2220
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2221 AGCATTTTCAGCTGACCTACCTGCTGCTTGTTCCTCCAGGAAATGTTTCAAGTTGCACAG 2280
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2281 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2341 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820
Db 2401 ATCAGTCTGACCGAGGAACTGAATATACAACTTTTCAAGGAGTCAAGTGCCTCCAGA 2460
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
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Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2521 GTGGTCTCCGAAGAGACAGACACACTTTTGTATGCCCGACCGAGCTGCGAGGAA 2580
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2581 GCTGCTTTCATCAGACTCTCTAAGGACTGGAAGTCAAGTCACTCATCTCAGAGCATTTGT 2640
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2641 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAAA 2691

RESULT 3

US-10-948-493-1
; Sequence 1, Application US/10948493
; Publication No. US20050064491A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIBKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0023 DIV
; CURRENT APPLICATION NUMBER: US/10/948,493
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-948-493-1

Alignment Scores:

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| Pred. No.: | 0 | Length: | 2694 |
| Score: | 4588.00 | Matches: | 897 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 19 | Gaps: | 0 |
| US-09-810-796-4 (1-997) x US-10-948-493-1 (1-2694) | | | |
| Qy | 1 | MetLysAspValcIuSerGlyArgGlyArgValLeuLeuAenSerAlaAlaAaArgGly | 20 |
| Db | 1 | ATGAAGGATGTGGAGTTCGGCCCGGCGCAGGGTGCTGTGTAACCTCGGCAGCGCCGAGGGGC | 60 |
| Qy | 21 | AspGlyLeuLeuLeuLeuGlyThrArgalaaIathrLeuGlyGlyGlyGlyGlyLeu | 40 |
| Db | 61 | GACGGCTCTGCTACTGTGGGCACCCGCGCGGCCACGCTTGTGTGGCGCGCGGTGGCGCTG | 120 |
| Qy | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaargMetSerLeuLeuLeuGlyLysProLeuSer | 60 |
| Db | 121 | AGGAGAGCGCCCGGGGCAAGCAGGGGGCCCGGATGAGCTGTCTGGGGAAAGCCGCTCTCT | 180 |
| Qy | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 |
| Db | 181 | TACACGAGTAGCACAGAGCTGCCGCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG | 240 |
| Qy | 81 | TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu | 100 |
| Db | 241 | TACAACGTGCTGGAGAGACCCCGCGGCTGGCGGCTTCATCTACCAACGCTTTCGTTTTCTC | 300 |
| Qy | 101 | LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 |
| Db | 301 | CTTGCTTTGGTTGCTTGATTTTTCAGTGTTTCTTACCATCCCTGAGCACACAAATG | 360 |
| Qy | 121 | AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 |
| Db | 361 | GCCTCAAGTTGCTCTTGATCTCGAGTTCTGTGATGATTGTGCTTTTGGTTGGAGTTCT | 420 |
| Qy | 141 | IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu | 160 |
| Db | 421 | ATCATTCGAATCTGGTCTCGCGGTTGCTGTGTTCGATATAGAGATGCGCAAGAGAACTG | 480 |
| Qy | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 |
| Db | 481 | AGGTTTGTCTGAAAGCCCTTCGTGCTTATAGATACCAATTGTTCTTATCGCTTCAATAGCA | 540 |
| Qy | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 |
| Db | 541 | GTTGTTTCTTGCAAAACTCAGGCTAATATTTTTTGGCACGCTCGCACTCAGAACTCTCCGT | 600 |
| Qy | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu | 220 |
| Db | 601 | TTCTTACAGATCCTCGCATGTCGCGATGACCGAAGGGAGGAGCATCTGGAAATTAAGTCTG | 660 |
| Qy | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu | 240 |
| Db | 661 | GGTTCACTGGTTATGCTCACAGCAAGAGATTAATCACAGCTTGGTACATAGATTTTTG | 720 |
| Qy | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| Db | 721 | GTTCTTATTTTTTTCGTTCTTCTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT | 780 |
| Qy | 261 | SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrIleGlyTyrGly | 280 |
| Db | 781 | TCTACATATATGCAGATGCTCTCTGGTGGGGGCAAAATACATTCGACAACTATTTGGCTATGGA | 840 |
| Qy | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
| Db | 841 | GACAAACTCCCCCTAACTGGCTGGGAAGATTGCTTCTGCGAGCGTTTGCACCTCCTTGGC | 900 |
| Qy | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| Db | 901 | ATTTCCTTTCTTTGCACTTCTCGCGGCACTTCTGGCTCAGGTTTGTGATTAAGTACAA | 960 |

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Db 2041 GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGGCGCCACACACCATTCGAAACCAA 2100
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2101 ATAAATACGGCACCCAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
Qy 721 AlalleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2161 GCCATCAAGCATCTGCCAGGCCAGAACTCTGACACCCCTAACCTTGCGAGGCTTACAGGAA 2220
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2221 AGCATTTCTGAGCTCACCACCTGCTTGTTCCTCCCAAGGAATATGTTACAGTTGCACAG 2280
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2281 TCAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2341 TTGCTCTGTCTGCCATGGTCCGAGGACCTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2400
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2401 ATCAGTTCGACCGAGGAACTGATATACAACTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy 821 GlySerGlnAspPheTyProLysTrpArgGluSerLysLysPheIleThrAspGluGlu 840
Db 2461 GGCAGCCCAAGATTTTACCCCAATATGGAGGGAATCCAAATTTGTTTATTAACATGATGAAGAG 2520
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2521 GTGGGTCCGAGAGACAGACACACTTTTGTATGCCGACCCAGCCCTGCCAGGGAA 2580
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2641 AAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691

RESULT 4
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Alignment Scores:
Pred. No.: 0 Length: 3137
Score: 4588.00 Matches: 897
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-810-796-4 (1-897) x US-10-661-629-1 (1-3137)
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Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 61 GACGGCTCTACTGCTGGGCACCCCGCGGCCACGCTCGGTGGCGCGCGCGCTGCGCTG 120
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaAsnMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGAGAGACCGCGGGGCAAGCAGGCGGCCCGGATGAGCTGCTGGGGAAGCCGCTCTCT 180
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCAGAGCTGCCCGGCCAACGTCAGGTACCGCGGGTGCAGAACTACCTG 240
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACAACGCTGTGGAGAGACCCCGCGCTGGCGCTTCATCTACCACGCTTTTCGTTTTCTC 300
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 301 CTGTCTTTTGGTGTCTTGATTTTGTCAAGTGTTCACCATCTCTGAGCACACAAAATTG 360
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTTGCCCTTTGATCTCTGGAGTTCGTGATGATTGCTGCTTTGGTGGAGTTC 420
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 421 ATCATTCGAATCTGCTGCTGGCGGTGCTGTGTGATATAGAGATGAGAGATGCAAGGAACTG 480
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTTCTCGAAAGCCCTTCTGTGTATAGATACCATGTTCTTAICGCTTCAATAGCA 540
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Db 541 GTTGTCTTCGCAAACTCAGGGTAAATATTTTGGCCACGCTGTCACATCAGAAAGTCTCCGT 600
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 601 TTCCTACAGATCTCCCGCATGGTGGCATGACCAAGGGAGGACATTTGGAATTTACTG 660
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTTATGCTCAGCAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 720
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Db 721 GTTCTTATTTTTCGTCTTCTTCTGCTATCTGTTGAAAAGAGATGCCAATAAAGAGGTTT 780
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 781 TCTACATATGAGATGCTCTCTGGTGGGCGCAATTCATTGACAACTATTGGCTATGGA 840
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAAACCTCCCTTAACCTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACATCTCTGGC 900
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 901 ATTTCTTTTTCGTCATCTTCTGCGGCATTTCTGGCTCAGGTTTGGCAATTAAGAGTACAA 960
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GAACAAACCCCGCAGAAACACTTTGAGAAAAGAGGAACCCAGCTGCTGCCAATCTCATTCAG 1020
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
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361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGluAlaSerSer 380
1081 CACTTGAAGGCCCTTGCACACCTCGACCCCTTACCAAGAAAGAACAGGGAAGCATCAAGC 1140
381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
1141 AGTCAGAGCTAAGTTTAAAGGAGCGAGTGCATGGCTAGCCCGAGGGGCCAGAGTATT 1200
401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
1201 AAGAGCCGCAAGCCCTCAGTAGTGCACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1260
421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
1261 GCGAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCTTCCGGCCC 1320
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1321 TCGCTGCCCTCAAAAGTTCTCAGCCAAACAGTGTAGATGCTGTGACACAGGCCCTTGGC 1380
461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
1381 ACTGATGATGATATGATCAAAAGGATGCCAGTGTGATGTATCAGTGGAAAGACCTCACC 1440
481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
1441 CCACCACTTAAACACTGTCTTCGAGCTATCAGATTATGAAATTTTCATGTTGCAAAACGG 1500
501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
1501 AAGTTTAAAGAAACATTACGTTCCATGATGTAAAGATGTCATTGAACATATTTCTGCT 1560
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601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
1801 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCCAACCTTTTGAATGTGAACAGACATCT 1860
621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
1861 GACTATCAAGCCCTGTGTGATAGCAAGATCTTTCGGGTTCGCAACAAAACAGTGGCTGC 1920
641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
1921 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTCGAGTTCATTTCTGACGCCAAAT 1980
661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
1981 GAGTTCAGTGCCAGACTTTCTACCGCTTACCCCTTACTATGCACAGTCAAGCAACACAG 2040
681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
2041 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGGAGGCCCAACACACCATTTGCCAAACCA 2100
701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
2101 ATAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740

2161 GCCATCAAGCATCTGCCAGGCCGAAACTCTGCACCCCTAACCCCTGCAGGCTTTACAGAA 2220
741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
2221 AGCATTTCTGAGCTCACCACCTGCTTGTGCTTCCCTCAAGGAAATGTTTCAGGTTGCACAG 2280
761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
2281 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAAACTCTCG 2340
781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
2341 TTGCTGTCTGTCCCATGGTCCGAGGACTTGGCAAAATCTTTGCTGTGTGCAAAACCTG 2400
801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
2401 ATCAGGTCGACCGAGGAATCAATATATCAACTTTTCAGGAGGTGAGTCAAGTGGCTCCAGA 2460
821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
2461 GGCAGCCAAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTATAACTGATGAAGAG 2520
841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
2521 GTGGTCCCGAAGAGACAGACAGACACTTTGTATGCCGACCCAGCCTCCACAGGAA 2580
861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
2581 GCTGCCITTCATCAGACTCTCTAAGGACTCGAAGGTCCAGATCATCTCAGAGCATTTGT 2640
881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691

RESULT 5
US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-1

Alignment Scores:
Pred. No.: 0 Length: 3071
Score: 4584.00 Matches: 896
Percent Similarity: 99.89% Conservative: 0
Best Local Similarity: 99.89% Mismatches: 1
Query Match: 99.91% Indels: 0
DB: 9 Gaps: 0

US-09-810-796-4 (1-897) x US-09-810-796-1 (1-3071)

QY 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| Db | 10 | ATGAAGGATGTGGAGTCGGGCGGCGAGGGTGTCTGTAACTCGGCAGCGCGAGGGC | 69 | Db | 1090 | CACTTGAAGGCGCTTGACACACCTGCAGCCCTCAACAGAAAGAACAAAGGGGAAGCATCAAG | 1149 |
| Qy | 21 | AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu | 40 | Qy | 381 | SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle | 400 |
| Db | 70 | GACGGCTGTCTACTGTGGGACCCCGCGGCCACGCTTGGTGGCGGCGGGTGGCTG | 129 | Db | 1150 | AGTCAGAGCTAAGTTTAAAGGAGGAGTGCATGGCTTAGCCCCAGGGCCAGAGTATT | 1209 |
| Qy | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 | Qy | 401 | LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu | 420 |
| Db | 130 | AGGAGAGCCCGCGGCAAGCAGGGGCGCGGATGAGCTGTCTGGGGAAGCGGCTCTCT | 189 | Db | 1210 | AGAGCCGACAGCCCTCAGTAGGTGACAGAGGTCCCAAGCACCCACATCATCAGCCGAG | 1269 |
| Qy | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu | 80 | Qy | 421 | GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro | 440 |
| Db | 190 | TACACGAGTACGACAGCTGCGGCGCAACGTCAAGTACCGCGGGTGCAGAACTACTG | 249 | Db | 1270 | GGCAGTCCCAACAAAGTCAGAGAGCTGGAGCTTCAACGACGAAACCCGCTTCGGGCC | 1329 |
| Qy | 81 | TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu | 100 | Qy | 441 | SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly | 460 |
| Db | 250 | TACAACGTGTGGAGAGACCCCGCGGCTGGGGTTCATCTACCAACGCTTTCGTTTTCTC | 309 | Db | 1330 | TCGCTCGGCTCAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGACACAGCCCTTGCC | 1389 |
| Qy | 101 | LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 | Qy | 461 | ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr | 480 |
| Db | 310 | CTTGCTTTGGTGTCTTGTATTTGTAGTGTTCATCCATCCCTGAGCACACAAATTG | 369 | Db | 1390 | ACTGATGATGATATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGAAGACCTCACC | 1449 |
| Qy | 121 | AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 | Qy | 481 | ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg | 500 |
| Db | 370 | GCCTCAAGTGTGCTCTTGATCTGGAGTTCGATGATGTGCTTGGTGGAGTTC | 429 | Db | 1450 | CCACCACTTAAAACTGTCTTCAGCTATCAGAAATTTAGAAATTTCTATGTGCAAAACGG | 1509 |
| Qy | 141 | IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu | 160 | Qy | 501 | LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla | 520 |
| Db | 430 | ATCATTCGAATCTGTCTCGGGTGTCTGTGATATAGAGGATGCAAGGAAGACTG | 489 | Db | 1510 | AGTTTAAAGAAACRTTACGTCCATATGATGATAAAGATGTCTATTGAACAATTTCTGCT | 1569 |
| Qy | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 | Qy | 521 | GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu | 540 |
| Db | 490 | AGGTTTGTCTGAAAGCCCTTCTGTATATAGATACCATTTGTCTTATCGCTTCATATGCA | 549 | Db | 1570 | GGTCATCTCGACATGTGTGTAGAAATTTAAAGGCTTCAACACGCTGTGTCAAAATCTTT | 1629 |
| Qy | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 | Qy | 541 | GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu | 560 |
| Db | 550 | GTGTGTTCTGCAAAACTCAGGGTAATATTTTGGCCACTGTCTGCACTCAGAACTCTCGT | 609 | Db | 1630 | GGAAAGGGCAATTCATCATAGATAGAGAGCGGAGAGAAATATACAGCAGAACATGAG | 1689 |
| Qy | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu | 220 | Qy | 561 | ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer | 580 |
| Db | 610 | TTCTACAGATCTCCGCAATGTGGCGATGGACCGAAGGGAGGACATTGGAAATTTACTG | 669 | Db | 1690 | ACCACAGCAGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC | 1749 |
| Qy | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu | 240 | Qy | 581 | IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer | 600 |
| Db | 670 | GGTTCAGTGGTTATGCTCACAGCAGGAATTAATCACAGCTTGGTACATAGGATTTTG | 729 | Db | 1750 | ATAGAAATCCAAGCTGGACTCCCTACTAGACATCTATCAACAGGTCTCTCGGAAAGGCTCT | 1809 |
| Qy | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 | Qy | 601 | AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer | 620 |
| Db | 730 | GTTCCTATTTTTCGTTCTTCTTCTATCTGTTGGTGAAGAGATGCCAATAAAGAGTTT | 789 | Db | 1810 | GCCTCAGCCCTCGTTTGGCTTCTATCCAGTCCACCTTTTGAATGTGAACAGACATCT | 1869 |
| Qy | 261 | SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 | Qy | 621 | AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys | 640 |
| Db | 790 | TCTACATATGACAGATCTCTGTGGTGGGCACAAATTACATTAACATTTGGCTATGA | 849 | Db | 1870 | GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGCGCAAAAACAGTGGCTGC | 1929 |
| Qy | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuGly | 300 | Qy | 641 | LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn | 660 |
| Db | 850 | GACAAACCTCCCTAATCTTGGCTGGGAGATTGCTTTCTGCGAGGCTTTCACCTCTTGGC | 909 | Db | 1930 | TTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTCGAGTTCATTCTGACGCCAAT | 1989 |
| Qy | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 | Qy | 661 | GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln | 680 |
| Db | 910 | ATTTCTTTCTTTCGACTCTCTGCGGCANTTCTTGGCTCAGTTTTCATTAAGATACAA | 969 | Db | 1990 | GAGTTTCAGTCCCGAGACTTTCTACGCGCTTACGCTTACTATGACAGTCAACAGCACAG | 2049 |
| Qy | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln | 340 | Qy | 681 | ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln | 700 |
| Db | 970 | GAAACACCCGCGAGAAACACTTTGAGAAAGAGGAAACCCAGCTGCCACCTCATTCAG | 1029 | Db | 2050 | GTGCCAATTTAGTAAAGCGATGGCTCAGCAGTGGCGGCCAACACACCATTTGCAACCCA | 2109 |
| Qy | 341 | CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro | 360 | Qy | 701 | IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro | 720 |
| Db | 1030 | TGTTTGGGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTCGAACTCTGGAAGCCA | 1089 | Db | 2110 | ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCA | 2169 |
| Qy | 361 | HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer | 380 | Qy | 721 | AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu | 740 |
| | | | | Qy | 2170 | GCCATCAAGCATCTGCCAGGCGCAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGNA | 2229 |

QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
DB 2230 AGCATTTCTGACGTACCACCTGCTGTTGCTCTCAAGAGAAATGTTTCAGGTTCACAG 2289
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
DB 2290 TCANATCTCACCCAGAGACCGTCTATGAGGAAAGCTTTGACATGGGAGGAAACTCTG 2349
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
DB 2350 TTGCTGCTGTGCCATGGTCCGAGAGACTTGGGCAAAATCTTTGCTGTGCAAAACCTG 2409
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
DB 2410 ATCAGGTCCGACGAGAACTGAATATACAACCTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2469
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
DB 2470 GCGACCAAGATTTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACCTGATGAGAG 2529
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
DB 2530 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGCGCACCGCAGCTGCCAGGAA 2589
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
DB 2590 GCTGCTTTTGATCATCAGACTCTCTAAGGACTTGAAGGTCCAGCATCATCTCAGAGCATTTGT 2649
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
DB 2650 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2700

RESULT 6

US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. US20020076809A1
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEROHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-148-1

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4574.00 Matches: 895
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 2
Query Match: 99.65% Indels: 0
DB: 9 Gaps: 0

US-09-810-796-4 (1-897) x US-09-813-148-1 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
DB 215 ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTCTGTAATCTCGCAGCCCGCAGGGGC 274

QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
DB 275 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCCACCGCTTGGTGGCGGGCGGCGCTG 334
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 335 AGGAGAGCCCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGAAGCCGCTCTCT 394
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 395 TACACGAGTACCCAGAGCTGCGCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 454
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 455 TACAACGCTGTGGAGAGACCCCGCGGCTGGGCTTCATCTACCAACGCTTTCGTTTTCTC 514
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 515 CTTGTCTTTGGTGTGCTTGTGATTTTGTCACTGTTTCTACCATCCCTGACACAAAATG 574
QY 121 AlaSerSerCysLeuLeuLeuPheValMetIleValPheGlyLeuGluPhe 140
DB 575 GCCTCAAGTTCGCTTCGATCCTCGAGTTCGTGATGATTGTCGCTTTGGTGGAGTTC 634
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 635 ATCATTCGAATCTGCTGCGGGTGTGTTGTCGATATAGAGGATGCAAGAAAGACTG 694
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAsnIleAla 180
DB 695 AGGTTTGTCTGAAAGCCCTCTGTGTTATATACCATGTTCTTATCGCTTCAATAGCA 754
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 755 GTTGTTCCTGCAAAACTCAGGGTAATATTTTGCACGCTGCTGCACTCAGAAGTCTCCGT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 815 TTCTTACAGATCTCCGCAATGCGCATGCGTACAGACCGGAGGAGGACCTTGAAATTTACTG 874
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 875 GGTTCAGTGGTTATGCTCACAGCAAGAAATTAATCACAGCTGTGTCATAGGATTTTG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 935 GTTCTTATTTTTCGCTCTTCCTTCTATCTGGTGGAAAGGATGCCAATAAGAGTIT 994
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 995 TCTACATATGAGATGCTCTCTGGTGGGSCACAATTAATTCACAACTATTGGCTATGGA 1054
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTCTTCGAGGCTTTGCATCTCTGGC 1114
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1115 ATTTCCTTTTTCGACTTCCTGCGGCAATCTTGGCTCAGGTTTGGCATTTAAAGTACAA 1174
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1175 GAACAACACCCCGAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1234
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380
DB 1295 CACTTGAAGGCTTGCACACCTGCGAGCCTACCAAGAAAGAAAGAACAGGGGAGCATCAGC 1354

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QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1355 AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGGCCAGAGTATT 1414
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1415 AAGAGCCGACAAAGCTCAGTAGTGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1475 GGCAGTCCCAACAAAGTGCAGAAAGAGTGGAGCTTCAACGACCGAACCCGCTCCGGCCC 1534
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1535 TCGTTCGCCCTCAAAAGTTCTCAGCCAAACACAGTATAGATGCTGACACAGCCCTTGGC 1594
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1595 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGTATCAGTGGAAAGACCTCAC 1654
QY 481 ProProLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaIleArg 500
Db 1655 CCACCACTTAAACACTGCTCATTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1714
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1715 AAGTTTAGGAAACATTACGTCCATCATGATGTAAAGATGTCATTGAACAATATTCGT 1774
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1775 GGTCTATCGGACATGCTGTAGTAATTAAGAGCCCTTCAACACCGTGTGTGATCAAAATCTT 1834
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1835 GGAAAGGCGCAATCAGATCAGTAAAGAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1894
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1895 ACCACAGACGATCTCAGTATGCTCGGTGGTGGTCAAGGTGAAAAACAGGTACAGTCC 1954
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1955 ATAGAATCCAAAGCTGAGCTGCTATCAGACATCTATCAACAGGTCTTCGGAAAGGCTCT 2014
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 620
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGATGTGAACAGACATCT 2074
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTCGGGTTCGGCACAAACAGTGGCTGC 2134
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2135 TTATCCAGATCAACTAGTGGCCAACTCTCGAGAGGCTGCACTTCATTCAGCGCCAAAT 2194
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2195 GAGTTCAAGTCCAGACTTTCAGCGCTTACCGCTTACCTATGCAGTCAAGCAACACAG 2254
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2255 GTGCCAATTAGTCAAAAGCGTGGCTCAGCAGTGGGCGGCGCCACCAACCACTTCAACACCA 2314
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2315 ATAAATACGGCCCAAGCCAGCCAGCCCAACAACTTTACAGATCCACCTCTCTCCCA 2374
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2375 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCTTAACTCTGCAGGCTTACAGGAA 2434
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
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Db 2435 AGCATTTCTGACGCTCACCACTCCCTTGTTCCTCCAAAGGAAATGTTCCAGTTGCACAG 2494
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2495 TCAAAATCTCACCAAGAGCCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2554
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2555 TTGCTGCTGTCTCCATGGTGGCCGAGGACTTGGGCAAAATCTTTGCTGTGCAAAACCTG 2614
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlnSerSerGlySerArg 820
Db 2615 ATCAGGTCGAGCCGAGGAACATGAAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAG 2674
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2675 GGAGAGCCAAATTTTACCCCAATGGAGGGAATCCAAATTTTATTAATGATGAAGAG 2734
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2735 GTGGTCCCAAGAGACAGAGACAGACACTTTTGTGTCGCGCACCGCAGCCTGCCAGGAA 2794
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2795 GCTGCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2854
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2855 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACGTGAAA 2905
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RESULT 7

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US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US2002010267A1
; GENERAL INFORMATION:
; APPLICANT: Jegia, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3
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Alignment Scores:

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 0 | Length: | 2667 |
| Score: | 4527.50 | Matches: | 887 |
| Percent Similarity: | 99.00% | Conservative: | 1 |
| Best Local Similarity: | 98.89% | Mismatches: | 0 |
| Query Match: | 98.68% | Indels: | 9 |
| DB: | 9 | Gaps: | 1 |

US-09-810-796-4 (1-897) x US-09-810-796-3 (1-2667)

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Db 1 ATGAAGATGTGGAGTCGGCGCGGCGAGGTGCTGTCTGAACCTCGGACGCCGCGAGGGGC 60
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
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Db 61 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCCACGCTTGGTGGCGGCGGCTGGCTG 120
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGGAGAGCGCGCGGGCAAGCAGGGGCGCGGATGAGCCTGCTGGGAAAGCCGCTCT 180
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCAGACGCTGCGCGGCAACGTCGAAGTACCGCGGGTGCAGAACTACCTG 240
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACACGCTGTGGAGAGACCGCGCGCTGGGGCTTCACTACACGCTTTCGTTTTCTC 300
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 301 CTTGTCTTTGGTGTCTGATTTTGTCAAGTGTTCCTACCATCCCTGAGCACAAATG 360
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTGTGCTTGAATCTGAGTTCGTGATGATGTGCTCTTTGGTTGGAGTTC 420
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 421 ATCATTCAATCTGCTGCGGTTGCTGTTCGATATAGAGATGGCAAGAAAGACTG 480
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCAATTTCTTATCGCTTCATAGCA 540
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTCTCTGCAAAACCTCAGGGTAATATTTTTCACGCTCTGCACTCAGAACTCCGT 600
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220
Db 601 TTCCTACAGATCCTCCGATGTCGCATGGACCAAGAGGAGGACCTTGGAAATACTG 660
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGTACATAGGATTTG 720
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTATTTTTCGCTCTTCCTGCTATCTGTGGTGAAGAGATGCCAATAAAGAGTTT 780
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 781 TCTACATATGCAGATGCTCTCTGGTGGGCGCAATTTACATTGACAACATTTGGCTATGGA 840
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAACTCCCTAACTTGGCTGGAGAGATGCTTCTTCGAGGCTTTGCACTCTCTGGC 900
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
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Qy 321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
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Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1081 CACTTGAAGGCGCTGCACACCTGCGAGCCCTACC----- 1113
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
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Db 1114 AATCAGAAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGGCCAGATATT 1173
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1174 AAGAGCCGACAAAGCCTCAGTAGTGCAGAGGAGTCCCCAAGCACGACATCAACAGCCGAG 1233
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1234 GGCAGTCCCAACAAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGCC 1293
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGACACAGCCCTTGGC 1353
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1354 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGATATCATGATGGAACCTCACC 1413
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1414 CCACCACTTAAACACTGCTCATTTGAGCTATCAGAATTATGAAATTTTCATGTTGCAAAACGG 1473
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1474 AAGTTTAAAGAAACGTTACGTTCCATATGATGTAAAGATGTCATTTGAACAATATTCGT 1533
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1534 GGTCACTGGACATGTTGTTAGTAATTAAGCCCTTCAACACACGCTGTTGATCAAAATCTT 1593
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1594 GGAAAGAGGCGCAATCACATCAGATAAGAGAGCCGAGAGAAATAACACAGCAGAACATGAG 1653
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 580
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Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1714 ATAGAGTCCAAGCTGGACTGCTACTACATCTATCAACAGGCTCTTCGGAAGGCTCT 1773
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1774 GCCTCAGCCCTCGCTTTGCTTTCATTCAGATCCCACTTTTGAATTTGAAACAGACATCT 1833
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCCGCAAAACAGTGGCTGC 1893
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1894 TTATCCAGATCAACTAGTGCACCAACATCTCGAGAGGCTCGAGTTTCAATCTGACGCCAAT 1953
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 1954 GAGTTAGTGCACGACTTCTTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2014 GTGCCAATTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACCAATTCGCAAAACCA 2073
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2074 ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2134 GCCATCAAGCATCTGCCCAGGCCGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAA 2193
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2194 AGCATTTCTGACGTCACCACTGCTGCTGCTCCCAAGGAAATGTTTCAGGTTGCACAG 2253

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QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
DB 2254 TCAATCTCACAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG 2313
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
DB 2314 TTGCTGTCTCCATGGTCCGAGGACTTGGCAAAATCTTTGTCTGTGCAAAACTG 2373
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
DB 2374 ATCAGTCCGACCGAGGAACCTGAATATACAACTTTCCAGGAGTGAAGTCAAGTGGCTCCAGA 2433
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
DB 2434 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTATTAACATGATGAAGAG 2493
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
DB 2494 GTGGTCCGAGAGACAGACAGACACTTTTGATGCCGACCGCAGCCTGCCAGGAA 2553
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
DB 2554 GCTGCCCTTGCATCAGACTCTCTAAGGACTCGAAGGTCAAGATCATCTCTCAGAGCATTTGT 2613
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
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RESULT 8

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US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20020042505A1el Human Ion Channel Protein and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
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Alignment Scores:

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Pred. No.: 0 Length: 2772
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservatives: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 9 Gaps: 1
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US-09-810-796-4 (1-897) x US-09-825-147-1 (1-2772)

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QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 166 GACGGCTGTCTACTGTGGGACCCCGCGGCCACCTCTGGTGGCGCGCGGTGGCTGT 225
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QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCACAGTACCGCGGGTGCAGAACTACCTG 345
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 346 TACAACGTGTGAGAGAGACCCCGCGGTGGCGCTTCATCTACCACGCTTCGTTTTTCTC 405
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 406 CTGTGCTTTGCTTGCTTGTATTTTGTGCTGATGATGCTGCTTTTGGTTTGGAGTTC 465
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 466 GCCTCAAGTTGCCCTCTTGATCTCGAGTTCGTGATGATGCTGCTTTTGGTTTGGAGTTC 525
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 526 ATCATTCGAATCTGCTCTCGGGTGTCTGTTGTCGATATAGAGATGCGCAGGAGACTG 585
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 586 AGGTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 645
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 646 GTTGTCTCGAAAACTCAGGGTAAATATTTTGGCCAGCTGCTGCTCAGAGTCTCCGT 705
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 706 TTCTACAGATCTCCGATGTTGGCGATGACCGAGGGGAGGACACTTGGAAATTAAGT 765
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 766 GGTTCAGTGGTTATGCTCAGCAGAGAAATTAATCAAGCTTGGTATCATAGGATTTTGT 825
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
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DB 886 TCTACATATGCAGATGCTCTCTGCGGCGCAATTAATGACAACTATTGGCTATGGA 945
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 946 GACAAAATCCCTTAACCTGGCTGGGAAGATTGCTTTCTGCGAGCTTTGCACTCCTTGGC 1005
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1006 ATTCTTCTTTGCACTTCTGCGGCAATTTCTGCTCAGGTTTGCATTAAGATACAA 1065
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1066 GAACAACACCCCGAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTCAG 1125
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1126 TGTGTTTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGNAGCA 1185
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380
DB 1186 CACTTGAAGGCTTGCACACCTGCGAGCCCTACC----- 1218
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
DB 1219 AATCAGAGCTAAGTTTTTAAGGAGCGAGTGGCGATGGCTAGCCCCAGGGGCGAGATATT 1278
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QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1279 AAGACCCCAAGCCTCAGTAGTCACAGGAGGTCCCCAAGCACCAGCATCACACCCGAG 1338
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1339 GGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1398
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1399 TCGCTGCGCCCTCAAAAGTTCTCAGCCAAAACCCAGTGATAGTCTGCACACAGCCCTTGGC 1458
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1459 ACTGATGATGATATGATGAAAAGAGTGCCAGTGTGATGTATCATGTGAAGACCTCAC 1518
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1519 CCACCACCTTAAACCTGCTATTCGACCTATCAGAAATATGAAATTCATGTTGCAAAACGG 1578
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1579 AAGTTTAAAGGAACATTAACGTCATGATGATGATAAGATGTCATTGAAACAATATTTCTGCT 1638
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1639 GGTCACTCGACATGTTGTGTAGAAATTAAGACCTTCAAAACGCGTGTGATCAAAATCTT 1698
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1699 GGAAGAGGCAATCATCATGATGAAGAGCGAGAGAAATTAACAGCAGACATGAG 1758
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
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Db 1819 ATAGAATCCAGCTGACGTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 1878
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1879 CCTCAGCCCTCGCTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1938
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1939 GACTATCAAGCCCTGTGATAGCAAGATCTTTCCGGTTCGCGACAAAACAGTGGCTGC 1998
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1999 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTCGCATTTCAATCTGACGCCAAT 2058
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2059 GAGTTCACTGCGCAGACTTCTACGCGTTAGCCCTTACTATGCAGTCAAGCAAGCAACAG 2118
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
Db 2119 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2178
QY 701 IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProLeuPro 720
Db 2179 ATAAATACGGCACCACCAAGCCAGCAGCCCAACACTTTTACAGATCCCACTCTCTCCA 2238
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2239 GCCATCAAGCATCTGCCCGAGCCAGAACTCTGCACCTTAACCTTGCAGGCTTACAGAA 2298
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2299 AGCATTTCTGACGTCAACACCTGCTGTTGCTTCCCTCAAGGAATGTTTCAGGTGGCAG 2358
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
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Db 2359 TCAAAATCTCAACAGGACCGTTCTATAGGAAAAAGCTTTGACATGGGAGGAGAACTCTG 2418
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2419 TTGTCGTCTGTCCCATGTCGCGAGGACTTGGCAATCTTTCTCTGTGCAAAACCTG 2478
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2479 ATCAGGTGCAGCGAGGAACCTGAATATACAACCTTTTCCAGGAGTGAGTCAAGTGGCTCCAG 2538
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2539 GGCAGCCCAAGATTTTACCCCAATGGAGGAATCCAATTTGTTATTAACCTGATGAAGAG 2598
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 860
Db 2599 GTGGGTCCCGAAGAGACAGACAGACACTTTTGATGCGCACCGCAGCTGCCAGGAA 2658
QY 861 AlaIlePheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2659 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGTATCATCTCAGAGCATTTGT 2718
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
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RESULT 9
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservatives: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 18 Gaps: 1

US-09-810-796-4 (1-897) x US-10-803-268-1 (1-2772)
QY 1 MetLysAspValGluSerGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
Db 106 ATGAAGATGTGGAGTCGGCGCGGCGAGGTGCTGCTGAACTCGGACGCCAGCGGCG 165
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaIleThrLeuGlyGlyGlyLeu 40
Db 166 GACGCGCTGTACTGTGCGGCGCCCGCCCGCTCGGTGCGCGCGCGGCGGCTG 225
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Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTACGACAGCTGCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 345
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACAACGGCTGGAGAGACCCCGGCGCTGGGCGTTTCATCTACCGCTTTTCGTTTTCCTC 405
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTGTGCTTGGTTCGTTGATTTGTTCAGTGTTCCTACCATCCCTGAGCACACAAATTG 465
Qy 121 AlaSerSerCysLeuLeuIleGluPheValMetIleValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGCCTTCGATCTCGAGTTCGTGATGATTGTCTGTTGGTTGGAGTTC 525
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
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Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTTGTCCGAAGCCCTCTGTGTTATAGATACCATTTGTTTCATCGCTTCAATAGCA 645
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheIleThrSerAlaLeuArgSerLeuArg 200
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Db 766 GGTTCAGTGGTTTATGCTCACGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 825
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Db 826 GTTCTTATTTTTCGTCCTTCCTGTCATCTGGTGGAAAGGATGCGCAATAAAGAGTTT 885
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATAGCAGATGCTCTCTGGTGGGGCAATTAATTGACAACATTTTGGCTATGGA 945
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 946 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCGAGCTTTTGCCTCTTGGC 1005
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTTTTCGCACTTCCCTCCCGCATCTTGGCTCAGGTTTTCGCAATTAAGATCAA 1065
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAACAAACCCCGCAAAACACTTTTGAGAAAGAGAGAACCCAGCTGCGCAACCTCATTTAG 1125
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1126 TGTGTTTGGCTAGTTACGACGTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1185
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380
Db 1186 CACTTGAAGGCGCTTGCACACCTGACGCTTACC----- 1218
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1219 AATCAGAGCTAAAGTTTTAAGAGCGAGTGGCATGGCTAGCCCCCAGGGGGCAGAGTATT 1278

Qy 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420
Db 1279 AAGAGCCGCAAGAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1338
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1339 GGCAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCGCTTCGGGCC 1398
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1399 TCGCTGGCCCTCAAAAGTTCTCAGCCAAACCACTGATAGTGTGACACAGCCCTTGGC 1458
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1459 ACTGATGATGATATGATGATAAAGAGTGCAGTGTGATGTATCAGTGGGAAGACTCAC 1518
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1519 CCACCACTTAAACTGTCTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1578
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1579 AAGTTTAAAGAAACATTTACGTCATATGATGATAAAGATGTCATTTGAACAATTTCT 1638
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1639 GGTTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAACACCGTGTGTGATCAAAATCT 1698
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1699 GGAAAGCGGCAAAATTCATCAGATGAAGAGCGGAGAGAAATAACAGCAGAACATGAG 1758
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 580
Db 1759 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAAGTTTGAACAGGTACAGTCC 1818
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1819 ATAGAATCCAAGCTGGACTGCTACTAGACATCTATCAACAGAGTCTTCGGAAGGCTCT 1878
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1879 GCCTCAGCCCTCGCTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1938
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1939 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTCCGACACAAACAGTGGCTGC 1998
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1999 TTATCCAGATCAACTAGTGGCCACATCTCGAGAGGCTGCGAGTTTCATTTCTGACGCCAAT 2058
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2059 GAGTTCAGTGGCCAGACTTTCACGCGCTTAGCCCTTACTATGCACAGTCAAGCAACACAG 2118
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2119 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCGCCACCAACACCATTTGCAAAACCA 2178
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2179 ATAAATACGGCACCCCAAGCCAGCAGCGCCCAACAACTTTACAGATCCCCACCTCTCTCCA 2238
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2239 GCCATCAAGCATCTGCCCGAGCCCAAGAACTCTGCAACCTTAACCTTCAGGCTTACAGAA 2298
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2299 AGCATTTCTGACGTCAACCATCTGCTTGTGCTCCCAAGGAAATGTTTCAGTTGACACAG 2358
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780

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Db 2359 TCANATCTCACAGACCGTTCTATGAGAAAGACTTTGACATGGGAGGAAACTCTG 2418
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2419 TTGCTGCTGTGCCATGTGCGGAGGACTTGGGCAATCTTTGCTGTGCAAAACCTG 2478
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820
Db 2479 ATCAGTCGACCGAGAACTGAATATACAACCTTTCCAGGAGTGAGTCAAGTGGCTCCAGA 2538
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2539 GCACCCCAAGATTTTACCCCAATGGAGGAAATCCAAATGTTTATTAACATGATGAAGAG 2598
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaLeuProGlnProAlaArgGlu 860
Db 2599 GTGGGTCCGAGAGACAGACACACTTTTGTATGCGCACCGCAGCTGCCAGGAA 2658
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2659 GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCAATTTGT 2718
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2719 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2769

RESULT 10
; US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No.: US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambriczy, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 9 Gaps: 1

US-09-810-796-4 (1-897) x US-09-825-147-3 (1-3111)
Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
Db 165 ATGAAGGATGTGAGTGTGGGCGGCGGAGGAGTGTGCTGTAAGTGGCAGCCCGGAGG 224
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGTACTGTGGCACCCCGCGGCGCACGCTCGGTGGCGGCGGTGGCTG 284
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Db 285 AGGAGAGACCCCGGGGCAAGCAGGGGCCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 344
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 345 TACACGAGTACCGAGAGCTGCGGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 404
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 405 TACACGCTGTGGAGAGACCCCGGGCTGGCGGTTCATCTACCAAGCTTTGTTTTTCTC 464
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTTGCTTTGTTGTTGCTGATTTTGTCAAGTGTTCCTACCATCCCTGAGCACACAAAATG 524
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTTGCTCTTGATCTCGAGTTCTGATGATGTCGTCCTTTGGTGTGGAGTTC 584
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 585 ATCATTCGAATCTGCTGCGGGTGTGTTGTCGATATAGAGGATGCAAGGAAGACTG 644
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 645 AGGTTTGTCTGAAAGCCCTCTGTGTTATATACCATTTGTTCTTATCGCTTCAATAGCA 704
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 705 GTTGTCTCTGCAAAAACCTCAGGGTAATATTTTTCACAGCTCTGCACCTCAGAAGTCTCCG 764
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyGlyThrTrpLysLeuLeu 220
Db 765 TTCTACAGATCTCTCCGATGTCGTCGATGACGAGGAGGAGGACCTTGAAATTAATCTG 824
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu 240
Db 825 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGATCATAGGATTTTGT 884
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTATTTTTCGTCCTCTCTCTGTCATCTGTTGGGAAAGGATGCCAATAAGAGTTT 944
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGAGATGCTCTCTGTTGGGGCAACAATTAATTCACAACTATTGGCTATGGA 1004
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAAACCTCCCTAACTTGGCTGGGAGATGCTTTCTGCAGGCTTTTGCACTCTCTTGGC 1064
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTCTTTCGCTCTCTGCGGCACTTCTGCTCAGGTTTGGCTATTAAGTACAA 1124
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCCCGAGAAACACTTTTGAGAAAAGAGAACCCAGCTGCCAACCCTCATTCAG 1184
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTGGCGTAGTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTTGGAGGCA 1244
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380
Db 1245 CACTTGAAGGCTTGCACACCTGCAGCCCTACC----- 1277
Qy 381 SerGlnLysLeuSerPhePheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1278 AATCAGAGCTTAAGTTTTTAAGAGCGAGTGGCATGCTAGCCCCCAGGGGCGCAGATATT 1337
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
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Db 1338 AAGAGCCGACAGCCTCAGTAGGTGACAGAGGTCCCAAGCACCAGCATCACAGCCGAG 1397
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheIleAsnAspArgThrArgPheArgPro 440
Db 1398 GGCAGTCCCAAGAGTGCAGAGAGGTGGAGCTTCAACGACCGAACCCTTCGGGCC 1457
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1458 TCGCTGCCCTCCAAAAGTTCTCAGCCAAACAGTATAGTATGCTGACACAGCCCTTGGC 1517
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1518 ACTGATGATGATATGATGAAAAGGATGCCAGTGTGATGATCATCAGTGAAGACCTCAC 1577
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1578 CCACCACCTTAAACCTGCTATTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1637
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1638 AAGTTTAAGGAAACATTACGTCATATGATGATAAAGATGTCATTTGAACAATATCTGCT 1697
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1698 GGTCTATCTGGACATGTTGTGTAGAAATTAAGAGCCTTCAACACAGCTGTGTGATCAAAATCTT 1757
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1758 GGAAAGGGCAAAATCACATCATGATAAGAGAGCCGAGAGAAATAAACAACAGACATGAG 1817
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValIleLysSer 580
Db 1818 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1877
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAATCCAGCTGCCTACTAGACATCTATCAACAGGTCTTCGGAAGGGCTCT 1937
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTGGCTTCATCTCCAGATCCACCTTTTGAATGGAACACATCT 1997
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGACACAAACAGTGGCTGC 2057
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTGCAGTTCATTTCTGACGCCAAT 2117
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTTCAGTCCACACTTTCACCGCTTAGCCCTTACTATGCAAGTCAAGCAACACAG 2177
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2178 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCGAGCCACCACACCATTTGCAAAACAA 2237
Qy 701 IleAsnThrAlaProLysProAlaIleProThrThrLeuGlnIleProProLeuPro 720
Db 2238 ATAAATACGGCCCAAGCCAGCCACCAACACTTTACAGATCCCACTCTCTCCCA 2297
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2298 GCATCAAGCATCTGCCAGGCCAGAACTCTGCACCTTAACCTTCAGGCTTACAGGA 2357
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2358 AGCAATTTCTGAGCTCACCACTGCTTGTGCTTCAAGGAAATATGTTTCAGGTTTCACAG 2417
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 780
Db 2418 TCAATCTCACCAAGGACCGTTCTATGAGAAAGCTTTGACATGGGAGGAGAAATCTCTG 2477
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Db 2598 GGCAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTATACTGATGAAGAG 2657
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Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2718 GCTGCCCTTTCATCAGACTCTCTAAGGACTTGAAGGTTCAGATCATCTCAGAGCATTTGT 2777
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RESULT 11

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US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3
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Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 18 Gaps: 1
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US-09-810-796-4 (1-897) x US-10-803-268-3 (1-3111)

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Db 165 ATGAAGGATGTGGAGTTCGGCCCGGCGCAGGGTGTCTGTAACCTCGGACGCCCGCGGGC 224
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyLeu 40
Db 225 GACGCGCTGCTACTGCTGGGCACCGCGCCACCGCTCGGTGGCGCGCGGTGGCTG 284
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Db 285 AGGAGAGCCGCGGGGCAAGCAGGGGCGCCGAGTAGCGCTGCTGGGAAGCCGCTCTCT 344
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 345 TACACGAGTAGCCAGAGCTGCGGGCGCAACGTCAGTAGTACCGGGGGTGCAGNACTACCTG 404
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Db 405 TACACAGGTGCTGGAGAGACCCCGCGCTGGCGGTTCATCTACACAGCTTCGTTTTTCTC 464
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Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTGTGCTCTGATCCTGAGTTCGTGATGATTGTCGTCCTTTGGTGGAGTTC 584
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
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Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 645 AGGTTTGTCTGAAAGCCCTTCGTGTATAGATACCATGTTCTTATCGCTTCAATAGCA 704
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Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 765 TTCTTACAGATCTCTCGCATGTGGCATGGACCGAAGGGAGGCACTTGGAAATTAATG 824
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Db 825 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTATAGGATTTTG 884
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTAATTTTCTGCTTCTGCTATCTGTTGGTGGAAAGGATGCCAATAAAGNGTTT 944
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGCAGATGCTCTCTGTGGGGGCAATATACATTGACAACTATTGGCTATGGA 1004
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAACCTCCCTTAACCTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCACTCTCTGGC 1064
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTCTTGGCTCTCTCGCGCATCTTGGCTCAGGTTTGGATTAAAGTAGTACA 1124
Qy 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCGCAGAAACACTTTGAGAAAAAGAGAAACCCAGCTGCGCAACCTCATTTCCAG 1184
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTTGGCGTAGTACGAGCTGATGAGAAATCTGTTTCATTGCAACCTGGGAAGCCA 1244
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1245 CACTTGAAGGCTTGCACACCTGACGCTTAC----- 1277
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1278 AATCAGAAGCTAAGTTTTAAGAGCGAGTGCATGGCTAGGCCCGGGCCAGAGTATT 1337
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420

Db 1338 AAGAGCCGCAAGGCTCAGTAGGTGACAGGAGGTCCCCAAGACCAGCATCACAGCCGAG 1397
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1398 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCGCTTCGGGCC 1457
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1458 TCGTGGCGCTCAAAAGTTCTCAGCCAAACACAGTAGTAGTGTGATCATGTGGAAGACCTCACC 1517
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1518 ACTGATGATGATATGATGATAAAGGATGCCAGTGTGATGATCATGTGGAAGACCTCACC 1577
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Db 1578 CCACCACCTTAAACCTGTCATTTCGAGCTATCAGAAATTATGAAATTCATGTTGCAAAACGG 1637
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1638 AAGTTTAAGGAACCATTCAGTCCATATGATGATAAAGATGTCAATTGAAACAATATTCGTCT 1697
Qy 521 GlyHisLeuAspMetLeuCysArgGlyLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1698 GGTCACTCGGACATGTTGTGTAGAAATTAAAGCCCTTCAACACGCTGTGATCAAAATCTT 1757
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1758 GGAAAGGGCAAAATCACATCAGATAGAAAGAGCCGAGAGAAATAAACAGCAGAACATGAG 1817
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1818 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1877
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAAATCCAAAGCTGGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1937
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1997
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCCTCCGCAAAACAGTGGCTGC 2057
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGCACCAACATCTCGAGAGGCTGCGAGTTCATTTGACGCCAAT 2117
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTTCAGTCCAGACTTTTCTACGCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2177
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGln 700
Db 2178 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCAA 2237
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2238 ATAAATACGGCACCCAGCCAGCCCAACACTTTACAGATCCCACTCTCTCTCCCA 2297
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2298 GCCATCAAGCATCTGCCCGAGCCAGAAACTCTGCACCCCTAACCCCTGCGAGGCTTACAGGA 2357
Qy 741 SerIleSerAspValThrThrCysLeuValLysSerLysGluAsnValGlnValAlaGln 760
Db 2358 AGCATTTCTGACGTCACCCACCTGCTTGTCCCTCCAAAGGAAAAATGTTTCAGTGTGCACAG 2417
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 780
Db 2418 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAAACTCTG 2477

Qy 273 rleuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe 293
Db 922 ATGTGCAACCAATCGGTATGTTGCAAGACACCGCACATGCTGGCGAGGTCTCTGGC 981
Qy 293 rAlaGlyPheAlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySe 313
Db 982 TGCTGGCTTCGCTTACTGGGATCTCTTTCTTCCCTGCTGCTGGCATCTTAGGCTC 1041
Qy 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333
Db 1042 CGGCTTTCGCTTGAAGGTCAGGAGCAGCCCGGAGAGCACTTCGAGAGCGGAGGAT 1101
Qy 333 nProAlaAlaLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp---GluLysSe 352
Db 1102 GCGGCGAGCCAACTTCATCCAGGCTGCTGGCGCTGTACTCCACCATATGAGCGGGC 1161
Qy 352 rValSerIleAlaThrTrp----- 358
Db 1162 CTACCTGACAGCCACTGGTACTACTATGACAGATATCTCCATCTTCAGAGAGCTGGC 1221
Qy 358 ----- 358
Db 1222 CCTCTTTTGAGCAGCTGCAACGGCGCGCAATGGGGCCCTACGGCCCTTGGAGGTGG 1281
Qy 359 -----LysProHisLeuLysAlaLeuHisTh 367
Db 1282 GCGGGCGCGGTACCAGCGAGACACCTCCGTTACCGCGCGTTGCCACTGTCACCG 1341
Qy 367 rCysSerProThrLysLysGluGlnGlyAlaSerSerSerGlnLysLeuSerPheLys 387
Db 1342 GCGGGCGAGCCTCTCTGCTGGCGTGGGGAAGCAGC-----CGATGGGATCAA 1392
Qy 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405
Db 1393 AGACCGCATCGCATGGGAGCTCCAGCGGGCGGAGCGGTCTCTCAAGCAGCAGCTGGC 1452
Qy 405 aSerValGlyAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424
Db 1453 ACCTCCAAATAGCCCACTCCCAAGCAGCAGCAGCGAGTGGGTGAGGCCACACCGCCAC 1512
Qy 424 rLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLe 444
Db 1513 CAAGGTGCAAAGAGCTGGAGTTCAATGACCGCCAGCGCTTCCGGGATCTCTGAGACT 1572
Qy 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464
Db 1573 C-----AAACCCCGCAGCTCTGCTGAGGATGCC---CCTCAGAGGAAGT 1614
Qy 464 lTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLys 484
Db 1615 AGCAGAGAGAGAGCTACCACTGTGAGCTCAGGTGGAGCAGCATCATGCTGCTGTGAA 1674
Qy 484 sThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysG1 504
Db 1675 GACAGTCATCGCTCCATCAGATTTCTCAAGTTCTGTGGCCAAAGAAATTCAGGA 1734
Qy 504 uThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAs 524
Db 1735 GACACTGGCAGCGTACGAGCGTGAAGGACGTCAATTGAGCAGTACTCAGCAGGCCACTGGA 1794
Qy 524 pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyG1 544
Db 1795 CATGTGGCGCGGATCAAGAGCTCCAACTCGGTGGACCAAAATTTGGGTGCGGGG-- 1852
Qy 544 nIleThrSerAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluTh 561
Db 1853 -----CCCGGGGACAGAGGCGCGGAGAGGCGGCGGCGCTTCGAGCGGAGGT 1908
Qy 561 rThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerI1 581
Db 1909 GGTGATGAATCAGCATGATGGGAGCGGTGTCAAGGTGAGAGAGGAGGTGAGTCCAT 1968
Qy 581 eGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAl 601

Db 1969 CGAGCACAAAGCTGACCTGCTGTTGGGCTTCTATTCCGCGCTGCTGCGCACCTC 2028
Qy 601 aSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAs 621
Db 2029 GGCC-----AGCTGGGCGCGTGCAGTGCCTGTTCCAGCCCGACATCACCTCCGA 2082
Qy 621 pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641
Db 2083 CTACACAGCCCTGTGGACCAACAGGACATCTCGTCTCCGACACGCTCAGC---AT 2139
Qy 641 uSerArgSerThrSerAlaAlaSerArgGlyLeuGlnPheIleLeuThrProAsnG1 661
Db 2140 CTCCGCTCGGTACCAACATCGAGCTGAGG----- 2173
Qy 661 uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681
Db 2173 ----- 2173
Qy 681 lProIleSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGlnI1 701
Db 2174 ----ACTTCTCAGAGCGAGCGCAGCACA----- 2197
Qy 701 eAsnThrAlaProLysProAlaAlaProThrThrLeu-GlnIleProProProLeuProA 721
Db 2198 -CGGCGCAGCCCGCGGCTGCGCTCCGACTGCGCTCTGAGCGCTCCGAGCTCCTCTCT 2256
Qy 721 lalIeLysHisLeuProArgProGluThrLeuHis 732
Db 2257 ACTTGAACCTCACTCCCTCACGGGAGAGAGACCAC 2291

RESULT 13
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-10-850-928-1

Alignment Scores:
Pred. No.: 3,89e-197 Length: 2335
Score: 2012.00 Matches: 437
Percent Similarity: 65.45% Conservative: 82
Best Local Similarity: 55.11% Mismatches: 136
Query Match: 43.85% Indels: 138
Gaps: 16

US-09-810-796-4 (1-897) x US-10-850-928-1 (1-2335)
Qy 8 ArgGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
Db 127 CGGGAGCGCCCGCGGAGCTAGTGGCGCTCAGCGC----- 165
Qy 28 ThrArgAlaAlaThrLeuGlyGlyGlyLeuArgGluSerArgArgGlyLys 47

[illegible]

| | | | |
|------|----|--|------|
| 1222 | Db | CCTCTTTGTGACACGTGCAACGGGCCCGCCAAATGGGGCCCTACGGCCCTCGAGGTGCG | 1281 |
| 359 | QY | -----LysProHisLeuLysAlaLeuHisTh | 367 |
| 1282 | Db | CGGGCGCGGTACCGACGGAGCACCTCCCGTTACCCGCGGTGGCCACCTGCACCG | 1341 |
| 367 | QY | rCysSerProThrLysLeuGlnGlyGluAlaSerSerGlnLysLeuSerPheLys | 387 |
| 1342 | Db | CGCGGGCAGCACCTCTCTTCTCGCTCGGGAAAGCAGC-----CGATGGGCATCAA | 1392 |
| 387 | QY | sGluArgValArgMetAlaSerProArgGlyGlnSerLysSerArgGln-----Al | 405 |
| 1393 | Db | AGACCGCATCCGATGGCAGCTCCAGCGCGGACGGGTCTCTCCAGCAGCAGCTGCG | 1452 |
| 405 | QY | aSerValGlyAspArgArgSerProSerThrAspLleThrAlaGluGly---SerProTh | 424 |
| 1453 | Db | ACCTCCAAACAATGCCACCTCCCAAGCAGCAGCAGGTGGGTGAGCCACCGACCCAC | 1512 |
| 424 | QY | rLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLe | 444 |
| 1513 | Db | CAAGGTGCAAAAGAGCTGGAGCTTCAATGACCCACCCGCTTCCGGGCATCTGTGACT | 1572 |
| 444 | QY | uLysSerSerGlnProLysProValLleAspAlaAspThrAlaLeuGlyThrAspAspVa | 464 |
| 1573 | Db | C-----AAACCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGAAAGT | 1614 |
| 464 | QY | lTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLys | 484 |
| 1615 | Db | AGCAGGAGAGAGACTACCAAGTGTGAGCTCCAGGTGGAGCAGCATCATGCTCTGTGAA | 1674 |
| 484 | QY | sThrValLeuArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGl | 504 |
| 1675 | Db | GACAGTCATCGCTCCATCAGGATTCCTCAAGTTCTCGTGTGCCAAAAGGAAATTCAGGA | 1734 |
| 504 | QY | uThrLeuArgProTyrAspValLysAspValLleGluGlnTyrSerAlaGlyHisLeuAs | 524 |
| 1735 | Db | GACACTGCGACCGTACGACGTGAAGACGTCATTGACGACTACTCAGCAGCCACCTGGA | 1794 |
| 524 | QY | pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnLleLeuGlyLysGlyGl | 544 |
| 1795 | Db | CATGCTGGCGCGGATCAAGACCTGCAAACTCGGTGACCAATTTGGTGGTGGGGG-- | 1852 |
| 544 | QY | nIleThrSerAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluTh | 561 |
| 1853 | Db | ---CCCGGGCAGCAGGAAGCCCGGAGAGGGCGCACAAGGGGCGCTCCACGCGGAGGT | 1908 |
| 561 | QY | rThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIl | 581 |
| 1909 | Db | GGTGGATCAATCAGCATGATGAGCAGCGGTGTCAGGTGGAGAGCAGAGTGCATCCAT | 1968 |
| 581 | QY | eGluSerLysLeuAspCysLeuLeuAspLleTyrGlnGlnValLeuArgLysGlySerAl | 601 |
| 1969 | Db | CGAGCACAAGCTGGACCTGCTGTTGGGTCTATTTCGCGCTGCTGGCTCTGGCAGCTC | 2028 |
| 601 | QY | aSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAs | 621 |
| 2029 | Db | GGCC-----AGCTGGCGCGCGTGCAGTCCGCTGTTCACCCCGGCATCACCCTCGA | 2082 |
| 621 | QY | pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAanSerGlyCysLe | 641 |
| 2083 | Db | CTACACAGCCCTGTGGACACGAGACATCTCCGTCTCCGACACAGACGCTCAGC---AT | 2133 |
| 641 | QY | uSerArgSerThrSerAlaAanLleSerArgGlyLeuGlnPheLleLeuThrProAanGl | 661 |
| 2140 | Db | CTCCCGCTCGGTGAGCAGCAACATGCACTGAGG | 2173 |
| 661 | QY | uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa | 681 |
| 2173 | Db | ----- | 2173 |
| 681 | QY | lProLleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAanGlnIl | 701 |
| 2174 | Db | ---ACTTCTCAGAGCAGCGGACAGACA----- | 219 |

Qy 701 eAsnThrAlaProLysProAlaAlaProThrThrLeu-GlnIleProProLeuProAla 721
Db 2198 -CGGCCAGCCCGCGCGCTGGCGCTCCGACTGCGCTCTGAGCGCTCCGCGACTCTCTCGT 2256
Qy 721 lalleLysHisLeuProArgProGluThrLeuHis 732
Db 2257 ACTTGAACCTACTCCCTCACGGGGAGAGACCAC 2291

RESULT 14
US-10-820-307-8
; Sequence 8, Application US/10820307
; Publication No. US20040175691A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB CO.
; TITLE OF INVENTION: USE OF KCNQ2 AND KCNQ3 GENES FOR THE DISCOVERY OF AGENTS USEFUL
; ; TITLE OF INVENTION: IN THE TREATMENT OF NEUROLOGICAL DISORDERS
; FILE REFERENCE: DM-7029 DIV
; CURRENT APPLICATION NUMBER: US/10/820,307
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/110,804
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: US 09/454,868
; PRIOR FILING DATE: 1999-12-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 5595
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-820-307-8

Alignment Scores:
Pred. No.: 6,31e-178 Length: 5595
Score: 1832.50 Matches: 419
Percent Similarity: 60.26% Conservative: 92
Best Local Similarity: 49.41% Mismatches: 196
Query Match: 39.94% Indels: 142
DB: 18 Gaps: 21

US-09-810-796-4 (1-897) x US-10-820-307-8 (1-5595)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db 1652 TCCACTCGGACGGCGCTACTATCGCGGCTCCGAGCGCCCAAG-----CGC 1702
Qy 37 GlyGlyGlyLeuArgGluSerArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 56
Db 1703 GCGAGCGTTTGTAGCAAGCCCGCGGACGGCGCGCGGAGCC-----GGG 1747
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysThrArgVal 76
Db 1748 AAGCCC-----CCAAAGCGCAAGCGCTTCTACCGCAAGCTG 1793
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 1784 CAGAAATTCCTATACAAGCTGTAGAGCGGCCCGCGCTGGCGGCTTCATCTACCAAGCC 1843
Qy 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db 1844 TACGGTGTTCCTTTAGTCTTCTCCGCGCTTGTGCTTTCGCTTTCACCATCAAGGAG 1903
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValPhe 136
Db 1904 TATGAGAGATTCGAGAGGGCCCTCTACATCTTGGAATCGTGACCATCGTGTATTC 1963
Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
Db 1964 GGTGTGTGAGTACTTTGTGAGAATCTGGCTGTCAGGCTGCTGCTGCGGTATCGAGGCTG 2023
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 176
Db 2024 AGGGCCCGGCTCAAGTTTCCAGGAAGCCATTCTGTGTATCGATCATCATGTGTGATT 2083

Qy 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 2084 GCCTCCATTGCTGCTGGCTGCTGGCTCCAGGGCAATGTCTTTGTGTACGCTCTGCACAT 2143
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216
Db 2144 CGGAGCTTGGGTTCTTACAAATCTTACGAGATGATCCGTATGGACCGGAGGGGGGACC 2203
Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
Db 2204 TGGAAAGCTCTGGGATCGGTGCTACGCTCACAGCAAGAGAGCTGGTGTGGTGTAC 2263
Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db 2264 ATTGGCTCTCTGCTCATCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2323
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThr 276
Db 2324 AATGACCACTTCGACACTACGCGGATGCACTCTGGTGGGTCTGATCACCCTGACAC 2383
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 2384 ATTGGCTACGGGACAAAGTACCCTCAGACCTGGAAACGGGAGGCTGTAGCAGCAGCTT 2443
Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 2444 ACCCTCATTTGCTGCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2503
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysPheGluLysArgGlnAsnProAlaAla 336
Db 2504 CTGAAAGTCCAAGAGCAGCATCGGCAAAACACATTTGAGAAACGGCGGAAATCTTCGGGCA 2563
Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIle 355
Db 2564 GGTCTGATCCAGTCTGCTGCGGATTTCTGCTACTAACCCTCTCAGCAGCCGACCTGCAC 2623
Qy 356 AlaThrTrpLys----- 359
Db 2624 TCCACGTGGCAGTACTACGAGCGGACAGTCACTGCTCCCATGATCAGCTCACAACACTCAA 2683
Qy 360 -----ProHisLeuLysAlaLeuHisThrCysSerProThr 371
Db 2684 ACCTATGGGCGCTCCAGACTCATTTCCGCTCTGAACCCAGCTGGAGAGTCTGAGGAATCTC 2743
Qy 372 LysLysGluGlnGly-----GluAlaSerSerSerGln 382
Db 2744 AAGAGCAATCTGACTCACTCTTCAGGAGGAGCCACAGCCAGAGCCATCACCAGTCTAG 2803
Qy 383 LysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSer 402
Db 2804 AAGGTCAAGTTTGAAGATCGTGTCTCTCCAGCGCCCGAGCGGTGCTGCCAAGGGG 2860
Qy 403 ArgGlnAlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGlu 420
Db 2861 AAGGGGTCTCCAGGCGCCAGACGCTCCGCGGTCTCCCGAGTGGAGATCAGAGTCTCAGT 2920
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 2921 GACAGCCCAAGCAGGTGCCCCAGAGCTGGAGCTTTGTTGACCGCAGCGCTGCGAGCCAG 2980
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 2981 GCTTTCGCTATCAAGGGCGCTGCTCCCGGAGAACTCAGAAAGAACGAGCAAGCTCCCTGG 3040
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 3041 GAGGATATCGTGGAGGCAACAGAGCTGTAACTGCGAGTTTGTGACTGAGAGATCTTACC 3100
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 3101 CTGGCTCAAGATCAGCATCAGAGCTGTGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3160

Db 2341 GGACCACGAGGAGCTGGAGCGTTCCTTCAGGGGCTTCAGCATCTCCAGTCCAGGAGAA 2400
Qy 806 uleuAsn 808
Db 2401 CCTGGAT 2407

Search completed: April 3, 2005, 17:27:36
Job time : 1273.53 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 02:34:27 ; Search time 6898.61 Seconds
(without alignments)
4949.353 Million cell updates/sec

Title: US-09-810-796-4

Perfect score: 4588
Sequence: 1 MKVSEGRVLLNSAARG.....SICKAGESTDALSLPHVCLK 897

Scoring table:

| | BLOSUM62 | Xgapop 10.0 | Xgapext 0.5 |
|-------------|----------|-------------|-------------|
| Ygapop 10.0 | | | 0.5 |
| Ygapop 6.0 | | | 7.0 |
| Delop 6.0 | | | 7.0 |

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09810796/runat_31032005_141121_18209/app query.fasta_1.2126
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0 -I=OOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09810796 @CGN 1 1 7935 @runat_31032005_141121_18209 -NCPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

| | 1: gb_est1:* |
|--------------|--------------|
| 2: gb_est2:* | |
| 3: gb_hic:* | |
| 4: gb_est3:* | |
| 5: gb_est4:* | |
| 6: gb_est5:* | |
| 7: gb_est6:* | |
| 8: gb_gsa1:* | |
| 9: gb_gsa2:* | |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 4509.5 | 98.3 | 2733 | 9 AY407013 | AY407013 Homo sapi |
| 2 | 4202 | 91.6 | 2729 | 9 AY407015 | AY407015 Mus muscu |
| 3 | 3079.5 | 67.1 | 2014 | 9 AY407014 | AY407014 Pan trogl |
| 4 | 2716 | 59.2 | 2276 | 3 AK033079 | AK033079 Mus muscu |
| 5 | 1528 | 33.3 | 1571 | 3 AK040190 | AK040190 Mus muscu |
| 6 | 1260.5 | 27.5 | 997 | 2 BB609854 | BB609854 BB609854 |
| 7 | 1225 | 26.7 | 797 | 6 CD629762 | CD629762 55049367J |
| 8 | 1161 | 25.3 | 732 | 6 CD629756 | CD629756 55049343J |
| 9 | 1150 | 25.1 | 742 | 6 CD629754 | CD629754 55049327J |

| | | | | | | |
|----|--------|------|------|---|----------|--------------------|
| 10 | 1121.5 | 24.4 | 864 | 7 | CK772601 | CK772601 961159 MA |
| 11 | 1112 | 24.2 | 717 | 6 | CD629766 | CD629766 55049391J |
| 12 | 1111 | 24.2 | 691 | 6 | CD629755 | CD629755 55049343H |
| 13 | 1101 | 24.0 | 678 | 6 | CD629758 | CD629758 55049351J |
| 14 | 1085 | 23.6 | 632 | 2 | BB624101 | BB624101 BB624101 |
| 15 | 1080 | 23.5 | 744 | 6 | CB244389 | CB244389 UI-M-FY0- |
| 16 | 1079.5 | 23.5 | 658 | 2 | BE158938 | BE158938 MRO-HT040 |
| 17 | 1074 | 23.4 | 724 | 6 | CD629752 | CD629752 55049303J |
| 18 | 1053.5 | 23.0 | 628 | 5 | EX917798 | EX917798 BX917798 |
| 19 | 1043.5 | 22.7 | 679 | 2 | BE647997 | BE647997 UI-M-BH1- |
| 20 | 1038.5 | 22.6 | 1766 | 9 | AY404832 | AY404832 Homo sapi |
| 21 | 1037 | 22.6 | 1742 | 9 | AY404834 | AY404834 Mus muscu |
| 22 | 1035 | 22.6 | 714 | 6 | CD629760 | CD629760 55049359J |
| 23 | 1031 | 22.5 | 599 | 6 | CD629765 | CD629765 55049303H |
| 24 | 1013.5 | 22.1 | 624 | 6 | CD629751 | CD629751 55049303H |
| 25 | 997 | 21.7 | 635 | 6 | CD629759 | CD629759 55049359H |
| 26 | 993.5 | 21.7 | 643 | 6 | CD629763 | CD629763 55049383H |
| 27 | 989 | 21.6 | 584 | 2 | AW049888 | AW049888 UI-M-BH1- |
| 28 | 983 | 21.4 | 1298 | 3 | CR681452 | CR681452 Tetraodon |
| 29 | 976.5 | 21.3 | 638 | 6 | CD216615 | CD216615 ppp2n.pk0 |
| 30 | 976 | 21.3 | 744 | 6 | CA368089 | CA368089 644157 NC |
| 31 | 966.5 | 21.1 | 737 | 6 | CD629764 | CD629764 55049383J |
| 32 | 963 | 21.0 | 594 | 6 | CD629757 | CD629757 55049351H |
| 33 | 925 | 20.2 | 734 | 4 | BG532543 | BG532543 602562103 |
| 34 | 907.5 | 19.8 | 570 | 4 | BI033850 | BI033850 QV2-NN200 |
| 35 | 902 | 19.7 | 547 | 4 | BI034993 | BI034993 QV2-NN200 |
| 36 | 892 | 19.4 | 914 | 2 | BF312386 | BF312386 601898926 |
| 37 | 864 | 18.8 | 908 | 2 | BF240146 | BF240146 601905649 |
| 38 | 858 | 18.7 | 659 | 5 | BX926684 | BX926684 BX926684 |
| 39 | 856.5 | 18.7 | 920 | 2 | BF317072 | BF317072 601903470 |
| 40 | 853 | 18.6 | 580 | 6 | CD629761 | CD629761 55049367H |
| 41 | 849 | 18.5 | 659 | 5 | EX919587 | EX919587 BX919587 |
| 42 | 835.5 | 18.2 | 634 | 1 | AI589812 | AI589812 tm74f08.x |
| 43 | 832 | 18.1 | 1431 | 9 | AY410850 | AY410850 Homo sapi |
| 44 | 831 | 18.1 | 506 | 4 | BF959996 | BF959996 QV2-NN004 |
| 45 | 827.5 | 18.0 | 1004 | 5 | BQ219245 | BQ219245 AGENCOURT |

ALIGNMENTS

| | | | | | |
|------------|---|-------------|-----|--------|-----------------|
| RESULT 1 | AY407013 | 2733 bp | DNA | linear | GSS 15-DEC-2003 |
| LOCUS | AY407013 | | | | |
| DEFINITION | Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence, | | | | |
| ACCESSION | AY407013 | | | | |
| VERSION | AY407013.1 | GI:39762984 | | | |
| KEYWORDS | GSS. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | 1 (bases 1 to 2733) | | | | |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarial, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. | | | | |
| TITLE | Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios | | | | |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) | | | | |
| PUBMED | 14571302 | | | | |
| REFERENCE | 2 (bases 1 to 2733) | | | | |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarial, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | | | | |
| COMMENT | This sequence was made by sequencing genomic exons and ordering them based on alignment. | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1..2733 | | | | |

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gene

ORIGIN

Alignment Scores:

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Pred. No.:      0      Length:      2733
Score:          4509.50  Matches:      884
Percent Similarity: 98.66%  Conservative: 1
Best Local Similarity: 98.55%  Mismatches: 3
Query Match:      98.29%  Indels: 9
DB:              9      Gaps: 1

US-09-810-796-4 (1-897) x AY407013 (1-2733)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAargGly 20
Db 67 ATGAAGGATGTGAGTCCGGCGGGCAGGGTGTCTGCTGAACCTCGGCAGCCGCCAGGGGC 126
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 127 GACGGCTGTCTACTGTGGGACCCCGCGCCACGCTCGGTGGCGGGGGTGGCTG 186
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 187 AGGGAGACCCGGGGGACAGAGGGGGCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 246
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgGValGlnAsnTyrLeu 80
Db 247 TACACGAGTAGCAGAGCTGCGCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 306
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 307 TACACGCTGTGGAGAGACCCCGCGCTGGCGGTTTCATCTACCAAGCTTTCGTTTTCTC 366
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 367 CTTGCTTTTGGTTGCTGATTTTGTGAGTGTTCACAGTGTTCACATCCCTGAGCACACAAATG 426
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
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Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 487 ATCATTCGAATCTGTGCTGCGGGTGTGCTGTGATATAGAGGATGGCAAGGAGACTG 546
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 547 AGTTTGTCTCAAGAGCCCTCTGTGTTATAGATACCATTTCTTATCCCTTCATAGCA 606
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 607 GTTGTCTTCTGCAAAACTCAGGTAATATTTTGGCACGCTCTGCACCTCAGAAGTCTCGT 666
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyTyrThrLysLeuLeu 220
Db 667 TTCCTACAGATCCTCCGATGTGGCGCATGAGCGAAGGGAGGCACCTTGGAAATTAATCTG 726
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db 727 GGTTCAGTGGTTATGCTTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGT 786
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 787 GTTCTTAATTTTCTGCTCTTCTCTCTATCTGTGTTGGAAGAGGATGCCAAATAAGAGATT 846
Qy 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
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Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 967 ATTTCTTTCTTGGCACCTTCTGCGGCATCTTGGCTCAGGTTTGGCATTAAGATACAA 1026
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1027 GAACAACACCCCGCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCCTCATTCAG 1086
Qy 341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
Db 1087 TGTGTTTGGGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCACCTGGAAGCCA 1146
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380
Db 1147 CACTTGAAGGCTTGGCACACCTGCGAGCCCTACC----- 1179
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1180 AATCAGAAAGCTTAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCGAGGGGCCAGAGTATT 1239
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1240 AAGAGCCGACAGAGCTCAGTAGGTGACAGAGGTTCCTCCAGCACCAGCATCACAGCCGAG 1299
Qy 421 GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro 440
Db 1300 GGCAGTCCCAAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1359
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1360 TCGCTGCGCCTCAAAAGTCTCAGCCAAACACAGTAGATGCTGATGATGATGATGATGATG 1419
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1420 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1479
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1480 CCACCACTTAAACCTGCTCAATTCGAGCTATCAGATTTATGAAATTTCAATTTGCAAAACGG 1539
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1540 AAGTTTAAAGGAAACATTACGTCATATGATGATGATGATGATGATGATGATGATGATGATG 1599
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1600 GGTCACTCGGACATGTTGTGTAGAAATTAAGCCCTTCAACACCGCTGTGTGATCAAAATCTT 1659
Qy 541 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1660 GGAAGAGGCGAAATCAGATCAGATAAGAGAGCGAGAGAAAATAACAGCAGAGAAACATGAG 1719
Qy 561 ThrThrAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1720 ACCACAGACCATCTCAGTATGCTCGGTGGGTGTCAAGGTTGANNNNNNNGTACAGTCC 1779
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1780 ATAGAATCCAAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1839
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1840 GCCTCAGCCCTCGCTTGGGTTCATTCCAGATCCACCTTTTGAATGTGAACACACATCT 1899
Qy 621 AspTyrGlnSerProValAspLeuSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
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Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrPheIleGlyPheLeu 240
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Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 790 GTTCTTATTTTTCATCTCTCTGCTATCTGTGGAAAGGATGCCAATAAAGAGTTT 849
Qy 261 SerThrTyrAlaAspAlaLeuTyrPheGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 850 TCGACATATGGGATGCTCTCTGGTGGGGCAATCAGACTGACAAACATTTGGCTATGGA 909
Qy 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 910 GACAAAACACCCCTAACCTGGCTGGGAAGACTGCTCTCTGAGGCTTCGACTCTCTGGC 969
Qy 301 IleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 970 ATTTCTTTCTTGGCACTTCTGCTGGCATTTCTGGCTCAGGTTTGGCATTAAGAATACAG 1029
Qy 321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1030 GAGCAGCACCGCCAGAACATTTTGAGAAAGAGAGAACCCAGCTGCCAACCCTCATCCAG 1089
Qy 341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
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Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
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Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420
Db 1243 AAGACACAGACATCATAGTAGTGACAGGAGATCCCGAGCAGCTGACATCACTGCCGAG 1302
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1303 GGCAGCCCCACCAAGATCCAGAAAGTTGGAGCTTCAACGACCGCAACCCGCTTCAGGCC 1362
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
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Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
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Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
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Db 1603 GGTCACTGGACATGCTTTGTAGATAAAGCCCTTCAGACAGC-----CAAAATCTT 1655
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1656 GGAAAGACAAATGACCTCAGATAAGAGAGCCGAGAGAAATAACACGACAGACACAG 1715
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1716 ACACAGATGACCCAGCATGCTCCCGGGTTGTGAAGGTTGAGAAACAGGTCCAGTCC 1775
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Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
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Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1836 GCCTCCGCGCTCACTCTGGCATCCTTTTCAGATCCGCGCTTTTGAATGTGAACAGACCTCT 1895
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1896 GACTATCAAGTCTCTGGATAGCAAGACCTGTGGCTCAGCACAAAACAGCGGCTGT 1955
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 1956 TTAACGAGGTGACGAGTGCCCAACATCTCAAGAGCGCTGCAGTTTCATCTTAACACCAAT 2015
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2016 GAGTTCACTGCTCAGACTTTCTATGCGCTTAGCCCTACTATGCACAGCAAGCTACCCAG 2075
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
Db 2076 GTACCCATGAGTCAAAATGACGCTCTCTCGGTAGCCCAATTAACATTGCAAAACCA 2135
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2136 ATAAGCGCGCACCAAGCAGCAGCCCAACACTTTACAGATCCCTCTCTCTCTCG 2195
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2196 GCCATCAAGCACTTGTCCAGGCCAGAACCTCTGCTCTCAAAACCCGCGGCTTCAAGAG 2255
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2256 AGTATTTCTGATGTCACACCTGCTTGTGTGCTCCCAAGGAAGTGTTCAGTTGCGACAG 2315
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 780
Db 2316 TCAAACTGACCAAGGACCGTTCTCTGAGGAAAAGTTTCGACATGGGAGGAGAACTCTG 2375
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2376 TTGTCTGTCCGCCCTTGTGTCGCCAAGGATTTGGGCAAACTCTGTCTGTACAAACCTG 2435
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2436 ATCAGTTCGACAGAAAGCACTGAACCTTACAGTTTCAGCAGCAGAGTCAAGCGCTCTCGA 2495
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2496 GGCAGTCAAGATTTTATCCCAAGTGGAGAAATCCAAATTTGTTTATAACTGATGAGGAG 2555
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaProGlnProAlaArgGlu 860
Db 2556 GTCGGTCCGGAAGAGACAGAAACAGATACTTTTCAGCGCACCCACCGCCCTGCGGGGAG 2615
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2616 GCTGCTTCTCATCAGACTCTCTAAGGACTGGAAGGTCAAGGTCTATCTCAGACATTTGT 2675
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeu 896
Db 2676 AAGACAGAGACAGTACAGACGCCCTCAGTTTGGCTTGCCTCAGCTCAAACTG 2723
RESULT 3
AY407014
LOCUS
DEFINITION Pan troglodytes KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407014
VERSION AY407014.1 GI:39762985
KEYWORDS GSS:
SOURCE Pan troglodytes (chimpanzee)
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| | | | | |
|---|--|------|---|------|
| ORGANISM | Pan troglodytes | 171 | AspThrIleValLeuIleAlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIle | 190 |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. | 481 | GATACCATTTGTTTATCGCTTCAATGACAGTGTCTTTCGCAAAACCTCAGGGTAATATT | 540 |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. | 191 | PheAlaThrSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMet | 210 |
| TITLE | Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios | 541 | TTTGCCACGCTGTCACACGAGTCTCCGTTCTCAGATCCTCCGATGGTGGCATG | 600 |
| JOURNAL | Science 302 (5652), 1960-1963 (2003) | 211 | AspArgArgGlyGlyThrTyrLysLeuLeuGlySerValValTyrAlaHisSerLysGlu | 230 |
| PUBMED | 14671302 | 601 | GACCGAAGGGGAGGCACCTTGGAAATTAATCGGTTTCAGTGGTTTATGCTCAGCAAGGAA | 660 |
| REFERENCE | 2 (bases 1 to 2014) | 231 | LeuIleThrAlaTyrTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyr | 250 |
| AUTHORS | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. | 661 | TTAATCAGCTTGGTACATAGGATTTTGGTTCTTATTTTTCGCTCTTCTCTGCTAT | 720 |
| TITLE | Direct Submission | 251 | LeuValGluLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTrpGly | 270 |
| JOURNAL | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | 721 | CTGTGGAAAGGATGCCAATAAAGATTTTCTACATATGCAATGCTCTCTGTGGGCG | 780 |
| COMMENT | This sequence was made by sequencing genomic exons and ordering them based on alignment. | 271 | ThrIleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArg | 290 |
| FEATURES | Location/Qualifiers | 781 | ACAAATTACATTGACAACCTATTGGCTATGGAGACAAAACCTCCCTTAACCTGGGAGA | 840 |
| source | 1..2014 | 291 | LeuLeuSerAlaGlyPheAlaLeuLeuGlyLysSerPheAlaLeuProAlaGlyIle | 310 |
| gene | /organism="Pan troglodytes" | 841 | TTGCTTTCTGCGAGCTTTGCACCTCTTGGCATTTCTTTTGTGCACTTCTCTGCGGCATT | 900 |
| | /mol_type="genomic DNA" | 311 | LeuGlySerGlyPheAlaLeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLys | 330 |
| | /db_xref="taxon:9598" | 901 | CTTGCGCTCAGGTTTGCATTAAAGATACAAACAACACCGCCAGAAACACTTTTGAGAAA | 960 |
| | <1..>2014 | 331 | ArgArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAspGlu | 350 |
| ORIGIN | /gene="KCNO5" | 961 | AGAAGGAACCCAGCTGCCACCTCATTCAGTGTGTTGGCGTAGTTATGCAGCTGATCAG | 1020 |
| | /locus_tag="HCM2749" | 351 | LysSerValSerIleAlaThrTyrLysProHisLeuLysAlaLeuHisThrCysSerPro | 370 |
| Alignment Scores: | | 1021 | AAATCTGTTTCCATTGCAACCTGGAAGCCACACTTGAAGGCTTGGCACCTCGAGCCCT | 1080 |
| Pred. No.: | 5,296-287 | 371 | ThrLysLysGluGlnGlyGluAlaSerSerGlnLysLeuSerPheLysGluArgVal | 390 |
| Score: | 3079.50 | 1081 | ACC-----AATCAGAGCTTAAGTTTTTAAAGAGCGAGTG | 1113 |
| Percent Similarity: | 90.59% | 391 | ArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArg | 410 |
| Best Local Similarity: | 90.44% | 1114 | CGCATGGCTAGCCCGGCGCCAGAGTATTAAAGAGCCGACAAAGCTCAGTAGGTGACAGG | 1173 |
| Query Match: | 67.12% | 411 | ArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrp | 430 |
| DB: | 9 | 1174 | AGGTCCCAAGCACCGACATCACAGCGGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGG | 1233 |
| US-09-810-796-4 (1-897) x AY407014 (1-2014) | | 431 | SerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlyProLys | 450 |
| | | 1234 | AGCTTCAACGACCAACCCGCTTCGGCCCTCGCTGGCCCTCAAAAGTCTCAGCAAAA | 1293 |
| | | 451 | ProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCys | 470 |
| | | 1294 | CCAGTGATAGATGNNNACACAGCCCTTGGCACTGATGATGATATGATGAAAAAGGATGC | 1353 |
| | | 471 | GlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAlaIle | 490 |
| | | 1354 | CAGTGTGATGATCAGTGGGAAGANNNTCAACCCACCACTTAAACCTGTCATTCGAGCTATC | 1413 |
| | | 491 | ArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyrAsp | 510 |
| | | 1414 | AGAAATTGAAATTTTCATGTTGCAAAACGGGAAGTTTAAAGGAACGTTACGTCCATATGAT | 1473 |
| | | 511 | VallysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLys | 530 |
| | | 1474 | GTAAAAAGATGCAATTGAACAATATTCTGCTGCTCATCTGGACATGTTGTGTAGAAATAAA | 1533 |

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| QY | 531 | SerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLys | 550 |
| Db | 1534 | ACCTTCAACACGTTGATCAATCTTGGAAAGGCAATCACATCAGATGAAG | 1593 |
| QY | 551 | SerArgGluLysIleThrAlaGluHisGluThrThrAspLeuSerMetIeuGlyArg | 570 |
| Db | 1594 | AGCCGAGAGAAATAACAGCAACATGAGACCACAGCATCTCAGTATGCTCGGTCGG | 1653 |
| QY | 571 | ValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeuAsp | 590 |
| Db | 1654 | GTGGTCAAGTNNNNNNNGTACAGTCCATGAGTCAAGCTCGAGCTGCTACTAGAC | 1713 |
| QY | 591 | IleTyrglnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGln | 610 |
| Db | 1714 | ATCTATCAACAGCTCTTCGGAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATCCAG | 1773 |
| QY | 611 | IleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAsp | 630 |
| Db | 1774 | ATCCCACTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGAT | 1833 |
| QY | 631 | LeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSer | 650 |
| Db | 1834 | CTTTCGGGTTCTGCACAAACAGTGGCTCTTATCCAGATCAACTAGTGCCCAATCTCG | 1893 |
| QY | 651 | ArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyzAlaLeu | 670 |
| Db | 1894 | AGAGCCTGCGATTCATCTGAGCCCAATGAGTTCAGTCCCGACATTTCTACGCGTT | 1953 |
| QY | 671 | SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAla | 690 |
| Db | 1954 | AGCCCTACTATGCACAGTCAAGCANCACAGGTGCNAATAGTCAAGCGGTGCTCAGCA | 2013 |
| RESULT 4 | | | |
| LOCUS | AK033079 | 2276 bp mRNA linear | HTC 03-APR-2004 |
| DEFINITION | Mus musculus adult male cortex cDNA, RIKEN full-length enriched library, clone:7730402H11 product:potassium voltage-gated channel, subfamily Q, member 5, full insert sequence. | | |
| ACCESSION | AK033079 | | |
| VERSION | AK033079.1 | GI:26328812 | |
| KEYWORDS | HTC; CAP trapper. | | |
| SOURCE | Mus musculus (house mouse) | | |
| ORGANISM | Mus musculus | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. | | |
| JOURNAL | Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | |
| MEDLINE | Genome Res. 10 (10), 1617-1630 (2000) | | |
| PUBMED | 20499374 | | |
| REFERENCE | 2 | | |
| AUTHORS | Carninci, P., Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer | | |
| JOURNAL | Genome Res. 10 (11), 1757-1771 (2000) | | |
| MEDLINE | 20530913 | | |
| PUBMED | 11076861 | | |
| REFERENCE | 4 | | |

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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AUTHORS

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JOURNAL

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2276)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. 2276

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:7730402H11"

/db_xref="taxon:10090"

/clone="7730402H11"

/sex="male"

/tissue_type="cortex"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

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/notes="unnamed protein product; potassium voltage-gated channel, subfamily Q, member 5 (MGDI)GI:1924937, GBAF263836, evidence: BLASTN, 99%, match=2186)

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Alignment Scores:

Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL MEDLINE 20499374
 PUBMED 11042159
 REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M., Sumi, I., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11): 1757-1771 (2000)

MEDLINE 20530913
PUBMED 11076861
FERENCE 4
AUTHORS
TITLE The RIKEN Genome Exploration Research Group Phase II Team and the
JOURNAL FANTOM Consortium.
FERENCE 5
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
FERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase 1 & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 1571)


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Db      285 TATCAGATTATGAATTTTCATGTTGCAAAACGGAGTTTAAAGGAAACATTACGTCCATA 226
Qy      509 rAspVallyLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgI1 529
Db      225 TGATGTAAGATGTGTCATTGAACATATTCCTGCTGTCATCTGGACATGTTGTGTAGAA 166
Qy      529 eLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLy 549
Db      165 TAAAGCCCTTCAACACGCTGTTGATCAAAATCTTGGAAAAGGGCAATCACAATCAGATAA 106
Qy      549 sLysSerArgGluLysIleThrAlaGluHisGlnThrThrAspAspLeuSerMetLeuG1 569
Db      105 GAAGAGCCGAGAGAAATAACACGACAGACATCAGACACACAGCATCTCAGTATGCTCGG 46
Qy      569 yArgVallyLysValGluLysGlnValGlnSerIleGluSer 583
Db      45 TCGGTGCTCAAGGTTGAAAACAGGTACAGTCCATAGATCC 3

RESULT 8
CD629756/c
LOCUS      CD629756              732 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 55049343J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD629756
VERSION    CD629756.1  GI:40278022
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 732)
AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE     Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES             source
            1..732
            Location/Qualifiers
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                /clone_lib="FLP"
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ORIGIN
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Score:          1161.00      Matches:    240
Percent Similarity: 97.56%      Conservative: 0
Best Local Similarity: 97.56%      Mismatches: 3
Query Match:    25.31%      Indels:     4
DB:              6      Gaps:      0

US-09-810-796-4 (1-897) x CD629756 (1-732)

Qy      339 IleGlnCysValTprArgSer-TyrAlaAlaAspGluLysSerValSerIleAlaThrTr 358
Db      731 ATTACGTGTGTTGGCGTAGTTAAACGACGTGATGAGAAATCTGTTCCATGCAACCTG 672
Qy      358 pLysProHisLeuLysAlaLeuHisThrCysSerProThr-LysLysGluGln-GlyGlu 377
Db      671 GAAGCCACATTTGAAGGCTTTGCACACCTGCAGCCCTACCCAGAAAGAAACAAGGGGAA 612
Qy      378 AlaSerSerGlnLysLeuSerPhelyGluArgValArgMetAlaSerProArgGly 397
Db      611 GCATCAACGACGTCAAGACTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCGAGGGGC 552
Qy      398 GlnSerIleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrThrAspIle 417
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Qy      418 ThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArg 437
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Qy      438 PheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThr 457
Db      431 TTCCGGCCCTCGCTGGCCCTCAAAAGTTCTCAGCCAAACACGAGTATAGATGCTGACACA 372
Qy      458 AlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGlu 477
Db      371 GCCCTTGGCACTGATGATATATATGATGAAAAGAGTCCAGTGTGATGATCATCAGTGAA 312
Qy      478 AspLeuThrProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisVal 497
Db      311 GACCTCACCCACCACTTAAACCTGTCTTCGAGCTATCAGAAATTATGAAATTTTCATGTT 252
Qy      498 AlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGln 517
Db      251 GCAAAACGGAAGTTTAAAGGAACATTACGTCATGATGATAAAGATGTCAATTGAACAA 192
Qy      518 TyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAsp 537
Db      191 TATTCTGCTGCTCATCTGGACATGTTGTGTAGATTAAAGCCTTCAAACACGCTGTGAT 132
Qy      538 GlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAla 557
Db      131 CAAATTTCTGGAAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAAATAACAGCA 72
Qy      558 GluHisGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGln 577
Db      71 GAACATGAGACACAGACAGATCTCAGTATGCTCGTGGTGGTGGTCAG-GTTGAAAAAACAG 13
Qy      578 ValGlnSerIle 581
Db      12 GTACAGTCCATA 1

RESULT 9
CD629754/c
LOCUS      CD629754              742 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 55049327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD629754
VERSION    CD629754.1  GI:40278020
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 742)
AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE     Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES             source
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                /clone_lib="FLP"
                /note="Vector: pDrive Cloning Vector"

ORIGIN
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Pred. No.:      1.48e-100      Length:      742
Score:          1150.00      Matches:    239
Percent Similarity: 96.76%      Conservative: 0
Best Local Similarity: 96.76%      Mismatches: 5
Query Match:    25.07%      Indels:     4

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Db 483 GTGTACTTGGCAGAGAGGGGAGAACGATCACTTTGATACCTACGCGGACGCACTCTGG 542
Qy 269 TrpGlyThrIleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrLeu 288
Db 543 TGGGGCTGTATCACTTGACCAACATTGGCTACGGGGACAGTACCCTCAGACCTGGNAC 602
Qy 289 GlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAla 308
Db 603 GGGAGGCTCTGGCAGCAGCTTCACCTCATCGGTGTCTCTCTTCCGCTCTCTCTGCT 662
Qy 309 GlyIleLeuGlySerGlyPheAlaLeuLysValGlnGluGlnHisArgGlnLysHisPhe 328
Db 663 GGCATTTTGGGGTCTGGCTTTGGCTTGGCTTCAAGAGTCAAGAGCAGCAGCCGTCAGAGCAGCTTT 722
Qy 329 GluLysArgArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAla 348
Db 723 GAGAAAGCGGAGACCCCGCAGAGCTCTGATCCAGTCCGCTGGAGTTCTATGCCACC 782
Qy 349 AspGluLysSerValSerIle---AlaThrTrpLys 359
Db 783 AACTGTGCGCAGCAGCAGCTGCACCTCCACGTGGCAG 818

RESULT 11
LOCUS CD629766/c 717 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049391J1 PFLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629766
VERSION CD629766.1 GI:40278032
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 717)
JOURNAL Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
COMMENT Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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Query Match: 24.24% Gaps: 0
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US-09-810-796-4 (1-897) x CD629766 (1-717)

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Db 715 AGTTACGAGCTGATGAGAAATCTGTGTCATTGCACTGGAGGCCACACTTGAAGCT 656
Qy 365 LeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSerSerGlnLysLeu 384
Db 655 TTGCACACTGCGCCCTACCAAGAAAGAACAGGGAAGCATCAAGCAGTCAGAAGCTA 596
Qy 385 SerPhe-LysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArg-G 404
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Db 595 AGTTATTAGAGCGAGTGGCATGGCTAGCCCCAGGGGCCGAGTATTATAGAGCCGAC 536
Qy 404 InAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGluGlySerProT 424
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Qy 424 hrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgL 444
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Db 415 TCAAAAGTTCTCAGCCAAACACAGTAGTAGTGTGACACAGCCCTTGGCACTGATGATG 356
Qy 464 alTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuL 484
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Db 235 AAACATTACGTCCATATGATGATAAAGATGTCATTGACATATTCCTGCTGCTCATCTGG 176
Qy 524 spMetLeuCysArgIleLysSerLeuGln-ThrArgValAspGlnIleLeuGlyLysGly 543
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LOCUS CD629755 691 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049343H1 PFLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629755
VERSION CD629755.1 GI:40278021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 691)
JOURNAL Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
COMMENT Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
Location/Qualifiers
source
1..691
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/clone_lib="PLP"
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ORIGIN
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Percent Similarity: 97.84%
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Best Local Similarity: 97.40% Mismatches: 4
 Query Match: 24.22% Indels: 3
 DB: 6 Gaps: 0

US-09-810-796-4 (1-897) x CD629755 (1-691)

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 Db 1 GCTCTCTGTTGGGGCACATTAACATTAATGCTATGGAGACAAATCCCTTA 60
 Qy 286 ThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyLysPhePheAla 305
 Db 61 ACTTGGCTGGGAAGATTCCTTCTGACAGCTTTGCACTCCTTGGCAATTTCTTTGCA 120
 Qy 306 LeuProAlaGlyLysLeuGlySerGlyPheAlaLeuLysValGlnGlnGlnHisArgGln 325
 Db 121 CTCTCTGCGGCAATTCCTTGGCTTCAGGTTTTCATTAAGATACAGAACACACCGCCAG 180
 Qy 326 LysHisPheGluLysArgArgAsnProAlaAlaAsnLeuLysGlnCysValTrpArgSer 345
 Db 181 AAACACTTTGAGAAAGAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGGTAGT 240
 Qy 346 TyrAlaAlaAspGluLysSerValSerileAlaThrTrpLysProHisLeuLysAlaLeu 365
 Db 241 TACGCGAGCTGATGAGAAATCTGTTTCCATTCGCACTGGAAGCCACACTTGAAGCCCTTG 300
 Qy 366 HisThrCysSerProThrLysLysGlnGlnGlyAlaSerSerSerGlnLysLeuSer 385
 Db 301 CACACTGCGCCCTACCAAGNAGAACAGGGNAGCATCAGCAGTCAGAGCTAAGT 360
 Qy 386 PheLysGluArgValArgMetAlaSerProArgGlyGlnSerileLysSerArgGlnAla 405
 Db 361 TTAAAGAGCGAGTGGCATGGCTAGCCCCAG-GGCCAGAGTATTAAAGAGCCGCAAGCC 419
 Qy 406 SerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu-GlySerProThrLys 425
 Db 420 TCAGTAGTGACAGAGATGCCAGACCCAGCATCACAGCGAGGGGCGATGCCACCA 479
 Qy 425 sValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLys 445
 Db 480 AGTGAGAGAGCTGGAGCTTCAAGCGCGAACCCGCTTCGGCCCTCGCTGGCGCTCA 539
 Qy 445 sSerSerGlnProLysProValileAspAlaAspThrAlaLeuGlyThrAspAspValty 465
 Db 540 AAGTCTCAGCCAAACCCAGTGATAGTGTGACACAGCCCTTGGCACTGATGATATA 599
 Qy 465 rAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysTh 485
 Db 600 TGATGAAAGAGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
 Qy 485 rValileArgAlaileArgileMetLysPhe 495
 Db 659 TGTCATTCAGCTATCAGAAATTGAAATTC 689

RESULT 13
 CD629758/c
 LOCUS 55049351J1 FLP Homo sapiens cDNA, mRNA sequence. EST 12-JAN-2004
 DEFINITION
 ACCESSION CD629758
 VERSION CD629758.1 GI:40278024
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 678)
 Fu.G.K., Wang.J.T., Yang.J., Au-Young,J. and Stuve,L.L.
 Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes
 Genomics 84 (1), 205-210 (2004)
 JOURNAL Contact: Fu GK
 COMMENT Incyte Genomics, Inc.
 3160 Porter Dr., Palo Alto, CA 94304, USA

FEATURES
 source
 1..678
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="PLP"
 /note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:
 Pred. No.: 7,24e-96 Length: 678
 Score: 1101.00 Matches: 223
 Percent Similarity: 99.12% Conservative: 1
 Best Local Similarity: 98.67% Mismatches: 1
 Query Match: 24.00% Indels: 2
 DB: 6 Gaps: 0
 US-09-810-796-4 (1-897) x CD629758 (1-678)
 Qy 360 ProHisLeuLysAlaLeuHisThr-CysSerProThrLysLysGlnGlnGlyGluAlaLe 379
 Db 677 CCACACTTGAAGGCTTGCACACCTCGAGCCCTACCAAGAAAGAACCAAGGGGAAGCATC 618
 Qy 379 rSerSerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSe 399
 Db 617 AAGCAGTCAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCGCCAGGCGCAGAG 558
 Qy 399 rLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAl 419
 Db 557 TATTAAAGGCGCAAGCCTCAGTAGGTGACAGAGGTTCCCAAGCACCAGCATCACAGC 498
 Qy 419 aGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheAr 439
 Db 497 CGAGGGCAGTCCCAAGTGCAGAGAGCTGAGAGCTTCAACGACCGAAACCCGCTTCCG 438
 Qy 439 gProSerLeuArgLeuLysSerSerGlnProLysProValileAspAlaAspThrAlaLe 459
 Db 437 GCCCTCGCTGGCCCTCAAAAGTTCTCAGCCAAACACAGTATGATGATGATGATGATGATGAT 378
 Qy 459 uGlyThrAspAspValTyArgGluLysGlyCysGlnCysAspValSerValGluAspLe 479
 Db 377 TGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 318
 Qy 479 uThrProLeuLysThrValileArgAlaileArgileMetLysPheHisValAlaLy 499
 Db 317 CACCCACCACTTAAACTGTTCATTCGAGCTATCAGAAATTATGAATTTCAATTTGCAAA 258
 Qy 499 sArgLysPheLysGluThrLeuArgProTyArgPheValLysAspValileGluGlnTySe 519
 Db 257 ACGGAAGTTTAAAGAAACATTACGTCATATGATGATGATGATGATGATGATGATGATGATGAT 198
 Qy 519 rAlaGlyHisLeuAspMetLeuCysArgGlyLysSerLeuGlnThrArgValAspGlnIl 539
 Db 197 TGCTGGTTCATCTGACATGTTGTGTAGAAATTTAAAGGCTTCAAAACACGTTGTGATCAAT 138
 Qy 539 eLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGluHi 559
 Db 137 TCTTGGAAAGGGCAATTCACATCAGATAGAGAGCGGAGAGAAATTAACAGGAGAAC 78
 Qy 559 sGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGl 579
 Db 77 TGAGACACACAGCATCTCAGTATGCTCGGTGGTGT-AAGGTTGAAAAACAGGTTACA 19
 Qy 579 nSerileGluSerLys 584
 Db 18 GTCCATAGAAATCCAGA 3

RESULT 14

BB624101

LOCUS

DEFINITION

BB624101 632 bp mRNA linear EST 26-OCT-2001
 BB624101 RIKEN full-length enriched, adult male cortex Mus musculus

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 744)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..744

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6832924"

/tissue_type="whole brain"

/dev_stage="embryo 13.5, 14.5, 16.5, 17.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is AGCGAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 9,18e-94 | Length: | 744 |
| Score: | 1080.00 | Matches: | 216 |
| Percent Similarity: | 91.46% | Conservative: | 9 |
| Best Local Similarity: | 87.80% | Mismatches: | 21 |
| Query Match: | 23.54% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-810-796-4 (1-897) x CB244389 (1-744)

| | | | |
|----|-----|--|-----|
| Qy | 631 | LeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnSer | 650 |
| Db | 7 | CTGTCTGGCTCAGACAAACAGCGGCTGTTTACGAGGTGAGCGAGTCCCAATCTCA | 66 |
| Qy | 651 | ArgGlyLeuGlnPheLeuThrProAsnGluPheSerAlaGlnThrPheTyAlaLeu | 670 |
| Db | 67 | AGAGGCTTGCAGTTCATCTCAACCAATGAGTTCAGTTCAGACTTTCTATGCGCTT | 126 |
| Qy | 671 | SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAla | 690 |
| Db | 127 | AGCCCTACTATGCACGACAGCTACCCAGGTACCCATGAGTCAAAATGACGGCTCTCC | 186 |
| Qy | 691 | ValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaPro | 710 |
| Db | 187 | GTGGTAGCCACCAATTAACATTGCAAAACCAATAAGCGCGCACCCAGCAGGCCCA | 246 |

| | | | |
|----|-----|--|-----|
| Qy | 711 | ThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGluThr | 730 |
| Db | 247 | ACAACTTTTACAGATCCCTCCCTCTCTCGGCCATCAGCACTTGTCCAGGCCAGAACCT | 306 |
| Qy | 731 | LeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuVal | 750 |
| Db | 307 | CTGCTCTCAAAACCCACCGGCTTACAAGAGAGTATTCTGATGTCAACACCTGCTTGT | 366 |
| Qy | 751 | AlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArg | 770 |
| Db | 367 | GCCTCCCAAGGAAGTGTTCAGTTTGCACAGTCACCAAGGACCGTTCCTCCTGAGG | 426 |
| Qy | 771 | LysSerPheAspMetGlyGlyLeuThrLeuLeuSerValCysProMetValProLysAsp | 790 |
| Db | 427 | AAAAGTTTCGACATGGGAGGAGAACTCTGTTGTCTGCCGCCATGGTGCCCAAGGAT | 486 |
| Qy | 791 | LeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGln | 810 |
| Db | 487 | TTGGGCAAAATCTCTGTCTGTACAAAACCTGATCAGGTGCGACAGAGAACTGAACCTTACAG | 546 |
| Qy | 811 | LeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTrpArg | 830 |
| Db | 547 | TTTTTCAGCGACGAGTCAAGCGGCTCTCGAGGCGAGTCAAGATTTTATCCCAAGTGGAGA | 606 |
| Qy | 831 | GluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAspThr | 850 |
| Db | 607 | GAATCCANATTTGTTTATAACTGATGAGGAGTCTCGAGGTCGGAAGAGACAGAACTACT | 666 |
| Qy | 851 | PheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThr | 870 |
| Db | 667 | TTTGACGGCACCCACCGCTCTCGGGGGAGGCTGCTTTCTCATCAGACTCTCTCCTAGGACT | 726 |
| Qy | 871 | GlyArgSerArgSerSer | 876 |
| Db | 727 | GGAAGGTCACGGTCACTCT | 744 |

Search completed: April 3, 2005, 11:13:04

Job time : 6922.61 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 06:38:16 ; Search time 348.733 Seconds
(without alignments)
4166.553 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547

Sequence: 1 MKDVESGRVLLNSAARG.....SICKAGESTDALSLPHVLK 888

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09810796/runat 31032005 141121 18218/app query.fasta_1.2126
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09810796 @CGN_1.1 147 @runat 31032005 141121 18218 -NCPUS=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 4547 | 100.0 | 2772 | 4 | US-09-825-147-1 |
| 2 | 4547 | 100.0 | 3111 | 4 | US-09-825-147-3 |
| 3 | 4527.5 | 99.6 | 3137 | 4 | US-09-590-304-1 |
| 4 | 4513.5 | 99.3 | 3074 | 4 | US-09-813-148-1 |
| 5 | 2007.5 | 44.1 | 2335 | 4 | US-09-492-361-1 |
| 6 | 1998.5 | 44.0 | 2196 | 4 | US-09-949-016-1823 |
| 7 | 1794 | 39.5 | 3237 | 3 | US-09-177-650-95 |
| 8 | 1792.5 | 39.4 | 3287 | 3 | US-09-105-058C-19 |
| 9 | 1790.5 | 39.4 | 2169 | 3 | US-09-105-058C-22 |
| 10 | 1788 | 39.3 | 3232 | 3 | US-09-177-650-1 |
| 11 | 1767 | 38.9 | 2273 | 3 | US-09-177-650-88 |
| 12 | 1587.5 | 34.9 | 2565 | 3 | US-09-105-058C-26 |

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|----|--------|------|-------|---|---------------------|--------------------|
| 13 | 1587.5 | 34.9 | 2914 | 3 | US-09-177-650-6 | Sequence 6, Appli |
| 14 | 1550.5 | 34.1 | 2814 | 3 | US-09-177-650-90 | Sequence 90, Appli |
| 15 | 1207.5 | 26.6 | 900 | 3 | US-09-105-058C-5 | Sequence 5, Appli |
| 16 | 1201.5 | 26.4 | 900 | 3 | US-09-105-058C-3 | Sequence 3, Appli |
| 17 | 1116.5 | 24.6 | 3181 | 3 | US-09-135-021-1 | Sequence 1, Appli |
| 18 | 1116.5 | 24.6 | 3181 | 3 | US-09-135-020-1 | Sequence 1, Appli |
| 19 | 1116.5 | 24.6 | 3181 | 3 | US-09-135-010A-1 | Sequence 1, Appli |
| 20 | 1116.5 | 24.6 | 3181 | 3 | US-09-444-871-1 | Sequence 1, Appli |
| 21 | 1116.5 | 24.6 | 3181 | 3 | US-09-597-735-1 | Sequence 1, Appli |
| 22 | 1116.5 | 24.6 | 3181 | 3 | US-09-444-295-1 | Sequence 1, Appli |
| 23 | 1116.5 | 24.6 | 3181 | 3 | US-09-597-732-1 | Sequence 1, Appli |
| 24 | 1116.5 | 24.6 | 3181 | 4 | US-09-597-731-1 | Sequence 1, Appli |
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| 26 | 1114 | 24.5 | 2028 | 4 | US-09-840-125-1 | Sequence 1, Appli |
| 27 | 1103.5 | 24.3 | 3182 | 3 | US-09-135-021-5 | Sequence 5, Appli |
| 28 | 1094 | 24.1 | 2734 | 3 | US-09-135-021-79 | Sequence 79, Appli |
| 29 | 1094 | 24.1 | 2821 | 3 | US-09-135-010A-115 | Sequence 115, App |
| 30 | 1094 | 24.1 | 2821 | 3 | US-09-597-735-115 | Sequence 115, App |
| 31 | 1094 | 24.1 | 2821 | 3 | US-09-597-732-115 | Sequence 115, App |
| 32 | 1094 | 24.1 | 2821 | 4 | US-09-597-731-115 | Sequence 115, App |
| 33 | 1094 | 24.1 | 2924 | 4 | US-09-949-016-32 | Sequence 32, Appli |
| 34 | 1085 | 23.9 | 930 | 3 | US-09-105-058C-17 | Sequence 17, Appli |
| 35 | 1027.5 | 22.6 | 2633 | 4 | US-09-949-016-3215 | Sequence 3215, Ap |
| 36 | 993.5 | 21.8 | 735 | 3 | US-09-105-058C-7 | Sequence 7, Appli |
| 37 | 901.5 | 19.8 | 896 | 3 | US-09-105-058C-1 | Sequence 1, Appli |
| 38 | 852 | 18.7 | 582 | 4 | US-09-495-050A-303 | Sequence 303, App |
| 39 | 731 | 16.1 | 575 | 4 | US-09-495-050A-305 | Sequence 305, App |
| 40 | 702.5 | 15.4 | 58543 | 4 | US-09-949-016-13565 | Sequence 13565, A |
| 41 | 475 | 10.4 | 1481 | 4 | US-09-949-016-4101 | Sequence 4101, Ap |
| 42 | 450 | 9.9 | 284 | 4 | US-09-495-050A-304 | Sequence 304, App |
| 43 | 387 | 8.5 | 251 | 4 | US-09-495-050A-296 | Sequence 296, App |
| 44 | 310 | 6.8 | 1080 | 4 | US-09-328-352-2971 | Sequence 2971, Ap |
| 45 | 260.5 | 5.7 | 1927 | 3 | US-09-336-643A-3 | Sequence 3, Appli |

ALIGNMENTS

RESULT 1

US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-825-147-1

Alignment Scores:
Pred. No.: 0
Score: 4547.00
Length: 2772
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 4
Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)

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| QY | 1 | MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAaArgGly | 20 | QY | 361 | HisLeuLysAlaLeuHisThrCysSerProThrAenGlnLysLeuSerPheLysGluArg | 380 |
| DB | 106 | ATGAAGGATGTGGAGTGGGGCGGGGAGGGTGTCTGAATCGCGAGCGCGCAGGGG | 165 | DB | 1186 | CACITTAAGAGGCTTGGCACACCTGAGCCCTACCAATCAGAAGCTAAGTTTTAAGCAGCGA | 1245 |
| QY | 21 | AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu | 40 | QY | 381 | ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp | 400 |
| DB | 166 | GACGGCTGCTACTGCTGGGACCCCGCGCGCCACGCTCGGTGGCGCGCGTGGCCGT | 225 | DB | 1246 | GTGGCATGGTGTAGCCCGAGGGGCGAGATTAAGAGCGGACAAAGCTCAGTAGGTGAC | 1305 |
| QY | 41 | ArgGluSerArgArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 | QY | 401 | ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer | 420 |
| DB | 226 | AGGGAGACCCCGGGGCAACAGGGGCGCCGAGTAGCCTGTGGGGAAGCCGCTCTCT | 285 | DB | 1306 | AGGAGGTCCCAAGCAGCAGCATCACAGCCAGGGGAGTCCCAACAAGTGCAGAGAGC | 1365 |
| QY | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu | 80 | QY | 421 | TyrSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro | 440 |
| DB | 286 | TACACAGTAGCCAGAGCTGCGCGGCAACGTCAAGTACCGCGGGTGCAGAACTACCTG | 345 | DB | 1366 | TGGAGCTTCAAGCAGCAGAACCGCTTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCA | 1425 |
| QY | 81 | TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu | 100 | QY | 441 | LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly | 460 |
| DB | 346 | TACAACTGCTGGAGAGACCCCGGGCTGGGCGTTCATCTACCAAGCTTTCGTTTTCTC | 405 | DB | 1426 | AAACCAAGTATAGATGCTGACACAGCCCTTGGCATGTATATATGATGAAAGGA | 1485 |
| QY | 101 | LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 | QY | 461 | CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla | 480 |
| DB | 406 | CTTGCTTTGGTTGCTGATTTGTCTGCTGCTTCTTACCATCCCTGAGCACACAAATG | 465 | DB | 1486 | TGCCAGTGTGATGATTCAGTGGAGAGCCTCACCCCAACCTTTAAACCTGCTATTGAGCT | 1545 |
| QY | 121 | AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 | QY | 481 | IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr | 500 |
| DB | 466 | GCCTCAAGTTGCTCTTGATCTCGAGTTCGTGATGATGTGCTGTTTTGGTTTGGAGTTC | 525 | DB | 1546 | ATCAGAAATATGAAATTTTCATGTTGCAAAACGAAAGTTTAAAGGAACATTACGTCCATAT | 1605 |
| QY | 141 | IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPngInGlyArgLeu | 160 | QY | 501 | AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle | 520 |
| DB | 526 | ATCATTCGAATCTGCTGCTGGGGTGTCTGTGTCATATAGAGTGGCAGGAGACTG | 585 | DB | 1606 | GATGTAAAGATGTCAATTAACCAATATTTCTGCTGCTCATCTGGACATGTTGTGTAGAATT | 1665 |
| QY | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 | QY | 521 | LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys | 540 |
| DB | 586 | AGGTTTGTCTCGAAGCCCTTCGTGTATATAGATACCAATGTTCTTATCGCTTCAATAGCA | 645 | DB | 1666 | AAAGGCTTCAACACAGTGTGATCAATTTCTTGGAAAGGGCAAAATCACAATCAGATAAG | 1725 |
| QY | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 | QY | 541 | LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly | 560 |
| DB | 646 | GTGTTTCTGCAAAAACCTCAGGGTAAATTTTTGTCACGTCTGCACTCAGAACTCCGT | 705 | DB | 1726 | AGAGCCGAGAGAAAATAACAGCAGAAACATGAGACCAACAGCACTCAGTATGCTCGT | 1785 |
| QY | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyTyrThrLysLeuLeu | 220 | QY | 561 | ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu | 580 |
| DB | 706 | TTCCTACAGATCTCCGATGTTGGCATGGAGCCGAGGAGGAGGACATTGGAATTAATCTG | 765 | DB | 1786 | CGGTGCTCAAGTTGAAACACAGGTACAGTCCATAGATCCAAAGCTGAGTGCCTACTTA | 1845 |
| QY | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu | 240 | QY | 581 | AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaSerPhe | 600 |
| DB | 766 | GGTTCAGTGTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATTTTGT | 825 | DB | 1846 | GACATCTATCAACAGGTCTCTCGAAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTTC | 1905 |
| QY | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 | QY | 601 | GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys | 620 |
| DB | 826 | GTTCCTATTTTTTCTGCTTCTCTCTATCTGTTGGTGAAGGATGCCAATAAAGAGTTT | 885 | DB | 1906 | CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAA | 1965 |
| QY | 261 | SerThrTyrAlaAspAlaLeuTyrPheGlyThrIleThrLeuThrIleGlyTyrGly | 280 | QY | 621 | AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle | 640 |
| DB | 886 | TCTACATATGATGCTCTGCTGGGGCACAATTAACATTCACAACTATGGCTATGGA | 945 | DB | 1966 | GATCTTTGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACATC | 2025 |
| QY | 281 | AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 | QY | 641 | SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla | 660 |
| DB | 946 | GACAAAACCTCCCTTAATCTGGCTGGGAAGATTCCTTTCTGAGGCTTTCGACTCTTGGC | 1005 | DB | 2026 | TCGAGAGCCCTGCAAGTTCATTTCTGACCCCAATGAGTTCAGTGCACAGACTTTCTACGCG | 2085 |
| QY | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 | QY | 661 | LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer | 680 |
| DB | 1006 | ATTCTTTCTTTGACATCTCTGCGGCATTTCTTGGCTCAGGTTTTCATTTAAAGATACAA | 1065 | DB | 2086 | CTTAGCCCTACTATGCAAGTCAAGCAACACAGGTGCAATTAGTCAAAAGCGATGGCTCA | 2145 |
| QY | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaLeuIleGln | 340 | QY | 681 | AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla | 700 |
| DB | 1066 | GAAACACACCGCCAGAACACTTTGAGAAAGAGGAACCCAGCTGCCAACCTCATTCAG | 1125 | DB | 2146 | GCAGTGGCAGCCCAACACACCATTTGCCAAACCAATAAATACGGCACCCCAAGCCAGCAGCC | 2205 |
| QY | 341 | CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro | 360 | QY | 701 | ProThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGlu | 720 |
| DB | 1126 | TGTGTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTCCATTTGCACTGGAAGCCA | 1185 | DB | 2206 | CCAACAACTTTACAGATCCCACTCTCTCCAGCCCATCAAGCATCTGCCCGAGCCAGAA | 2265 |
| QY | | | | QY | 721 | ThrLeuHisProAsnProAlaGlyLeuGlnLysSerIleSerAspValThrThrCysLeu | 740 |

Db 2266 ACTCTGCACCCCTTAACCCCTGCAGCCTTACAGGAAGACATTTCTGACGTCCACACCTGCCTT 2325
Qy ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2326 GTTGCTCCAGGAAATGTTTCAGGTTCACAGTCAAAATCTCACCAAGGACGGTCTATG 2385
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2386 AGGAAAGCCTTTGACATGGAGGAGAAACTCTGTGTCTGTCTGCCATGTGCGGAAG 2445
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuLeuArgSerThrGluGluLeuAsnIle 800
Db 2446 GACTTGGGCAATCTTTGTCTGTGCACAACTGATCAGTGCACCGAAGAACTGAAATATA 2505
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTyr 820
Db 2506 CAACCTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGACGCAAGATTTTACCCTCAATGG 2565
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2566 AGGGAATCCAAATGTTTATTAACATGATGAAGAGTGGGTCCCGAAGACAGACAGAC 2625
Qy 841 ThrPheAspAlaAProGlnProAlaAArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2626 ACTTTTGAATGGCGACCGACCTCCAGGAGGAGTGGCTTTGCAATCAGACTCTCTAAGG 2685
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2686 ACTGGAAGTCACGATCATCTCAGAGCATTTGTAAGGACGAGGAAGATACAGATGCCCTC 2745

RESULT 2

US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-3 (1-3111)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20

Db 165 ATGAAGGATGTGGAGTTCGGGCGGGGAGGTGTCTGTAACCTCGGACGCCCGGAGGCGC 224
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGTCTACTGTGGGCAACCCGCGGGCAGCTCGGTGGCGGGCGGGTGGCTG 284
Qy 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 285 AGGAGAGCCCGGGGCAAGCAGGGGCGCGGATGAGCCTGTGGGAAAGCCGCTCTCT 344
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 345 TACACGAGTAGCCAGAGCTGCGCGGCAACGTCAAGTACCAGCGGGGTGCAGAACTACCTG 404
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 405 TACAACGTGTGGAGAGACCCCGCGGTGGGGTTCATCTACACGCTTTCGTTTTTCTC 464
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTTGTCTTGGTGTCTGATTTTGTAGTGTTCAGTGTTCATCATCCCTGAGCACACAAATTG 524
Qy 121 AlaSerSerCysLeuLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTTCGCTTCTGATCCTGGAGTTCGTGATGATGTCTTTCGTTTGGAGTTC 584
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 585 ATCAATCGAATCTGGTCTGGCGGTTCGTGTGATATAGAGGATGCAGAGAGACTG 644
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 645 AGGTTTGTCTGAAAGCCCTTCGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 704
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 705 GTTGTTCCTGCAAAACCTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAACTTCGGT 764
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
Db 765 TTCCTACAGATCCTCCGATGTCGCGATGCACGAGGGGAGGACACTTGGAAATTAATG 824
Qy 221 GlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db 825 GGTTCAGTGGTTTATGTCTACAGCAAGAAATTAATACAGCTTGTGTATATAGGATTTTG 884
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTATTTTTCGTCCTTCCTGTCATCTGGTGGAAAGGATGCCAATAAAGAGTTT 944
Qy 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGCAGATGCTCTCTGGTGGGCAACATTAATGACAACTATTTGGCTATGGA 1004
Qy 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAACTCCCTAACTTGGCTGGGAAGATGTCTTCTGCAAGCTTTGCACTTCCTTGGC 1064
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTTTCGTCATCTTCCTGCGGCAATCTTGGCTCAGGTTTTCGATTTAAAGATCAA 1124
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCCAGAAACACTTTGAGAAAGAGGAACCCAGCTGCCCACTCATTCAG 1184
Qy 341 CysValTyrArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTyrLysPro 360
Db 1185 TGTGTTTGGCGTAGTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCA 1244
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380

Db 1245 CACTTGAAGGCGCTTGCACACCTGCAGCCCTACCAATCAGAACTAAGTTTTAAAGGAGCGA 1304
Qy 381 ValArgMetAlaSerProArgGlyClnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1305 GTGCGCATGGCTAGCCCGAGGGGCGAGATATTAAAGCCGACCAAGCTCTAGTAGGTGAC 1364
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1365 AGGAGGTCCTCCCAAGCAGCATCACAGCCGAGGCGAGTCCACCAAGTGCAGAGAGC 1424
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1425 TGGAGCTTCAACGACCGAACCGCTTCGCGCCCTCGCTGCGCCCTCAAAAGTTCTCAGCCA 1484
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1485 AAACAGGTGATAGATGCTGCACAGCCCTTGCGACTGATGATGATATGATGATAAAGGA 1544
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
Db 1545 TGCCAGTGTGATGATCAGTGGAGACCTCACCCACCCACCTTAAACCTGTCATTCGAGCT 1604
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProThr 500
Db 1605 ATCAGAAATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAACATTACGTCCATAT 1664
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1665 GATGTAAAGATGATGATGAACAATTTCTGCTGCTCATCTGGACATGTTGTGATGAAT 1724
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1725 AAAAGCCTTCAACACAGGTGTTGATCAATTTCTGGAAAAGGCAAAATCACATCAGATAAG 1784
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCCACAGACGATCTCAGTATGCTCGGT 1844
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1845 CGGTGGTCAAGTTGAAAACAGTACAGTCCATAGNATCAAGCTGGAGTGGCTACTA 1904
Qy 581 AsplIleTyrGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1905 GACATCTATCAACAGGTCTCTTCGGAAGAGCTCTGCCTCAGCCCTCGCTTGGCTTCATTC 1964
Qy 601 GlnIleProProPheGluCysGluClnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCACACCTTTGAAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 2024
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTCGGGTTCCGCAAAACAGTGGCTGCTTATCCAGATCACTAGTGGCCACATC 2084
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGCCCTGCAGTTCATTCGAGCCAAATGAGTTTCAGTGCCACGACTTCTACGCG 2144
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2145 CTTAGCCCTTACTATGCACAGTCAAGCAACAGAGGTGCCAATTAGTCAAAAGCGATGGCTCA 2204
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2205 GCAGTGGCAGCCACCAACACCATTCGCAAAACCAATAAATAGGCNCCCAAGCCAGCAGCC 2264
Qy 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2265 CCAACAACTTTACAGATCCACCTCTCTCCAGGCATCAAGCATCTGCCAGGCGCAGAA 2324
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrCysLeu 740
Db 2325 ACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAAGCATTTCTGACGTCAACCACTGCCTT 2384

Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2385 GTTGCCTCCAAGGAAATGTTAGTTTGCACAGTCAAACTCTCACCAGGACCGTTCTATG 2444
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2445 AGGAAAAGCTTTGACATGGGAGGAGAACTCTGTTGTTCTGTCTGCTCCCATGGTCCGAAG 2504
Qy 781 AsplLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2505 GACTTGGGCAAACTTTGTTCTGTGCAAAACCTGATCAGGTGCGACCGAGGAACCTGAATATA 2564
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTyr 820
Db 2565 CAACCTTCAGGAGTGATCAAGTGGCTCCAGAGGCGAGCAAGATTTTATCCCAATGG 2624
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2625 AGGGAATCCAAATTTGTTATACTGATGAAGAGTGGTCCCGAAGAGACAGACAGAC 2684
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2685 ACTTTGATCCGACCGCAGCTGCCAGGAAAGCTGCTTTGCAATCAGACTCTCTAAGG 2744
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2745 ACTGGAAGTTCAGCATCATCTCAGAGCATTTGTAAGCGCAGGAGAAAGTACAGATGCCCTC 2804
Qy 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGCTCATGTCAAACTGAAA 2828

RESULT 3

US-09-590-304-1

; Sequence 1, Application US/09590304

; Patent No. 6649371

; GENERAL INFORMATION:

; APPLICANT: JENTISCH, Thomas

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS

; FILE REFERENCE: 2815-0136P

; CURRENT APPLICATION NUMBER: US/09/590,304

; CURRENT FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3137

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2691)

US-09-590-304-1

Alignment Scores:

Pred. No.: 0 Length: 3137

Score: 4527.50 Matches: 887

Percent Similarity: 99.00% Conservative: 1

Best Local Similarity: 98.89% Mismatches: 0

Query Match: 99.57% Indels: 9

DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x US-09-590-304-1 (1-3137)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20

Db 1 ATGAAGGATGTGGAGTCGGGCCGGGCGAGGTGCTGCTGAACCTCGGACGCCCGCAGGGGC 60

Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40

Db 61 GACGGCTGTCTACTGCTGGGCACCCGCGCGGCACGCTCGGTGGCGCGCGGTGGCTG 120

Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60

Db 121 AGGGAGACCCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCTCTCT 180
Qy 61 TyrThrSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAGATACCGCGGGTCGACGACTACCTG 240
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACACGCTGCTGGAGAGACCCCGCGCTGGCGCTTCATCTACCAACGCTTCCTTTTCTC 300
Qy 101 LeuValPheGlyCysLeuIleuSerValPheSerThrIleProGluHisThrIysLeu 120
Db 301 CTGTGCTTTGGTGTCTGATTTGTGAGTGTCTTACCATCCCTGAGCACACAAAATG 360
Qy 121 AlaSerSerCysLeuIleuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTGCCTTCGATCCTGGAGTTCGTGATGATGTCGTCCTTTGGTGTG 420
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 421 ATCATTCGAATCTGGTCTGCGGGTGTCTGTGTCGATATAGAGGATGCAAGGAAGCTG 480
Qy 161 ArgPheAlaArgIysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTGTCTGAAAGCCCTTCGTGTTATAGATACCATGTGCTTATCGCTTCAATAGCA 540
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTTCCTGCANAACTCAGGTAATATTTTGCACGCTGCACTCAGAACTCCGT 600
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 601 TTCTCTACAGATCCTCCGATGTCGCGATGCGATGACCAAGGGAGGCACCTGGAAATCTG 660
Qy 221 GlySerValValTyrAlaHisSerIysGluIleuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 661 GGTTTCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATAGGATTTTG 720
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTATTTTTCGCTCTTCCTGCTATCTGTTGGTGAAGAGGATCCCAATAGAGTTT 780
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 781 TCTACATATGAGATGCTCTCTGTTGGGGCACAATTACATTCAACATTTATGGCTATGGA 840
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgGluLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAACCTCCCTAACTTGGCTGGGAAGATGCTTCTGCAAGGCTTTGCACTCTCTGGC 900
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 901 ATTTCTTTCTTTCGATCTTCCTGCGGCATCTTGGCTCAGGTTTGGCATTAAGATACAA 960
Qy 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GAACAACACCGCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCGCAACTCATTCAG 1020
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTTGGCGTAGTTCAGCAGCTGATGAGAAATCTGTTCCATTGCAACCTGGAAGCCA 1080
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1081 CACTTGAAGGCTTGCACACTGACGCTTACCAGAAAGAACAGAGGGAAGCATCAAGC 1140
Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAAGCTAAAGTTTAAAGAGGCGAGTGGCATGGCTAGCCCGAGGGGCGAGAGTATT 1200
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411

Db 1201 AAGAGCCGACAGAGCCTCAGTAGGTGACAGGAGGTCCCCCAAGCAGCAGCATCACAGCCGAG 1260
Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCGCTTCCGGGCC 1320
Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTGGCGCTCAAAAGTTCTCAGCCAAACCAAGTGTAGATGCTGACACAGCCCTTGGC 1380
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1441 CCACCACCTTAAACCTGTCATTTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1500
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1501 AAGTTTAAAGGAACATTTACGTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1561 GGTCTATCTGGACATGTTGTGTAGAAATTAAGACCTTCAACACGCTGTGTGATCAAAATCTT 1620
Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1621 GGAAGAGGGCAATTCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 1680
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValLysValGluLysGlnValGlnSer 571
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1740
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1741 ATAGAAATCCAGCTGGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 1801 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1861 GACTATCAAGCCCTGCTGGATAGCAAGATCTTTCCGGGTCCCGCACAAAACAGGTGGCTGC 1920
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1921 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTGCGAGTTCATTTCTGACGCCAAT 1980
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1981 GAGTTTCAGTGGCCAGACTTTCTACGCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040
Qy 672 ValProLysSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGln 691
Db 2041 GTGCAATATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCAA 2100
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2101 ATAAATACGGACCCAGCCAGCCAGCCCAACAACTTTACAGATCCCACTCTCTCTCCA 2160
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2161 GCCATCAAGCATCTGCCCGAGCCAGAACTCTGACCCCTAACCCCTGCGAGGCTTACAGGAA 2220
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2221 AGCATTTCTGACGTCAACCATCTGCTTGTCCCTCCCAAGGAAATGTTTCAGGTGTCACAG 2280
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
Db 2281 TCAATCTCAACAGGACCGTTCTATAGGAAAAAGCTTTGATGGGAGGAGAAACTCTG 2340

QY 772 LeuSerValCysProMetValProlyAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
DB 2341 TTGTCGTCTCTCCATGTCGCCGAGACTTGGCAAAATCTTGTCTGTGCAAAACCTG 2400
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 811
DB 2401 ATCAGTCCGACCGAGGAACCTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460
QY 812 GlySerGlnAspPheTyrProLysThrArgGluSerLysLeuPheIleThrAspGluGlu 831
DB 2461 GCGACCCCAAGATTTTACCCCAATGGAGGAATCCAAATGTTTATAACTGATGAAGAG 2520
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
DB 2521 GTGGTCCCGAAGACAGACAGACACTTTTGTATGCGCGACCGACCTGCCAGGGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
DB 2581 GCTGCTTTGCAATCAGACTCTTAAGGACTGGAAGTCAAGATCATCTCAGAGCATTTGT 2640
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
DB 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAAA 2691

RESULT 4

US-09-813-148-1
; Sequence 1, Application US/09813148
; Patent No. 6617131
; GENERAL INFORMATION:
; APPLICANT: STEINMEYER, Klaus
; APPLICANT: LERCHE, Christian
; APPLICANT: SCHERER, Constanze
; APPLICANT: SEEBOHM, Guiscard
; APPLICANT: BUSCH, Andreas E.
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM
; FILE REFERENCE: 38005-119
; CURRENT APPLICATION NUMBER: US/09/813,148
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: DE 100 13 732.6
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/194,041
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-148-1

Alignment Scores:

Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
DB 215 ATGAAGGATGTGAGTCGGCGCGGACAGGCTGCTGAACTCGGACCGCGGAGGCG 274
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 275 GACGCGCTGCTACTGCTGGGACCCCGCGGCGACGCTTGTGGCGCGGCTGGCTG 334
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 335 AGGAGAGCCCGCGGCGGACGAGGGGCGGCGGATGAGCTGCTGGGAGCGCGCTCTCT 394

QY 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 395 TACACGAGTAGCCAGAGCTCCCGCGCAACGTCGAAGTACCGCGGGTGCAGAACTACCTG 454
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 455 TACAACGTGTGGAGAGACCCCGCGGTGGCGTTCACTACCAACGCTTTCGTTCCTC 514
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 515 CTTGTCTTTGCTGCTTGAATTTTGTCTAGTGTCTTCTACCAATCCTCTGAGCACACAAAATTG 574
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 575 GCCTCAAGTTGCTCTTTGATCCTTGGAGTTCGTGATGATTGCTGCTCTTGTGTTGGAGTTC 634
QY 141 IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 635 ATCATTCGAATCTGGTCTGGCGGTGCTGTGTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA 754
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 695 AGGTTTCTCGAAAGCCCTTCTGTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA 754
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 755 GTTGTCTTCGCAAAACTCAGGGTAAATATTTTGGCCACGCTGTCACCTCAGAACTCCGT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220
DB 815 TTCTACAGATCCTCCGATGGTGGCATGGACCGAAGGGGAGGCATCTTGGAAATTAAGT 874
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
DB 875 GGTTCAAGTGTATTATGCTCAGCAGAGGAATTAATCAGAGTGTGTATAGGATTTTG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 935 GTTCTTATTTTTCCTTCTTCTTCTATCTGTGTGAAAGGATGCGCAATAAAGAGTTT 994
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 995 TCTACATATGAGATGCTCTCTGTGTGGGCAATTAATCAGAGTGTGTATAGGATTTTG 1054
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 1055 GACAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCCTTTGGC 1114
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1115 ATTTCTTTTCTTTCCTTCTTCTGCGGCAATCTTGTGCTCAGGTTTGTCAATTAAGAGTACA 1174
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCGCTGCCAATCATTTAG 1234
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1235 TGTGTTGGCGTAGTACGACGCTGATGAGAAATCTGTGTTCCATTGCAACCTGGAAGCCA 1294
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1295 CACTTGAAGGCTTTGCAACCTGCAAGGCTTACCAGAAAGAACCAAGGGAGGCATCAAGC 1354
QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
DB 1355 AGTCAGAGCTTAAGTTTTAAGACGAGTGGCGCATGTGCTAGCCCCAGGGGCCAGATATT 1414
QY 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
DB 1415 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1474


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Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1475 GGCAGTCCCAAGAGTGCAGAGAGCTGGAGCTTCAACGACCGGAAACCGCTTCGGGCC 1534
Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1535 TCGCTGCCCTCAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGCACACAGCCCTTGGC 1594
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1595 ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1654
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1655 CCACACATTAAACCTGTCATTCGAGCTATCAGAAATTTAGAAATTTTCATGTTGCAAAACGG 1714
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1715 AAGTTTAAGGAACATTACGTCATATGATGTAAGATGTCATTGAACATATTCGCT 1774
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1775 GGTCACTGGACATGCTGTGTAGATTTAAAGCCCTTCAACACAGCGTGTGATCAAAATTCCT 1834
Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1835 GGAAGAGGCAAAATCACATCATGATAAGAGAGCCGAGAGAAATAACACAGCAACATGAG 1894
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1895 ACCACAGACGATCTCAGTATGCTCGTGGTGGTCAAGGTTGAAAGATGTAACAGTACAGTCC 1954
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1955 ATAGAATCAAGCTGGACTGCTACTACATCATCAACAGGTCCTTCGGAAAGGCTCT 2014
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATTCCAGATCCACACCTTTTGAATGTGAACAGACATCT 2074
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTCGGGTTCGGCAAAACAGTGGCTGC 2134
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTCGAGTTCATTCTGACGCCAAT 2194
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTTCAGTGGCCAGACTTCTACGCGCTTACGCTTACTATGCACAGTCAAGCAACACAG 2254
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTAGTCAAGCGATGGCTCAGAGTGGCGCCACCAACCATTTGCAAAACCA 2314
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
Db 2315 ATAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCA 2374
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2375 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTTAACCTTCGAGGCTTACAGAA 2434
Qy 732 SerIleSerAspValThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2435 AGCATTTCTGACGTCAACCTGCTGTTGCTTCCCAAGGAAATGTTTCAGGTTGCACAG 2494
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
Db 2495 TCAATCTCAACCAAGACCGTCTCATGAGAAAGCTTTGATCGGGAGGAGAACTCTG 2554
Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
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Db 2555 TTGCTGTCTCTCCATGGTCCGAGGACTTTGGCAAAATCTTTGCTGTGCAAAACCTG 2614
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 811
Db 2615 ATCAGGTCGACCGAGGAACCTGAATATATCAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2674
Qy 812 GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2675 GGCAGCCCAAGATTTTACCCCAAAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2735 GTGGTCCCGAAGACAGACAGACACTTTTGTATGCCGCCACCGCCCTGCCAGGAA 2794
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2795 GCTGCTTTGTCATCAGACTCTCTAAGGACTCGAAGGTCAAGTATCATCTCAGAGCATTTGT 2854
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2855 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2905

RESULT 5
US-09-492-361-1
; Sequence 1, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492.361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

Alignment Scores:
Pred. No.: 5,98e-203 Length: 2335
Score: 2007.50 Matches: 434
Percent Similarity: 65.32% Conservative: 82
Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
DB: 4 Gaps: 16

US-09-810-796-5 (1-888) x US-09-492-361-1 (1-2335)
Qy 8 ArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
Db 127 CGGGAGCGCCCGCGCGGAGTAGTGGCGCTACGGC----- 165
Qy 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 47
Db 166 ---CGTCAGAGCGAAACAGGGCGAGCGG-----CGGGGGCGG 201
Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
Db 202 CTCGCCGCGCGCTCGGCTCTCTGGCAGCCCTTCGCCCGCGCGCGCGCTCCCTCCCTGG 261
Qy 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLys 73
Db 262 GCCGGGCTCCGGCTCGGGCTCCGGCTCGGGCGCAGGCTCTCTCGCGCGCGCACACGCTA 321
```


; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1823

Alignment Scores:
Pred. No.: 4,86e-202 Length: 2196
Score: 1998.50 Matches: 426
Percent Similarity: 66.14% Conservative: 78
Best Local Similarity: 55.91% Mismatches: 124
Query Match: 43.95% Indels: 134
Gaps: 4

US-09-810-796-5 (1-888) x US-09-949-016-1823 (1-2196)

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Qy 35 GlyGlyGlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeu 54
Db 52 GCGGGGGGCGGCTCCCGGC-----CGCTCGGCTC 84

Qy 55 LeuGlyLysProLeu-----Ser 60
Db 85 CTGGGCGACCCCTCGCGCGCGCGCGCTCCCTCGGCGCGGCTCGGCTCGGCTCC 144

Qy 61 TyrThrSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 145 GCCTCGGCGCGAGCTCTCGCGCGCGCGCGCTCCCGCTCGGCGCGCTCGGCGCGG 204

Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheLeuTyrHisAlaPheValPheLeu 100
Db 205 TACAACTGCTGGAGCGCGCGCGGCTGGGCTTCTGCTACCGCTTCATATTTTG 264

Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 265 CTGGTCTTCAGTCTGCTGCTGTGTGTCTGCTCCACTATCCAGGAGCACCGAACTT 324

Qy 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPhe 140
Db 325 GCCAACAGTGTCTCTCATCTTGAATTCGTGATGATCGTGGTTTCGGCTTCGAGTAC 384

Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 385 ATCTGCGGGTCTGGTCCGCGGATGTGCTGCTGCGCTACCGAGATGGCAGGTTCGCTC 444

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 445 CGCTTTGCCAAGACCCCTCTGTGTATCATCTGCTCATCTGCTGCTGCTGCTGCTGCTG 504

Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 505 GTCATCGCGCGGGTACCCAGCGGCAACATCTTCGCCACGCTCGCGCTCGCAGATCGC 564

Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
Db 565 TTCTTCAGATCTTCGGCATGGTGGCATGGACCGCGCGCGGCGGACCTGGAGCTGCTG 624
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Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db 625 GGCTCAGTGTCTACGGCGCATAGCAAGAGCTGATCACCGCTGGTACATCGGGTTCCTG 684

Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 685 GTGCTCATCTCGCTCTCTCTGCTTACCTGGCTGAGAAGAGCGCAACTCCGACTTC 744

Qy 261 SerThrTyrAlaAspAlaLeuThrTyrGlyThrIleThrLeuThrIleGlyTyrGly 280
Db 745 TCCTCTCTACGCGGACTCGCTCTGGTGGGAGCATTACATTGACAACCATCGGTATGGT 804

Qy 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 805 GACAAGACACCGCACATCGCTGGGAGGGTCTGCTGCTGCTGCTGCTGCTTACTGGGC 864

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 865 ATCTCTTTCTTTGGCTGCTGCTGCGGCATCTAGGCTCGGCTTGGCTTGGCTGCGAG 924

Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 925 GAGCAGCACCGCGAGAAGCACTTCGAGAAGCGGAGGATGCGGCGAGCAACTCATCCAG 984

Qy 341 CysValTyrArgSerTyrAlaAlaAsp---GluLysSerValSerIleAlaThrTyr--- 358
Db 985 GCTGCTTGGGCGCTGTACTCCACGATATGAGCGCGGCTTACTTACGACAGCCACTGGTAC 1044

Qy 358 ----- 358
Db 1045 TACTATGACAGTATCTCCATCTCTTCAGAGAGCTGGCCCTCTTGTGTGACGACGTGCAA 1104

Qy 358 ----- 358
Db 1105 CGGSCCGCAATGGGGGCTTACGGCCCTCGAGGTGGGGGGCGCGGTACCCGACGGA 1164

Qy 359 -----LysProHisLeuLysAlaLeuHisThr-----Cys 368
Db 1165 GCACCTCTCCGTTACCGCGCGCTTGCACCTGCCCGCGCGCGGCGAGCACCTCTCTTCGC 1224

Qy 369 SerProThrAsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGly 388
Db 1225 CTGGGGAAGACCGCGATGGGCATCAAGACCGCATTCGCATCGGCGAGCTCCAGCGG 1284

Qy 389 GlnSerIleLysSerArgGln-----AlaSerValGlyAspArgArgSerProSerThr 406
Db 1285 CGGACGGGTCTCTTCCAGCAGCATCTGCACCTCCACAATGCCACCTCCCAAGCAGC 1344

Qy 407 AspIleThrAlaGluGly---SerProThrLysValGlnLysSerTyrSerPheAsnAsp 425
Db 1345 GAGCAGGTGGGTGAGGGCCACCGAGCCCAAGGTGCAAAAGAGCTGGAGCTTCAATGAC 1404

Qy 426 ArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAsp 445
Db 1405 CGCACCGCTTCCGGGATCTCTGAGACTC-----AAACCCCGGACCTCT 1449

Qy 446 AlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspVal 465
Db 1450 GCTGAGGATGCC---CCCTCAGAGAGTAGCAGAGGAGAGAGTACCAGTGTGAGCTC 1506

Qy 466 SerValGluAspLeuThrProLeuLysThrValIleArgAlaIleArgIleMetLys 485
Db 1507 ACGGTGACGACATCATGCTGCTGTGTGAGACAGTATCCGCTCCATCAGGATTTCTCAAG 1566

Qy 486 PheIleValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspVal 505
Db 1567 TTCTGTGGCCAAAGAAATTCAGGAGACATCGGACCGGTACGAGCTGAAGACGCTC 1626

Qy 506 IleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThr 525
Db 1627 ATTGAGCAGTACTCAGCAGCGCCACTGTGACATGTGGCGCGGATCAAGAGCTGCACAACT 1686

Qy 526 ArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlu--- 544
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Db 1687 CGGGTGGACCAAAATTGGTGGTGGGGG-----CCCGGGGACAGAGGCGCGGAGAG 1740
Qy 545 -----LysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArgVal 562
Db 1741 GCGCAAGGGCGCCCTCCGACGCGAGGTGGTGAATGAATCAGCATATGCGGCGCGGTG 1800
Qy 563 VallysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeuAspIle 582
Db 1801 GTCAAGTGGAGAGCAGTGCAGTCCATCAGACACAGCTGGACCTGCTGTGGGCTTC 1860
Qy 583 TyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIle 602
Db 1861 TATTGCGCTGCTGCGCTCTGGCACTCGGCC-----AGCCTGGGCGCGGTGCAAGTG 1914
Qy 603 ProProGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeu 622
Db 1915 CCGTGTTCGACCCGACATCACCTCCGACATCACAGCCCTGTGGACCAAGGACATC 1974
Qy 623 SerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArg 642
Db 1975 TCCGTCTCCGACAGACGCTCAGC---ATCTCCGCTCGGTGAGCACCACATGACTGA 2031
Qy 643 GlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSer 662
Db 2032 GGG----- 2034
Qy 663 ProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaVal 682
Db 2035 -----ACTTCTCAGAGCGGCGGAGCACA--- 2058
Qy 683 AlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThr 702
Db 2059 -----CGGCCAGCCCGCGGCTGGCGCTCCGACT 2088
Qy 703 ThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGluThrLe 722
Db 2089 GCGCTCTGAGCGCTCCGACTCCTCTCGTACTTGAATCACTCCCTCAGCGGAGAGAGA 2148
Qy 722 uHis 723
Db 2149 CCAC 2152
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RESULT 7

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US-09-177-650-95
; Sequence 95, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 95
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2917)
US-09-177-650-95
Alignment Scores: 6,328-180 Length: 3237
Pred. No.: 1794.00 Matches: 432
Score:
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Percent Similarity: 56.22% Conservative: 106
Best Local Similarity: 45.14% Mismatches: 225
Query Match: 39.45% Indels: 195
DB: 3 Gaps: 26
US-09-810-796-5 (1-888) x US-09-177-650-95 (1-3237)
Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db 227 TCCACCCGGGACGCGGCGCTGCTGATCGCCGGCTCCGAGGCCCCCAAG-----CGC 277
Qy 37 GlyGlyGlyLeuArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuGly 56
Db 278 GGCAGCATCTCAGCAAAACCTCGCGGCGCGCGCGCC-----GGG 322
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
Db 323 AAGCCC-----CCCCAAGCGCAACGCTTCTACCGCAAGCTG 358
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 359 CAGATTTCTCTACACAGTGTGGAGGCGCGCGCTGGGCGTTTCATCTACCAGCC 418
Qy 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db 419 TACGTGTTCTCTCTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPhe 136
Db 479 TATGAGAAGAGCTCGGAGGGGGCCCTCTACATCTCGAAATCTGAGTATCGTGGTGT 538
Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
Db 539 GCGTGGAGTACTTCTGCGGATCTGGGCGCGAGCTGCTGCTGCGGTACCGTGGCTGG 598
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
Db 599 AGGCGCGCGCTCAAGTTTGGCCGAAACCGTTCTGTGTGATTGACATCATGCTGCTCATC 658
Qy 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 659 GCCTCCATTCGGGTGCTGGCGCGCGCTCCAGGGCAACGCTTTTGGCAATCTGCGCTC 718
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216
Db 719 CGGAGCTGCGCTTCTCTGAGATTTCTCGGATGATCGCATGGACCGCGGGAGGCACC 778
Qy 217 TrpLysLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
Db 779 TGGAAAGCTGCTGGGCTCTGTGCTATGCCACAGCAAGAGAGCTGCTGCTGCTGCTGCT 838
Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db 839 ATCGGCTTCTTTGCTCTCATCTGCGCTCGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 898
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThr 276
Db 899 AACGACCACCTTGGACACCTACGCGGATGCACTCTGTTGGGCGCTGATCAGCTGACCACC 958
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 959 ATTGGCTACGCGGACAAAGTACCCCGACACCTGGAAACGCGGAGCTTCTTGGCGCAACCTTC 1018
Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 1019 ACCCTCATCGGTGCTCTCTCTTCTGCGCTGCTGCGCATCTTGGGGTCTGGGTTTGGC 1078
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
Db 1079 CTGAAGGTTCAAGAGAGCAGCAGGAGACACTTTGAGAAGAGGCGGAAACCCGCGAGCA 1138
Qy 337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 349
```

Db 1139 GGCCTGATCAGTCGGCTGGAGATTCTACGCCACCAACCTCTCGGCACAGACCTGCAC 1198
Qy 350 -----GluysSerValSerIleAlaThrTrpLys----- 359
Db 1199 TCCAGTGGCAGTACTACGAGCGAAGCTGACCGTGCCTGTCAGTTCGCAAACTCAA 1258
Qy 360 -----ProHisLeuLysAlaLeuHisThr----- 367
Db 1259 ACCTACGGGGCTCCAGACTTATCCCGCTGAAACCAAGCTGCTGAGGAACCTC 1318
Qy 367 ----- 367
Db 1319 AAGAGTAAATCTGGACTCGCTTTCAGGAAGACCCCGCGGACCGCTCTCCAAGTAA 1378
Qy 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
Db 1379 GGCAGCCCGTGCAGAGGGCCCTGTGTGGATGCTGCCCGGACGCTCTAGCAGAAAGTGC 1438
Qy 376 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 395
Db 1439 AGTTGAAGATCGTGTC---TTCTCCAGCCCCGAGGGCGTGTGCTGCAAGGGGGAAGGG 1495
Qy 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGluGlySer 413
Db 1496 TCCCGCAGGCCAGACTGTGAGGCGGTCAACCCAGCGCGACGAGCTCGAGGACAGC 1555
Qy 414 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 433
Db 1556 CCCAAGAGTGGCCCAAGAGCTGGAGCTTCGGGAGCCGACGCGGGCAGCGAGCTTTC 1615
Qy 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp 453
Db 1616 CGCATCAAGGTGGCGCGCTCAGCGGAGAACTCAGAA---GAAGCAAGCTCTCCCGGAG 1672
Qy 454 AspValTyrAspGluLysGlyCysGlnCysValSerValGluAspLeuThrProPro 473
Db 1673 GACATTGGATGACAGAGCTGCCCTGCGAGTTGTGACCGAGACCTGACCCCGGCG 1732
Qy 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493
Db 1733 CTCAAAGTCAGCATCAGAGCGCGTGTGTCTGTCGTTCTGTTCTCAAGCGGAAGTTC 1792
Qy 494 LysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHis 513
Db 1793 AAGGAGACCTCGCGCCCTACGACGTGATGACGTCATCGACGATCTACGCGGCCAC 1852
Qy 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 533
Db 1853 CTGGACATGCTGTCCTCCGATTAAGAGCTGTCAGTCCAGAGTGGACCATGCTGGGGCGG 1912
Qy 534 GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGluThrThr 553
Db 1913 GGCCCGCATCACGAC---AAGGACCGCACCAAGGGCCCGCGGCGGAGCTGCC 1969
Qy 554 AspAspLeuSerMetLeuGlyArgValLysValLysValGluLysGlnValGlnSerIleGlu 573
Db 1970 GAGGACCCCATGATGGAGCGCTCGGGAAGTGGAGAGCAGAGTCTTGTCTCATGAG 2029
Qy 574 SerLysLeuAspCysLeuLeuLysIleTyrGlnGlnValLeuArgLysGlySerAlaSer 593
Db 2030 AAGAGCTGGACTTCCTGGTGAATATCTACATGCG---CGATGGGC----- 2074
Qy 594 AlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys----- 607
Db 2075 -----ATCCCCCGACAGACGAGCGGCTACTTTGGGCGC 2110
Qy 608 -----GluGlnThrSerAspTyrGlnSerProValAspSerLysLeuSerGly 624
Db 2111 AAAGAGCGGAGCGCGCGCTGATGAGTGGAGAGTGGAGAGCAGCTTGTCTCATGAG 2161
Qy 625 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 644
Db 2162 CATGTCGACAGGACGCGGTGATGTCGAAGATCGTGGCTCCAGCAGCTCCACGCGC--- 2218

Qy 645 GlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThr 664
Db 2218 ----- 2218
Qy 665 MethisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAla 684
Db 2218 ----- 2218
Qy 685 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeu 704
Db 2219 -----CAGAAGAATCTTCTCGGCGCCCGCGCGCGCC---CCTGTC 2257
Qy 705 GlnIleProPro-----ProLeuProAlaIleLysHis 715
Db 2258 CAGTGTCCGCTCCACCTCTGCGCAGCCACAGAGCCACCGCGC---CCAGGGCCAGCGAC 2316
Qy 716 LeuProArg-----ProGluThr-----LeuHis---ProAsnProAlaGlyLeuGlnI 731
Db 2317 CTCCCCGTGGGACACACGGCTCCTGTGGTGGATCCCGCGCGCTGCCACGAGG 2376
Qy 731 uSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaG 751
Db 2377 GTGCTGTGCGCTACGCGGGGGCAACCGCGCCAGCATGAGTTCCTCGCGCAGGAG 2436
Qy 751 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGly 769
Db 2437 CACCCCGGCTGTCAGGCGCCCGCGGAGAACCTCGCGGACAGC-----GA 2481
Qy 769 uThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValG 789
Db 2482 CACCTCATCTCCATCCGCTCCGTGGACCCAGGAGCTGGAGCGTCTCTCAGCGGCTT 2541
Qy 789 nAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerG 809
Db 2542 CAGCATCTCCAGTCCAGGAGAACCTGGATGCTCTCAACAGCTGCTACGCGCGCTGC 2601
Qy 809 ySerArgGlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAs 829
Db 2602 GCCTTGTCGCAAGTCAAGCCCTACATTCGCGAGGAGAGTCAAGC-----ACCGA 2652
Qy 829 pGluGluVal-----GlyPro-----GluGluThrG 838
Db 2653 CTCCGACCTGTGTACCCGTCGCGGCGCCCGCCACGCTCGGCCCGGAGGTCCTT 2712
Qy 838 uThrAspThrPheAspAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSe 858
Db 2713 TGGTGACGTGGCTGGCGCGCGCGCGGAGAGTGAAGCGCGCTGGGC----- 2764
Qy 858 rLeuArgThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGly 874
Db 2765 ---CAGTGGACCGCGCGCGCTCTCAGCAGCGTCTCCGAGGT 2809

RESULT 8

US-09-105-058C-19
; Sequence 19, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blauar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105.058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1


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Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349
Db |||||
1012 GGTCTGATCCAGTCGTGCGTGGAGATTCTATCTACTAACTCTCAGCACCGACCTGCAC 1071
Qy |||||
350 -----GluLysSerValSerIleAlaThrTrpLys-----ProHis 361
Db |||||
1072 TCCAGCTGGCAGTACTACGAGCGGACAGTCACTGTCCCATGTACAGACTCATCCCACT 1131
Qy |||||
362 LeuLysAlaLeuHisThrCys----- 368
Db |||||
1132 CTGAACAGCTGGAGCTCTGAGGAATCTCAAGAGCAAAATCTGAGCTCACCTTCAGGAAG 1191
Qy -----SerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
Db |||||
1192 GAGCACAGCCAGAGCCATCACCA---AGTCAGAGGTCAGTTCAAGATCGTGC--- 1245
Qy 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp----- 400
Db |||||
1246 TTCTCCAGCCCGAGGATGCTGCCAAGGAAAGGGTCTCCCGCAGGCCAGACGGTC 1305
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db |||||
1306 CGGCGGTCCCCAGTCGCGAGTCAGAGTCTTGATACAGCCCGCAGCAAGTGCCTCAAGAGC 1365
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db |||||
1366 TGGAGCTTTGGTACCGCGCAGCGCACCGCAGGCTTTCGCATCAAGGGTGTCTGCATCC 1425
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db |||||
1426 CGGCAGATTCAGAAGCAAGCTCCCT---GGGGAGGACATCGTAGAGGACAACAAGAGC 1482
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
Db |||||
1483 TGTAACTCGAGTTGTGACTGAGAGATCTTACCCCTGGCCCTCAAGTTAGCATCAGAGCT 1542
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGlyGlnThrSerAspLys 500
Db |||||
1543 GTGTGTATTATCGCTTCTTGTATCTAAGCGAAGTTCAAGAGAGTCTGGGCCATAT 1602
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db |||||
1603 GATGTGATGGACGTCATCGAAGCAGTACTCGCTGAGACATTGGATATGTTCTCCCGCATC 1662
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnThrSerAspLys 540
Db |||||
1663 AAGACCTTCAGTCCAGAGTGGACAGATTGTGGCGGGGGCCCAACATAACGGAT--- 1719
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db |||||
1720 AAGGATCGCACCAAGGCGCCAGCGAAGACGAGCTGCCCGAAGACCCCGCATGATGGGA 1779
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db |||||
1780 CGGCTTGGGAAGGTGGAGAAACAGTCTTGTCATGGAAGAAAGACCTCGACTTCTGTGTG 1839
Qy 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaLeuAlaLeuAlaSerPhe 600
Db |||||
1840 AGCATCTATACAG-----AGATGGGC----- 1863
Qy 601 GlnIleProProPheGluCys-----GluGlnThrSer 611
Db |||||
1864 ---ATCCACACAGACAGACAGAGCGCTATTTTGGGGCCAAAGAGCGCTGAGCGCGCACCA 1920
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db |||||
1921 CCTTACCACACCCAGAGAGCAGCGGTGAC-----CATGCAGACAAGCATGGGTGT 1971
Qy 632 -----LeuSerArgSerThrAlaAsnIleSerArgGlyLeuGlnPheIleLeu 648
Db |||||
1972 ATCATTAAGATCGTCGCTCCACAGCTCT----- 2001
Qy 649 ThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGln 668
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Db 2002 -----ACGGCCAGAGGAAGTACGACGACCCCGCCAGCATC-----CCC 2040
Qy 669 AlaThrGlnValProIleSerGlnSer 677
Db |||||
2041 CTGCCCAGTGTCTCTCCCTCCACCTCG 2067

RESULT 10
US-09-177-650-1
; Sequence 1, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (975)..(976)
; OTHER INFORMATION: There is an insertion of a GT between nucleotides
; OTHER INFORMATION: 975 and 976 in kindred KI504.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (978)
; OTHER INFORMATION: The mutation A to G occurs at this base in kindred
; OTHER INFORMATION: K3904.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1043)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K1705.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1691)..(1703)
; OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
; OTHER INFORMATION: deleted in kindred K3369.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1039)
; OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1846)
; OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1459)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K1525.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1094)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K4443.
; FEATURE:
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| | | | |
|----|------|---|------|
| Qy | 277 | IlseGlyTyrGlyAspLysThrProLeuThrTrrPLeuGlyArgLeuLeuSerAlaGlyPhe | 296 |
| Db | 959 | ATTGGGTTACGGGACAAAGTACCCCCAGACCTGGAACGGCAGGCTCTCTTGGCGCAACCTTC | 1018 |
| Qy | 297 | AlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla | 316 |
| Db | 1019 | ACCTCATCGGTGTCTCTTCCTCGCGCTCCCTGCAAGGCATCTTGGGTCCTGGGTTGGCC | 1078 |
| Qy | 317 | LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla | 336 |
| Db | 1079 | CTGAAGGTTTCAGGAGCAGCACAGCGAAGACACTTTTGAGAAGAGCGGCAACCCGGCAGCA | 1138 |
| Qy | 337 | AsnLeuIleGlnCysValTrrArgSerTyrAlaAlaAsp | 349 |
| Db | 1139 | GGCCTGATCAGTCCGGCTTGGAGATTCTACGCCCAACCACTCTCGCGCAGACACCTGCAC | 1198 |
| Qy | 350 | -----GluTyrSerValSerIleAlaThrTrpLys | 359 |
| Db | 1199 | TCCACGTGGCAGTACTACGAGCGAAGCGGTCAACGTCGCCCATGATACAGTTCGCAAACTCAA | 1258 |
| Qy | 360 | -----ProHisLeuLysAlaLeuHisThr | 367 |
| Db | 1259 | ACCTACGGGCTCCAGACTTATCCCCCGCTGAACCACTGAGCTGTGAGTGTCTGAGGAACCTC | 1318 |
| Qy | 367 | ----- | 367 |
| Db | 1319 | AAGAGTAAATCTGGACTCGCTTTTCAGGAAGGACCCCGCGGAGCGCTCTCCAAGTAAA | 1378 |
| Qy | 368 | -----CysSerPro-----ThrAsnGlnLysLeu | 375 |
| Db | 1379 | GGCAGCCCGTCGACAGGGGCCCTGTGTGGATGCTGCCCGGACGCTCTAGCCAGAAGGTC | 1438 |
| Qy | 376 | SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln | 395 |
| Db | 1439 | AGTTTGAAGATCGTGTCTCCAGCCCGGAGCGCTGTGCTGCCAAGGGGAAGGGG | 1495 |
| Qy | 396 | AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGluGlySer | 413 |
| Db | 1496 | TCCCGCGGACCCACAGACTGTGAGCGGTCAACCAGCGCGCACCAAGAGCTTCGAGGACAGC | 1555 |
| Qy | 414 | ProThrLysValGlnLysSerTrrSerPheAsnAspArgThrArgPheArgProSerLeu | 433 |
| Db | 1556 | CCAGCAAGGTGCCAAGAGCTGGAGCTTCGGGGACCGCAGCGCGGACGCCAGGCTTTC | 1615 |
| Qy | 434 | ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp | 453 |
| Db | 1616 | CGCATCAAGGTGCCCGCTCAGCGCAACTCAGAA---GAACCAAGCTTCCCGGAGAG | 1672 |
| Qy | 454 | AspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro | 473 |
| Db | 1673 | GACATTGTGATGACAAGAGCTGCCCTCGCGAGTTGTGTGACCGAGGACCTGACCCCGGGC | 1732 |
| Qy | 474 | LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe | 493 |
| Db | 1733 | CTCAAAATCAGCATCAGACCGGTGTGTCTATCGCGTCTCTGTGTGTCTCAAGCGGAAGTTC | 1792 |
| Qy | 494 | LysGluThrLeuArgProTrrAspValLysAspValIleGluGlnTrrSerAlaGlyHis | 513 |
| Db | 1793 | AAGGAGGCTTCGGCCCTACACGACGATGAGAGCTCATCGACAGCTACTCAGCCGGCCAC | 1852 |
| Qy | 514 | LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys | 533 |
| Db | 1853 | CTGCACATGCTGTCCCGAATTAAAGACCTGCAGTCCAGAGTGCACAGACTCGTGGGCGG | 1912 |
| Qy | 534 | GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGluThrThr | 553 |
| Db | 1913 | GGCCCAAGCATCACGAC---AAGGACCGCACCAAGGGCCCGCGGCGGAGCTGCC | 1969 |
| Qy | 554 | AspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlu | 573 |
| Db | 1970 | GAGGACCCACGATGAGGACGCGCTCGGGAAGTGTGAGAAGCAGGTCTTGTTCATGGAG | 2029 |
| Qy | 574 | SerLysLeuAspCysLeuLeuAspIleTrrGlnGlnValLeuArgLysGlySerAlaSer | 593 |

Db 892 ACCCTCATTTGGTGTCTGTTCTTTGCTCTTCCGGCTGCAATTTGGGATCGGCTTTGCC 951
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
Db 952 CTGAAGTCCAAAGACAGCATCGGCAAAACACATTTGAGAAACGCGGAAACCTTCGGCA 1011
Qy 337 AsnLeuLeuGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 1012 GGTCTGATCCAGTCTGCTCGAGATTCATGCTACTAACTCTCAGCCACCGACTGCGAC 1071
Qy 350 -----GluLysSerValSerAlaAlaThrTyrLysProHisLeuLys 363
Db 1072 TCCAGTGGCAGTACTACGAGCGNACAGTCACTGTCCCATGTACAGCTCACAACTCAA 1131
Qy 364 -----AlaLeuHisThrCysSerProThrAsnGln----- 373
Db 1132 ACCTATGGGGCTCCAGACTCATCCACTCTGAACACAGCTGGAGCTGCTGAGGAATCTC 1191
Qy 374 -----LysLeuSerPheLysGluArgValArg-----MetAlaSerPro 386
Db 1192 AAGAGCAATCTGGACTCACTTTCAGGAAGAGAGCCACAGCCAGAGCCATCCAGGCC 1251
Qy 387 ArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp-----ArgArgSerPro 404
Db 1252 CGAGGCTGGCTGCCAAGGGAAAGGGTCTCCCGAGGCCAGCGTCCGGCGGTCCGCC 1311
Qy 405 SerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTyrPheAsn 424
Db 1312 AGTCGGATCAGAGCTTGTGACAGCCGAGCAAGGTGCCAGAGCTGGAGCTTTGGT 1371
Qy 425 AspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIle 444
Db 1372 GACCGACCCGACACCGCCAGCTTTCGCATCAAGGGTGTGCATCCCGCGCAATTCATCA 1431
Qy 445 AspAlaAspThrAlaLeuGlyThrAspValTyrAspGluLysGlyCysGlnCysAsp 464
Db 1432 GAAGAGCAAGCTCCCTGGGAGGACATCTAGAGGACACAGAGCTGTAACTGGAG 1491
Qy 465 ValSerValGluAspLeuThrProLeuLysThrValIleArgAlaIleArgIleMet 484
Db 1492 TTTGTGACTGAAGATCTTACCCTCGCTCAAGTCTCAAGAGAGTCTGCGCCCATATGATGTGATGAC 1551
Qy 485 LysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAsp 504
Db 1552 CGGTTCTTGGTATCTTAAGCGAAAGTCAAGAGAGTCTGCGCCCATATGATGTGATGAC 1611
Qy 505 ValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGln 524
Db 1612 GTCATCGAACAGTACTCGGCTGGACATTTGGATATGTTGTCCTCCGATCAAGAGCTGCGAG 1671
Qy 525 ThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlu 544
Db 1672 ACCAGAGTGGACAGATTTGGGGGGGGGGCCCAACAATAACGGAT---AAGATCGCAC 1728
Qy 545 LysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValLys 564
Db 1729 AAAGCCCGACCGGAAACGAGCTGCGCCGAAGACCCAGCATGATGGGACGCTTGGGAAG 1788
Qy 565 ValGluLysGlnValGlnSerIleGluSerLysLysLeuAspCysLeuLeuAspIleTyrGln 584
Db 1789 GTGGAGAAACAGGTTTGTTCATGAGAAAGAGCTCGACTCTTGGTGAGCATCTATACA 1848
Qy 585 GlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPro 604
Db 1849 CAG-----AGAATGGCATCCACAGCAGAGACAGAGCCCTATTTTGGGGCCCAAG--- 1899
Qy 605 PheGluCysGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 624
Db 1900 ---GAGCCTGAGCCGCGCACCCCTTACCACAGCCAGAGGACAGCCGTGAC----- 1947
Qy 625 SerAlaGlnAsnSerGlyCys-----LeuSerArgSerThrSerAlaAsnIleSer 641
Db 1948 CATGCAGACAAGCATGGCTGTATCATTAAGATCTGCTCCGCTCCACCGACTCTACGG--GCC 2005

Qy 642 ArgGly-----LeuGlnPheIleLeuThrProAsnGlu 652
Db 2006 AGAGGAAGTACGACACACCCCAACCATCCCTCCCTGCGCAGTGTCTCTCCCTCCACCTCGT 2065
Qy 653 PheSerAlaGlnThr-----PheTyr 659
Db 2066 GGCGGAGAGCACACAGGCGCATGCGACCTCCCTGTGGGAGACCATGGTCACTGGTATC 2125
Qy 660 AlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGly 679
Db 2126 GCATCCCACTCTCCCTGACACAGAGCGGTGCTGTCTGCT----- 2167
Qy 680 SerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsn---ThrAlaProLysPro 698
Db 2168 ---ACGGTGGGGGCAACAGAGCCAGTACCGAGTTCCTTGGAGCTGGAGGCGACCCAGCCT 2224
Qy 699 AlaAlaProThrThrLeu 704
Db 2225 GCAGGCCCTCTGAGGCTG 2242

RESULT 12

US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360

GENERAL INFORMATION:

; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME

; FILE REFERENCE: 3053-4052

; CURRENT APPLICATION NUMBER: US/09/105,058C

; CURRENT FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 60/055,599

; PRIOR FILING DATE: 1997-08-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26

; LENGTH: 2565

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-105-058C-26

Alignment Scores:

Pred. No.: 4,24e-158 Length: 2565
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
DB: Gaps: 28

US-09-810-796-5 (1-888) x US-09-105-058C-26 (1-2565)

Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGly 22
Db 91 GACGTGGAGCAA-----GTCACCTTGGCGCTCGGGCGCGGAGCCGCAAGACGCGG 141
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
Db 142 ACCCTGCTGCTG-----GAGGGCGGGCGCGCGACGAGGGG 177
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 178 CAGCGGAGGAGCCCGCAGGGG-----ATCGGGTCTCTGGCCAGACCCCGCTGAGCGCG 231
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 232 CCAGTCAAG-----AGAAACAACGCCAAGTACCGCGCGCATCCAACTTTGATCTAC 282


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Db 2263 CGAATCTCCCGCCGAG-----AGACGTAGCATCAGC 2295
Qy 766 MetGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSer 785
Db 2296 CGAGACAGTGACACACCTCTGTCCCTG-----2322
Qy 786 LeuSerValGlnAsnLeuLeuArgSerThrGluGluLeuAsnLeuGlnLeuSerGlySer 805
Db 2323 ATGTCGGTCAACCAC-----GAGGAGCTGGAGAGGTCTCCAAGTGGCTTC 2367
Qy 806 GluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTyrArg 821
Db 2368 AGCATCTCCAGGACAGAGATGATGTTCGCCCCCAATGGGGGTGCGAGCTGGATG 2427
Qy 822 GluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAspThr 841
Db 2428 AGGGAGAAGCGGTACTCTGCCGAG-----GGTGAGACGGACACAGACGACGCC 2478
Qy 842 Phe 842
Db 2479 TTC 2481

RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.

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US-09-177-650-6
Alignment Scores:
Pred. No.: 5,37e-158 Length: 2914
Score: 1587,50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
DB: 3 Gaps: 28

US-09-810-796-5 (1-888) x US-09-177-650-6 (1-2914)
Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAalaArgGlyAspGly 22
Db 163 GACCTGGAGCAA-----GTCACCTTGGCGTCGGGGCCGAGCGACAAAGACGGG 213
Qy 23 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlu 42
Db 214 ACCCTGTGCTG-----GAGGGCGCGCGCGCGACGAGGGG 249
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 250 CAGCGGAGGACCCCGCAGGGC-----ATCGGGCTCTTGGCCCAAGACCCCGTGAGCCGC 303
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 304 CCAGTCAAG-----AGAAACAACGCCCAAGTACCGCGCATCCAAACTTTGATCTAC 354
Qy 82 AsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
Db 355 GACCCCTGGAGAGACCGCGGGCTGGCGCTGTTTACCACCGCGTGGTGTCTCTGAT 414
Qy 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
Db 415 GTCTCGGGGTCTTGATTTCTGGCTGCTGACCATTCATCAAGGAGTATGAGACTCTCTCG 474
Qy 122 SerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPheIle 141
Db 475 GGAGACTGGCTTCTGTACTGGAGACATTTCTCTATTTTCTTTGGAGCGAGTTGTGT 534
Qy 142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyValArgLeuArg 161
Db 535 TTGAGGATCTGGGCTGTGGATGTTGTCGCATACAAAGCTGGCGGGGCGGACTGAAG 594
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db 595 TTTGCCAGGAAGCCCTGTGCTATCTGGACATCTTTGTGCTGATTGCTCTGTGCGCAGTG 654
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db 655 GTTCTGTGGGAAACCAAGGCAATGTTCTGGCCACCTCC---CTGCGAAGCCTGCGCTTC 711
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuGly 221
Db 712 CTGAGATCTTCCGCAATGCTCGGATGGACCGAGAGGTGGACCTGGAAGCTTCTGGGC 771
Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
Db 772 TCAGCCATCTGTGCCACAGCAAGAACTCATACGGCTGTGTATCGTTCCTGTCGACA 831
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla-----256
Db 832 CTCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 891
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTrpGlyThr 271
Db 892 CAAGGAGAGAGATGAAGAGAGTTTGAGACCTATGCAATGCGATGCTGTGTGGGGCTG 951
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeu 291
Db 952 ATCACACTGGCCACCATTTGGCTATGGACAAAGACACCCAAACGTTGGGAAGCGCTGTG 1011
Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPheAlaLeuProAlaGlyIleLeu 311

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Db 1072 GGGTCGGGGCTGGCGCCCTCAAGGTGCAGAGCAACACCGTCAGAGCACTTTTGGAAAGG 1131
Qy 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAspGluLys 351
Db 1132 AGGAAGCCAGCTGCTGAGCTCATTCAGGCTCCCTGGAGGTATATGTACCAACCCCAAC 1191
Qy 352 SerValSer---IleAlaThrTriPlys-----ProHisLeu 362
Db 1192 AGGATTGCGGTGGCGACATGGAGATTTTATGAATCAGTCGTCTCTTTTCTTCTTC 1251
Qy 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
Db 1252 AGGAAGAACAGCTGGAGGAGCAGCATCCAGCCAAAGCTGGTCTCTTGGATCGGGTTGCG 1311
Qy 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402
Db 1312 CTTTCTAATCTCTGTGTAGCAATACTAAA-----GGAAAGCTATTT 1353
Qy 403 SerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTriPser 422
Db 1354 ACCCTCTGAATGTAGATGCCATAGAGAAAGTCTTCTTAAGAAACCAAGCCTGTGTGC 1413
Qy 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLys----- 436
Db 1414 TTAACCAATAAGAGCGTTCCCGACGGCTTCGCGATGAAAGCCTACGCTTTCTGGCAG 1473
Qy 437 SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspValTyr 456
Db 1474 AGTTCTGNA-----GATGCCGGGACAGT-----GACCCCATGGCG 1509
Qy 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476
Db 1510 GAAGACAGGGGCTATGGGAATGACTTCCCATCGAAGACATGATCCCCACCTGAAAGCC 1569
Qy 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496
Db 1570 GCCATCCGAGCGCTCAGAAATTCATAATTCGCTCTCTATAAAAAAATCAAGGAGACT 1629
Qy 497 LeuArgProTyrAspValLysAspValIleGluIntyrSerAlaGlyHisLeuAspMet 516
Db 1630 TTGAGGCTTTACGATGTGAAGATGTGATTGAGCAGATTTCTGCGGSCATCTCGACATG 1689
Qy 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536
Db 1690 CTTTCCAGGATAAAGTACCTTCAGACGAGATAGATATGATTTTCAACCCCTGGACCTCCC 1749
Qy 537 ThrSerAspLysLysSerArg----- 543
Db 1750 TCCAGCCAAACACAAAGAGTCTCAGAAAGGTCAGCATTCACCTTCCCATCCAGCAA 1809
Qy 544 -----GluLysIleThrAlaGluHisGluThr-----AspAspLeuSer 557
Db 1810 TCTCCAGGATGAACCATATGTACCCAGACATCCACATCAGAAATCGAAGACCAAGC 1869
Qy 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577
Db 1870 ATGATGGGAAGTTTGTAAAAGTTGAAAGACAGAGTTTCAGGACATGGGGAAGAGCTGGAC 1929
Qy 578 CysLeuLeuAspIleTyrGlnGluValLeuArg----- 588
Db 1930 TTCCTCGGGATATGCATGCATCAACATGAAAGCGTTGCGAGTGCAGGTCAAGGAGTAT 1989
Qy 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPhe 605
Db 1990 TACCAACCAAGGACCTCTCTCG-----CCAGCT 2019
Qy 606 GluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySer 625
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RESULT 14

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US-09-177-650-90
; Sequence 90, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 90
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (202)..(2811)
US-09-177-650-90

Alignment Scores:

Pred. No.: 4, 43e-154 Length: 2814
Score: 1550.50 Matches: 382
Percent Similarity: 54.43% Conservative: 109
Best Local Similarity: 42.35% Mismatches: 245
Query Match: 34.10% Indels: 167
DB: 3 Gaps: 27

US-09-810-796-5 (1-888) x US-09-177-650-90 (1-2814)

Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAaArgGlyAspGly 22
Db 340 GACGTGGAGCAA-----GTCACTTGGCGCTAGGCGCGGAGCCGACAAAGACGGG 390
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
Db 391 ACCCTGCTGCTG-----GAGGCGCGTGGCGCGGAGAGGGG 426
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 427 CAGAGGAGACCCCGCAGGCG-----ATCGGGCTCTGGCAAGACCCCTGAGCGCG 480
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 481 CCAGTCMAAG-----AGNAACAACGCCAAGTACAGCGCGCATCCAACTTTTGATCTAT 531
Qy 82 AsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeuLeu 101
Db 532 GACGCCCTGGAGAGACCGCGGGCTGGCGCTCTTACCACGGCGCTTGTGTCTCGATT 591
Qy 102 ValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
Db 592 GTCTGGAGATGCTTGATTCTGGCGCTGCTCACCACCTTCAGGAATATGACACTGTGTCT 651
Qy 122 SerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPheIle 141
Db 652 GGAGACTGGCTTTTGTCTGTGMAACAATTGTCTATTCTTTTGGAGCTGAGTTTGTCT 711
Qy 142 IleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeuArg 161
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Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db 772 TTGCGCAGAGCCCTCTGCAATGTTGACATCTTCGTACTGATTCCTCTGTGCCAGTG 831
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db 832 GTTGGCGTGGAAACACAGGGCAATGTCTTGCCACCTCC---CTGCGAAGCTTCGCTTC 888
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeuGly 221
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Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
Db 949 TCGGCTATCTGTGCCCAACAGAAAGACTATCATCTGCTGCTGATAGGCTTCTTGACA 1008
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256
Db 1009 CTCATCTTTTCTTCACTTTCTGTCTACCTGTGGTGGAGAGGATGTGCCAGAAATGGATGCC 1068
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThr 271
Db 1069 CAAGGAGAGGAGATGAAGGAGGAGTTTGAGACCTATGACAGATGCTCTGTGGTGGGCGCTG 1128
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeu 291
Db 1129 ATCACATGGCCACCATTTGGTTATGGACRAGACACCTAAACCTGGGAAGGAGCTGTG 1188

Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeu 311
Db 1189 ATTGCTGCCACCTTTTCTTAATGGCGCTCTCTTTTGGCCTTCCGGCAGCATCTT 1248
Qy 312 GlySerGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGlyLysArg 331
Db 1249 GGCTCAGACTGGCGACTGAAGTTTCAGAGCAGACCGCTCAGAGCATCTTTGAGAAGAGA 1308
Qy 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLys 351
Db 1309 AGGAAGCCAGCTGCGGAACCTCATCCAGCTCGCTGGAGATATTATGCTACCAACCCCAAC 1368
Qy 352 SerValSer---IleAlaThrTrpLys-----ProHisLeu 362
Db 1369 AGGTGGATCTGGTGGCAACCTGGAGATCTTGAATCAGTTGTCTTTTCCCATCTTTC 1428
Qy 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
Db 1429 AGGAAGAACAACTGGAGACGACGCCCAAGCTGGGTCTCTTGGATCGGGTTCGC 1488
Qy 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402
Db 1489 CTTTCTAATCTCTGTTAGCAATACTAAA-----GGAAAGCTATT 1530
Qy 403 SerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrpSer 422
Db 1531 ACCCTCTGTAATGTAGATGCCATAGAAAGACCTTCCAAAGAGACCAAGCTTGTGGC 1590
Qy 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer----- 437
Db 1591 TTAACAAATAAAGACGGTTTCCGACCGCTTCCGCAAGAAAGCTACGCTTTCTGGCAG 1650
Qy 438 ---SerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456
Db 1651 AGWTCTGAA-----GATCTGGGACAGC-----GACCCCATGGCA 1686
Qy 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476
Db 1687 GAAGACAGGGCTATGGGAATGACWTCTCATTMAGACATGATCCCTTCCTTAAAGCT 1746
Qy 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496
Db 1747 GCCATCGAGCTGTCAGAAITTCAGTTCGCTCTATATAAAGAAAGTTCAAGAGACG 1806
Qy 497 LeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet 516
Db 1807 TTGAGGCTTATGATGTGAAGATGTGATTCAGCAGTATTCGGCCGACATCTTGACATG 1866
Qy 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536
Db 1867 CTTTCCAGATAAAGTACCTACAGACAAGATAGATATGATTTTTCACCCCTGGACCTCCA 1926
Qy 537 ThrSerAspLys---LysSerArgGluLysIleThr----- 547
Db 1927 TCCACTCCAAACATAAAGAGTCTCAGAAAGGACAGCATTTTACTACCCATCCGAGCAG 1986
Qy 548 -----AlaGluHisGluThrThrAspAspLeuSer 557
Db 1987 TCTCCAAGGAATGAACCATATGTAGCCAGGGCAGCCACATCAGAACTGAAGACCAAGC 2046
Qy 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577
Db 2047 ATGATGGGAAGTTTGAAGATTGAAGACAGGTTTATGATCATGATGGGGAAGAAATCGGAC 2106
Qy 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588
Db 2107 TYCTCGTGGACATGTCATATGCATATGCATATGAAACGCTTACAGGTACATGTCACTGAGTAC 2166
Qy 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPhe 605
Db 2167 TACCAACTAARGGGGCTCTCTCC-----CCAGCC 2196

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QY 606 GluCySGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeu-SerGlySe 625
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QY 2197 GAAGGGGAGAGAAAGAACACAGGTACTCT---GATTGAAACCATCATCTGCCAC 2253
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 625 rAlaGlnAnSerGlyCysLeuSerArgSerThrSerAlaAnlleSerArgGlyLeuG1 645
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2254 TACTCAGACAGAGGGCCCTGACCTCCTTACAGCTTCCACCCAGGTGCCATCGACAGA 2313
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QY 645 nPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMe 665
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2314 GTTGGCCCTTACGGG-----TTTTTGACATGATCCCT--- 2346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 665 thisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaLath 685
Db : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2347 -----GTGAAACTGACCCGAGGGGACCCAGTCTCTACAAAGGCTCA 2387
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 685 rAnThrThrIleAlaAnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuG1 705
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2388 AGCTAACCTTCCCTCC-----TCGGGAAGTACATATGCAGA 2423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 705 nIleProProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAs 725
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2424 GAGGCCACAGTCTGCCATCTTGACTCTCTGACATCATGTGAGCTACCAC----- 2478
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 725 nProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaLaserLysG1 745
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2479 -----TCCACAGC 2486
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QY 745 uAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAs 765
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 765 pMetGlyGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSe 785
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2544 TAGGCACAGTGATACCTCTGTCCCTC----- 2571
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 785 rLeuSerValGlnAnLeuLeuArgSerThrGluGluLeuAnlleGlnLeuSerGlySe 805
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2572 -ATGTCCTGCAATCAC-----GAGGAACGGAGCGGTCTCCAAGTGGCTT 2615
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 805 rGluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTrpAr 821
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2616 CAGCATCTCAGACAGAGATGATTATTTGGCCCCAGTGGGGGATCGAGCTGGAT 2675
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 821 gGluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAspTh 841
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2676 GGGGAAAAGCGGTACCTGGCTGAA-----GGAGAAACGGACACGACACAGACCC 2726
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 841 rPhe 842
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2727 CTTC 2730
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RESULT 15

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US-09-105-058C-5
; Sequence 5, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven.
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; PRIOR FILING DATE: 1998-06-26
; CURRENT FILING DATE: 1998-05,599
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
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; LENGTH: 900
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5
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Alignment Scores:

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| Percent Similarity: | 83.88% | Conservative: | 28 |
| Best Local Similarity: | 74.67% | Mismatches: | 40 |
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US-09-810-796-5 (1-888) x US-09-105-058C-5 (1-900)

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GenCore version 5.1.6
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Run on: April 3, 2005, 06:10:16 ; Search time 9606.32 Seconds
(without alignments)
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Title: US-09-810-796-5

Perfect score: 4547

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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ACCESSION AR565635
VERSION AR565635.1 GI:53981668
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
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AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehls,M.C., Friedrich,G.,
Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;
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Query Match: 100.00% Indels: 0
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ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B.,
Zambrowicz, B. and Sands, A.T.
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Lexicon Genetics Incorporated (US)
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DEFINITION AX268476
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Lexicon Genetics Incorporated (US)
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ORGANISM Homo sapiens
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AUTHORS Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and Gribkoff,V.K.
TITLE Human kcnq5 potassium channel, methods and compositions thereof
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392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
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412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
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692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
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Qy      852   AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
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DEFINITION   Sequence 1 from patent US 6649371.
ACCESSION   AR430568
VERSION     AR430568.1  GI:40191384
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 3137)
AUTHORS    Jentsch,T.J.
TITLE      Potassium channel KCNQ5 and sequences encoding the same
JOURNAL    Patent: US 6649371-A 1 18-NOV-2003;
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Best Local Similarity: 98.89%      Mismatches: 0
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US-09-810-796-5 (1-888) x AR430568 (1-3137)

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Qy      21   AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db      61   GACGGCTGTCTACTGTGGGCACCGCGCGCCACGCTCGGTGGCGGGCGGTGGCGCTG 120
Qy      41   ArgGluSerArgGlyGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyValProLeuSer 60
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Qy      61   TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
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Qy      81   TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db      241  TACACGTGTCTGGAGAGACCGCGGGCTGGGCGTTCATCTACCGCTTTCTGTTTTCTC 300
Qy      101  LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db      301  CTTGTCTTTGGTGTCTGAATTTGTAGTGTCTTCTACATCCCTTGAGCACACAAATG 360
Qy      121  AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
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Qy      141  IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
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Qy      181  ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
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Qy      201  PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
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AX056817
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DEFINITION Sequence 1 from Patent WO0077035.
ACCESSION AX056817
VERSION AX056817.1 GI:12309758
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Patent: WO 0077035-A 1 21-DEC-2000;
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Alignment Scores:
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Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 99.57% Indels: 9
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US-09-810-796-5 (1-888) x AX056817 (1-3137)

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RESULT 8

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LOCUS Homo sapiens potassium voltage-gated channel, KQT-like subfamily,
DEFINITION member 5 (KCNO5) mRNA, complete cds.

ACCESSION AF202977 GI:7798695

VERSION AF202977.1

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3137)

Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and

Jentsch,T.J.

mediates M-type currents

KCNO5, a novel potassium channel broadly expressed in brain,

J. Biol. Chem. 275 (31), 24089-24095 (2000)

2 (bases 1 to 3137)

Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and

Jentsch,T.J.

Direct Submission

Submitted (09-NOV-1999) ZMNH, Hamburg University, Martinstrasse

85, Hamburg 20246, Germany

Location/Qualifiers

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ORIGIN

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ACCESSION
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SOURCE
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Unclassified.
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AUTHORS
Steinmeyer,K., Lerche,C., Scherer,C., Seeborn,G. and Busch,A.E.
TITLE
Nucleic acid molecule encoding the potassium channel protein, KCNQ5
JOURNAL
Patent: US 6617131-A 1 09-SEP-2003;
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DEFINITION Sequence 1 from Patent WO0170811.
ACCESSION AX253254
VERSION AX253254.1 GI:16073802
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lerche, C., Scherer, C., Seeborn, G., Busch, A. and Steinmeyer, K.
TITLE potassium channel protein kcnks, a target for diseases of central nervous system and cardiovascular system
JOURNAL Patent: WO 0170811-A 1 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
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Best Local Similarity: 98.66% Mismatches: 2
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DEFINITION Sequence 5 from Patent WO0232960.
ACCESSION AX456864
VERSION AX456864.1 GI:21715731
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Argentieri, T. M. and Sheldon, J. H.
TITLE Methods of selecting compounds for modulation of bladder function
JOURNAL Patent: WO 0232960-A 5 25-APR-2002;
WYETH (US)
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Score: Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
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DEFINITION cds.
ACCESSION AF249278
VERSION AF249278.1 GI:9651966
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REFERENCE 1 (bases 1 to 3074)
AUTHORS Lerche,C., Scherer,C.R., Seebom,G., Derst,C., Wei,A.D., Busch,A.E.
and Steinmeyer,K.
TITLE Molecular cloning and functional expression of KCNO5, a potassium
channel subunit that may contribute to neuronal M-current diversity
J. Biol. Chem. 275 (29), 22395-22400 (2000)
MEDLINE 20357367
PUBMED 10787416
REFERENCE 2 (bases 1 to 3074)
AUTHORS Lerche,C., Scherer,C.R., Seebom,G., Derst,C., Wei,A.D., Busch,A.E.
and Steinmeyer,K.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2000) Cardiovascular Diseases, Aventis Pharma
Deutschland GmbH, Building H824, Frankfurt a. M. 65926, Germany
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QY 888 Lys 888
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RESULT 15
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 LOCUS Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,
 DEFINITION partial cds.
 ACCESSION AF263836
 VERSION AF263836.1 GI:8132998

KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 3108)

REFERENCE Kniazeva,M. and Han,M.
 AUTHORS A new gene of the voltage-gated potassium channel KCNQ family,
 TITLE KCNQ5, is a candidate gene for retinal disorders

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3108)

AUTHORS Kniazeva,M. and Han,M.
 TITLE Direct Submission

JOURNAL Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
 Porter Biosciences Bldg., Boulder, CO 80309, USA

FEATURES Location/Qualifiers
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/db_xref="taxon:10090"

/sex="male"

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/dev_stages="9-11 weeks"

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ORIGIN

Alignment Scores:

Pred. No.:

1.89e-283 Length: 3108

Score: 4227.50 Matches: 827
 Percent Similarity: 95.90% Conservative: 14
 Best Local Similarity: 94.30% Mismatches: 27
 Query Match: 92.97% Indels: 9
 DB: 10 Gaps: 1

US-09-810-796-5 (1-888) x AF263836 (1-3108)

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Search completed: April 3, 2005, 16:36:47
Job time : 9670.32 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 2, 2005, 23:56:51 ; Search time 1110.87 Seconds
(without alignments)
4732.082 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547
Sequence: 1 MOVESGRVLLNSAARG.....SICKAGESTDALSLPHVKLK 889

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N_Geneseq_16Dec04 -QWTF=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 3: geneseqn2000as:*
- 4: geneseqn2001as:*
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- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 4547 | 100.0 | 2772 | Aah43633 | Aah43633 Human ion |
| 3 | 4547 | 100.0 | 3111 | Aah43634 | Aah43634 Human ion |
| 4 | 4527.5 | 99.6 | 2694 | Aas14652 | Aas14652 Human cDN |
| 5 | 4527.5 | 99.6 | 2694 | Aad27192 | Aad27192 Human pot |

| | | | | | | |
|----|--------|------|--------|----|----------|-----------|
| 6 | 4527.5 | 99.6 | 3137 | 4 | AAC85414 | Human KCN |
| 7 | 4523.5 | 99.5 | 3071 | 4 | AAS14651 | Human cDN |
| 8 | 4513.5 | 99.3 | 3074 | 4 | AAH49499 | Human KCN |
| 9 | 4513.5 | 99.3 | 3074 | 10 | ADB78684 | Human pot |
| 10 | 4346.5 | 95.6 | 3718 | 3 | AAC64371 | Human KCN |
| 11 | 2007.5 | 44.1 | 2335 | 3 | AAA47618 | Pot |
| 12 | 2007.5 | 44.1 | 2335 | 10 | AD311698 | Human 323 |
| 13 | 1810 | 39.8 | 5595 | 13 | AD311698 | Rattus no |
| 14 | 1798 | 39.5 | 7407 | 10 | ADB78687 | Human pot |
| 15 | 1797 | 39.5 | 7407 | 10 | ADB78687 | Human pot |
| 16 | 1797 | 39.5 | 7407 | 10 | ADB78688 | Human pot |
| 17 | 1797 | 39.5 | 7407 | 10 | ADB78688 | Human pot |
| 18 | 1797 | 39.5 | 7407 | 10 | ADB78688 | Human pot |
| 19 | 1797 | 39.5 | 7411 | 10 | AD329557 | Human tum |
| 20 | 1797 | 39.5 | 7420 | 11 | ADN38963 | Cancer/an |
| 21 | 1797 | 39.5 | 7420 | 11 | ADP65810 | Human mRN |
| 22 | 1797 | 39.5 | 7420 | 11 | ADP65731 | Human pot |
| 23 | 1797 | 39.5 | 7420 | 12 | ADL06495 | Human tum |
| 24 | 1797 | 39.5 | 7863 | 10 | ADJ56529 | Human cDN |
| 25 | 1794 | 39.5 | 3237 | 2 | AAJ57145 | Human mut |
| 26 | 1792.5 | 39.4 | 3287 | 2 | AAJ26587 | Nucleotid |
| 27 | 1790.5 | 39.4 | 2169 | 2 | AAJ26588 | Nucleotid |
| 28 | 1790 | 39.4 | 2565 | 2 | AAJ81548 | Human bra |
| 29 | 1790 | 39.4 | 3195 | 5 | AAJ74831 | DNA encod |
| 30 | 1788 | 39.3 | 3232 | 2 | AAJ57057 | Human KCN |
| 31 | 1788 | 39.3 | 3232 | 10 | AAJ58489 | Human pot |
| 32 | 1788 | 39.3 | 3232 | 13 | AD317844 | Human KCN |
| 33 | 1780 | 39.1 | 3232 | 5 | AAJ74830 | DNA encod |
| 34 | 1775 | 39.0 | 7413 | 5 | AAJ74832 | DNA encod |
| 35 | 1767 | 38.9 | 2273 | 2 | AAJ57140 | Mouse KCN |
| 36 | 1762 | 38.8 | 3029 | 2 | AAJ81547 | Human bra |
| 37 | 1750 | 38.5 | 4512 | 10 | ADJ56528 | Rat cDNA |
| 38 | 1667.5 | 36.7 | 125910 | 3 | AAJ64370 | Human KCN |
| 39 | 1611 | 35.4 | 1848 | 12 | ADH51119 | Potassium |
| 40 | 1611 | 35.4 | 1848 | 12 | ADM77995 | KCNQ2-15b |
| 41 | 1604 | 35.3 | 1878 | 12 | ADH51117 | Potassium |
| 42 | 1604 | 35.3 | 1878 | 12 | ADM77993 | KCNQ2-15b |
| 43 | 1602 | 35.2 | 1932 | 12 | ADH51115 | Potassium |
| 44 | 1602 | 35.2 | 1932 | 12 | ADM77991 | KCNQ2-15b |
| 45 | 1587.5 | 34.9 | 2565 | 2 | AAJ26596 | Nucleotid |

ALIGNMENTS

RESULT 1

| | |
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| AAS14653 | |
| ID | AAS14653 standard; cDNA; 2667 BP. |
| AC | AAS14653; |
| XX | |
| DT | 18-DEC-2001 (first entry) |
| XX | |
| DE | Human cDNA encoding a voltage gated potassium channel hKCNQ5-2. |
| XX | |
| KW | Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic; |
| KW | cerebroprotective; neurotropic; analgesic; vision disorder; |
| KW | central nervous system disorder; epilepsy; migraine; hearing disorder; |
| KW | psychotic disorder; seizure; learning disorder; memory disorder; stroke; |
| KW | pain; gene therapy; splice variant. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PH | Key |
| CDS | Location/Qualifiers |
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| FT | /*tag= a |
| FT | /product= "hKCNQ5-2" |
| XX | |
| PN | WO200170759-A1. |
| XX | |
| PD | 27-SEP-2001. |
| XX | |
| PF | 20-MAR-2001; 2001WO-US009328. |
| XX | |

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Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
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Db 2041 CGAGTGGAGCCACCAACCATTTGCAACCAATTAATATGAGCACCCCAAGCCAGCAGCC 2100
Qy 701 ProThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2101 CCAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2160
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
Db 2161 ACTCTGCAACCTTAACCTTGCAGGCTTACAGGAAAGCATTTCTGACGTCCACCCCTGCCTT 2220
Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2221 GTTGCTTCCAGGAAAATGTTGAGTTGACAGTCAATCTCACCAAGGACCGTCTATG 2280
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2281 AGSAAAAGCTTTGACATGGAGGAGAACTCTGTGTCTGTCTGCCATGTGTCGCGAAG 2340
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeulleArgSerThrGluGluLeuAsnIle 800
Db 2341 GACTTGGCAAAATCTTTCTGTGTCGCAAAACCTGATCAGTGCAGCGAGGAACTGAATATA 2400
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
Db 2401 CACTTTGAGGAGTGTGAGTCAAGTGGCTCCAGAGGCGACCAAGATTTTATCCCAATGG 2460
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2461 AGGGAATCCAAATGTTTATTAACATGATCAAGAGGTGGTCCCGAAGACAGACAGACAGAC 2520
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860

Db 2521 ACTTTGATGCGCCAGCCAGCCTGCCAGGAAGCTGCTTTGCATCAGACTCTCTAAGG 2580
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2581 ACTGGAAGGTCAACATCATCTCAGACGATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640
Qy 881 SerLeuProHisValLysLeuLys 888
Db 2641 AGCTTGCTCATGTCAAACTGAAA 2664
RESULT 2
AAH43633
ID AAH43633 standard; cDNA; 2772 BP.
XX
AC AAH43633;
DT 21-JAN-2002 (first entry)
XX
DE Human ion-channel forming protein ORF.
XX
XX Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS Homo sapiens.
XX
FN WO200175108-A1.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010875.
XX
PR 03-APR-2000; 2000US-0194255P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Kleke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI; 2001-656987/75.
XX
XX P-PSDB; AAB47678.
XX
PT New human ion channel protein and polynucleotides encoding the protein,
PT useful in diagnosing or treating diseases, in drug screening, and in
PT clinical trial monitoring.
XX
PS Claim 1; Page 34-35; 41pp; English.
XX
CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.
CC The protein shares structural similarity with mammalian ion channel
CC proteins, particularly voltage-gated potassium channel proteins. The
CC protein is expressed in many human cell lines including fetal brain,
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
CC be used in the diagnosis or treatment of diseases, in drug screening, and
CC in clinical trial monitoring. The oligonucleotides may be used as
CC hybridization probes for screening libraries, and assessing gene
CC expression patterns (particularly using a micro array or high throughput
CC chip format). The nucleic acids and novel protein can also be used in the
CC identification, selection and validation of novel molecular targets for
CC drug discovery, to screen collections of genetic material from patients
CC who have a particular medical condition, to identify mutations associated
CC with a particular disease, as a diagnostic or prognostic assay, and to
CC screen for drugs which can be used to treat symptomatic or phenotypic
CC manifestations of perturbing the normal function of novel human protein.
XX The polypeptides are further used in generating antibodies
SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0


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Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
US-09-810-796-5 (1-888) x AAH43633 (1-2772)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAArgGly 20
Db 106 ATGAAGATGTGGAGTCGGCGCGGCGAGGTGCTGCTGAACTCGGACGCGCGAGGGGC 165
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 166 GACGCGCTGCTACTGCTGGGACCCGCGCGCCACGCTCGGTGGCGCGCGGTGGCGCTG 225
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGAGAGCCCGCGGGGACAGGGGCGCGGATGAGCTGCTGGGAGACCCGCTCTCT 285
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTGCAGAGCTGCGCGCGCAACGCTCAAGTACCGCGGCGTGCAGAACTACCTG 345
Qy 81 TyrAsnValLeuGluAArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACAACGCTGCTGGAGAGACCCCGCGCGCTGGCGGTTCATCTACACGCTTTCGTTTTCTC 405
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTTCGCTTGGTGTGCTGATTTGTCAGTGTTTCTACCATCCCTGAGCACACAAATG 465
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGCCCTCTTCATCTCGAGTTCGTGATGATGTGCTTTTGGTTTGGAGTTC 525
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 526 ATCAATTCGAATCTGGTCTCGCGGTGCTGTTGTCATATAGAGTAGGATGCAAGGAGACTG 585
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTGCTCGAAGACCCCTCTGTTGATATAGATACCATTTGTTTCTATCGCTTCAATAGCA 645
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTTCCTGCAAAAACCTCAGGGTAATATTTTGGCACGTCTGCACCTCAGAACTCCGT 705
Qy 201 PheLeuGlnIleLeuAArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 706 TTCTTACAGATCTCCGTCATGGTGGCATGGTGGACCGAAGGGAGGACCTTGGAAATTTACTG 765
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db 766 GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 825
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTATTTTTTTCGCTCTTCCTGCTATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 885
Qy 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGAGATGCTCTCTGGTGGGCGCAATATCATTTGACAACTATTTGGCTATGGA 945
Qy 281 AspyLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 946 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTCGCAGGCTTTGCACTCCTTTGGC 1005
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTTCTTTCGCACTTCTGCGCGCATTTCTGGCTCAGGTTTGGCATTAAAGATACAA 1065
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAAACACACCGCCAGAAACACTTTGAGAAAAGAGAGAACCCAGCTGCGCAACTCATTCAG 1125
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Qy 341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1126 TGTGTTTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1185
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1186 CACTTGAAGGCTTTGCACACCTGCGAGCCCTACCAATCAGAAGCTTAAGTTTTTAAGAGCGCA 1245
Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1246 GTGCGCATGGCTAGCCCCAGGGCCAGAGTATTAAAGCCGACCAAGCTCTAGTAGGTGAC 1305
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1306 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCAACAAAGTGCAGAGAGC 1365
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1366 TGGAGCTTCAACGACCCGAAACCCGCTTCGCGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCA 1425
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1426 AAACAGTGTAGATGCTGACACAGCCCTTGGCACTGATGATGATATGATGATAAAGGA 1485
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
Db 1486 TGCCAGTGTGATGTATCAGTGGAGAGACTCACCCCAACCACTTAAACCTGTCTATTCGAGCT 1545
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1546 ATCAGAAATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACATTACGTCCATAT 1605
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1606 GATGTAAGAATGTCATTTGAAACAGTATTCGCTGCTCATCTGGACATGTTGTGTAGAAAT 1665
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1666 AAAAGCCTTCAACACACGTGTTGATCAAAATCTTGAAAAGGGCAATCACATCAGATAAG 1725
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCCGAGAGAAAATAACAGCAAGACATGAGACCAACAGATCTCAGTATGCTCGGT 1785
Qy 561 ArgValValLysValGluLysGlnValClnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1786 CGGTGCTCAAGTTGAAAACAGTACAGTCCATAGATCCCAAGCTGGACTGCTACTA 1845
Qy 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAspPhe 600
Db 1846 GACATCTATCAACAGGTCTTTCGAAAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1905
Qy 601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1906 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGACAA 1965
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 1966 GATCTTTTCGGGTTCCGCAACAAACAGTGGCTGCTTATCCAGATCACTAGTGCACCAATC 2025
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2026 TCGAGAGCCCTGCGAGTTCAITTCGACGCAAAATGAGTTGATGATGATGATGATGATGATG 2085
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2086 CTTAGCCCTTACTATGCAAGTCAAGACACACAGGTGGCAATTAGTCAAGCGATGGCTCA 2145
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2146 GCAGTGGCAGCCCAACCAACCATTCGAAACCAATAAATACGGCACCCACCCAGCAGCC 2205
Qy 701 ProThrThrLeuGlnIleProProLeuProIleLysHisLeuProArgProGlu 720
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Db 2206 CCAACAACTTTACAGATCCCACTCTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAGAA 2265
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
Db 2266 ACTCTGCACCCCTAACCTCTGAGGCTTACAGGAAGCATTTCTGAGGTCAACACCTGCTT 2325
Qy 741 VallalaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2326 GTTGCTCCAAAGGAAATGTTTCAGGTTGCAGATCAAAATCTCACCAGGACCGTTCTATG 2385
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2386 AGGAAAGCTTTGACATGGAGGAGAACTCTGTGTCTGTCTGTCCTCATGTCCTGCGAAG 2445
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2446 GACTTGGGCAAACTCTTCTGTGTCGCAAACTGATCAGTGCAGCGAGGAACCTGAATATA 2505
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyProLysTrp 820
Db 2506 CAACCTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGAGCAAGATTTTATCCCAATGG 2565
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2566 AGGGAATCCAAATGTTTATTAACCTGATGAAGAGTGGTCCGAGAGACAGACAGAC 2625
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2626 ACTTTGATGCGCACCGCAGCTGCCAGGAGCTGCTTGGCATCAGATCTCTAAGG 2685
Qy 861 ThrGlyArgSerArgSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2686 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCCCTC 2745
Qy 881 SerLeuProHisValLysLeuLys 888
Db 2746 AGCTTGCTCATGTCAAACTGAAA 2769

RESULT 3
AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
AC AAH43634;
XX
XX
DT 21-JAN-2002 (first entry)
XX
DE Human ion-channel forming protein coding sequence.
XX
KW Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..2831
FT /*tag= a
FT /product= "Human ion-channel forming protein"
XX
XX WO200175108-A1.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010875.
XX
XX 03-APR-2000; 2000US-0194255P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
XX Sands AT;
XX
XX WPI; 2001-656987/75.

```

DR P-PSDB; AAB47678.

XX New human ion channel protein and polynucleotides encoding the protein,
 PT useful in diagnosing or treating diseases, in drug screening, and in
 PT clinical trial monitoring.

XX Disclosure; Page 37-38; 41pp; English.

XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.
 CC The protein shares structural similarity with mammalian ion channel
 CC proteins, particularly voltage-gated potassium channel proteins. The
 CC protein is expressed in many human cell lines including fetal brain,
 CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can
 CC be used in the diagnosis or treatment of diseases, in drug screening, and
 CC in clinical trial monitoring. The oligonucleotides may be used as
 CC hybridization probes for screening libraries, and assessing gene
 CC expression patterns (particularly using a micro array or high throughput
 CC chip format). The nucleic acids and novel protein can also be used in the
 CC identification, selection and validation of novel molecular targets for
 CC drug discovery, to screen collections of genetic material from patients
 CC who have a particular medical condition, to identify mutations associated
 CC with a particular disease, as a diagnostic or prognostic assay, and to
 CC screen for drugs which can be used to treat symptomatic or phenotypic
 CC manifestations of perturbing the normal function of novel human protein.
 CC The polypeptides are further used in generating antibodies

SQ Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3111
 Score: 4547.00 Matches: 888
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-810-796-5 (1-888) x AAH43634 (1-3111)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20
 Db 165 ATGAAGGATGTGGAGTCGGCGCGGCGAGGTGCTGCTGAACTCGGACGCCAGCGGC 224
 Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 Db 225 GACGGCTGCTACTGCTGGGCACCGCGCGCCACGCTCGGTGGCGGCGGTGGCGCTG 284
 Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 Db 285 AGGAGAGCCCGCGGCGCAGCAGGCGCGCGGATGAGCTGCTGGGGAAGCGCGCTCT 344
 Qy 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
 Db 345 TACACGAGTAGCAGAGCTGCGCGCGCAACGCTCAAGTACCGCGCGGTGCAGAACTAC 404
 Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
 Db 405 TACAACGTGCTGGAGAGACCCCGCGCTGGCGGTTCATCTACCGCGCTTTCGTTTTCTC 464
 Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
 Db 465 CTGTGCTTTGGTGTGATTTTGTGATGTTTCTACCATCCCTGACGACACACAAATTTG 524
 Qy 121 AlaSerSerCysLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
 Db 525 GCCTCAAGTTGCTTGTGATCCTGGAGTTCGTGATGATTGTCGTTTGGTTTGGAGTTC 584
 Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
 Db 585 ATCATTCGAATCTGGTCTGCGGTTGCTGTGTGATATAGAGGATGTCAGAGGAGACGTG 644
 Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
 Db 645 AGGTTTGTCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTTATCGCTTCAATAGCA 704

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QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 705 GTTGTTTCTGCMNAACCTCAGGGTAATATTTTGGCACGCTGCACTCAGAACTCCCGT 764
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 765 TTTCCTACAGATCCTCCGCGATGTCGCGATGGACCGAGGGAGGCACTTGGAAATTAATCTG 824
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 825 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTGTGTATACATAGGAATTTTG 884
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTATTTTTCGTCCTTCCTGCTATCTGGTGGAAAGATGCCAATAAAGAGTTT 944
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGCAGATGCTCTCTGGTGGGCGACAATTAACATTGACAACATTATGGCTATGGA 1004
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAGGGCTTTGCACCTCCTTGGC 1064
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTCTTGGCATCTTCTGCGCGCAATCTTGGCTCAGGTTTGGCATTAAGATACAA 1124
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCCGACAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAACCCTCATTCAG 1184
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTTGGCGTAGTACGACGCTGATGAGAAATCTGTTTCCATTGGCAACCTGGAAGCCA 1244
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1245 CACTTGAAGGCTTGCACACCTGCAGCCCTACCAATCAGAGACTAAGTTTAAAGAGCGCA 1304
QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1305 GTGCGCATGGGTAGCCCCAGGGGGCCAGAGTATTAAAGCCGACCAAGCCTCAGTAGGTGAC 1364
QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1365 AGGAGTCCCCAAGCACCGACATCACGCCGAGGGCAGTCCCAACCAAAAGTGCAAGAGAGC 1424
QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1425 TGGAGCTTCAACGACCGAACCCGCTTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCCA 1484
QY 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1485 AAACAGTGATAGATGCTGCACACAGCCCTTGGCACTGATGATGATATATGATGATAAAGGA 1544
QY 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
Db 1545 TGCCAGTGTGATGATATCAGTGAAGACCTCACCCACCACTTAAACACTGTATTGAGACT 1604
QY 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1605 ATCAGAAATATGAATTTTCATGTTGCNAACCGAAGTTTAAAGGAACATTACGTCCATAT 1664
QY 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1665 GATGTAAAGATGTCAATTGAACAATATCTGCTGGTCACTCTGGACATGTTGTGTAGAATT 1724
QY 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1725 AARAGCCTTCAACACACGTTGTGATCAAAATTTTGGAAAGGGCAAAATCACATCAGATAG 1784
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RESULT 4

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QY 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACACACAGACGATCTCAGTATGCTCGGT 1844
QY 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1845 CGGGTGGTCAAGTTGAAAACACAGTACAGTCCATAGAAATCAAGTCCAGCTGCTACTA 1904
QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAspPhe 600
Db 1905 GACATCTATCAACAGGCTCTTCGAAAGGCTCTCCCTCAGCCCTCGCTTTGGCTTCATTC 1964
QY 601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCACCTTTTGAATGTGAACACACATCTGACTATCAAAAGCCCTGTGGATAGCAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTTGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCCAACATC 2084
QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGCCCTGCACTTTCATTTCCAGCCCAAAATCAGTTCACTGAGTGGCCAGACTTTCTACGCG 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2145 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAAAGCATGGCTCA 2204
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2205 GCAGTGGCAGCCACCAACACCATTTGCAAAACAAAATAAATACGGCACCCCAAGCCAGCAGCC 2264
QY 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2265 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2324
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
Db 2325 ACTCTGCACCTTAACCTTCAGCGCTTACAGAAAGCATTTCTGACGTCACCACTGCTT 2384
QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2385 GTTGCCTCCAAAGGAAAATGTTTCAAGTTTGCACAGTCAAATCTCACAAAGGACCGTTCTATG 2444
QY 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2445 AGGAAAAGCTTTGACATGGGAGGAGAAACTCTGTGTCTGTCTGCTCCATGGTCCCAAG 2504
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2505 GACTTGGGCAAACTTTTGTCTGTGCAAAACCTGATCAGTCAAGTCCGAGGAACCTGAATATA 2564
QY 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTyr 820
Db 2565 CAATTTTCAAGGAGTGAGTCAAGTGGCTCCAGAGCAGCCCAAGATTTTATCCCAAAATGG 2624
QY 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2625 AGGAAATCCAAATTTGTTTATACTGATGAAGAGTGGGTCCCGAAGAGACAGACAGACAGAC 2684
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2685 ACTTTTGTATGTCGCGCACCGCAGCCCTGCCAGGGAAGCTGCCCTTTGTCATCAGACTCTCTAAGG 2744
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2745 ACTGGAAGGTCAACATCATCTCAGAGCATTTGTTAAGCGAGGAGAAAGTACAGATGCCCTC 2804
QY 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGGCTCATGTCAAACTGAAA 2828
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| | |
|------------------------|--|
| AA514652 | AA514652 standard; cDNA; 2694 BP. |
| XX | AC |
| XX | AA514652; |
| XX | 18-DEC-2001 (first entry) |
| XX | Human cDNA encoding a voltage gated potassium channel hKCNQ5-1. |
| XX | Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic; |
| KW | cerebroprotective; neurotropic; analgesic; vision disorder; |
| KW | central nervous system disorder; epilepsy; migraine; hearing disorder; |
| KW | psychotic disorder; seizure; learning disorder; memory disorder; stroke; |
| KW | pain; gene therapy; splice variant. |
| XX | Homo sapiens. |
| OS | |
| XX | Key Location/Qualifiers |
| FT | CDS 1..2994 |
| FT | /*tag= a |
| FT | /product= "hKCNQ5-1" |
| XX | WO200170759-A1. |
| XX | 27-SEP-2001. |
| XX | 20-MAR-2001; 2001WO-US009328. |
| XX | 21-MAR-2000; 2000US-0190954P. |
| XX | (ICAG-) ICAGEN INC. |
| XX | Jegla TJ; |
| XX | WPI: 2001-611467/70. |
| DR | P-PSDB; AA09020. |
| XX | polypeptides and polynucleotides of potassium channel KCNQ5 for |
| PT | identifying a compound modulating ion flux in eukaryotic cell or cell |
| PT | membrane expressing the protein, comprises KCNQ approximately alpha- subunits. |
| XX | Claim 5; Page 62-63; 78pp; English. |
| XX | The invention relates to an isolated polypeptide comprising an alpha- |
| CC | subunit of a KCNQ potassium channel, with a subsequence having 65% |
| CC | sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence |
| CC | and forms a KCNQ potassium channel having the characteristic of voltage- |
| CC | gating with at least an additional KCNQ alpha-subunit. Also included in |
| CC | the scope of the invention are the nucleic acids encoding hKCNQ5 |
| CC | (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression |
| CC | vectors encoding them, antibodies against them, the use of 3-dimensional |
| CC | computer modelling to identify molecules that bind to a KCNQ containing |
| CC | potassium channel and modulate ion flux through the channel. The KCNQ |
| CC | polypeptide is useful for identifying a compound that increases or |
| CC | decreases ion flux through a potassium channel expressed in an eukaryotic |
| CC | host cell or cell membrane. The compound (and the KCNQ nucleic acid when |
| CC | used in gene therapy) is useful as a pharmaceutical agent for treating |
| CC | diseases involving abnormal ion flux, such as disorders of the central |
| CC | nervous system, such as epilepsy, migraines, hearing and vision problems, |
| CC | psychotic disorders, seizures, learning and memory disorders, stroke and |
| CC | pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a |
| CC | human tissue and the use of a nucleotide sequence of KCNQ5 to search |
| CC | computer databases to find variants of the sequence which are associated |
| CC | with disease states, is useful for screening mutations of KCNQ5. The |
| CC | present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1 |
| XX | Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other; |
| SQ | |
| XX | Alignment Scores: |
| Pred. No.: | 0 |
| Score: | 4527.50 |
| Percent Similarity: | 99.00% |
| Best Local Similarity: | 99.89% |
| Length: | 2694 |
| Matches: | 887 |
| Conservative: | 1 |
| Mismatches: | 0 |

| | | | |
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| Query Match: | 99.57% | Indels: | 9 |
| DB: | 4 | Gaps: | 1 |
| US-09-810-796-5 (1-888) x AA514652 (1-2694) | | | |
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| Qy | 21 | AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu | 40 |
| Db | 61 | GACGGCTGTACTGTCTGGGACCCCGCGCGCCACGCTTGTGTGGCGGGGTGGCTG | 120 |
| Qy | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 |
| Db | 121 | AGGGAGAGCCCGGGGCAAGCAGGGGGCCGGATGAGCCCTGTGGGGAAGCCCTCTCT | 180 |
| Qy | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 |
| Db | 181 | TACACGAGTAGCCAGAGCTGCCGGCGCAAGCTCAAGTACCGCGGGTGCAAGAACTCTG | 240 |
| Qy | 81 | TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu | 100 |
| Db | 241 | TACAACTGTGGAGAGACCCCGCGGCTGGGGTTCATCTACCAACGCTTTCGTTTTCTC | 300 |
| Qy | 101 | LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 |
| Db | 301 | CTTGCTTTTGGTTGATTTTGTCTAGTGTGTTTCTACCATCCCTCGACACACAAAATTG | 360 |
| Qy | 121 | AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 |
| Db | 361 | GCCTCAAGTTGCCCTTGTGATCTGGAGTTCTGTGATGATTTGCTTTTGGTTTGAGTTC | 420 |
| Qy | 141 | IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTyrGlnGlyArgLeu | 160 |
| Db | 421 | ATCATTCGAATCTGGTCTGGGGTGTCTGTGTGATATAGAGATGSCAAGGAGACTG | 480 |
| Qy | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla | 180 |
| Db | 481 | AGGTTTCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTTATCGCTTCAATAGCA | 540 |
| Qy | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 |
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| Qy | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu | 220 |
| Db | 601 | TTCTACAGATCTCTCCGATGTCGCGCATGSCACCGAAGGGAGGCACCTTGGAAATTACTG | 660 |
| Qy | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu | 240 |
| Db | 661 | GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCAAGCTTGGTACATAGGATTTTGT | 720 |
| Qy | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| Db | 721 | GTCTCTATTTTTCGTCTTCT | 780 |
| Qy | 261 | SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 |
| Db | 781 | TCTACATATGAGATGCT | 840 |
| Qy | 281 | AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
| Db | 841 | GACAAAACTCCCTTAACTTGGCTGGGAGATTTGCTTCTGCAAGGCTTTCCTCTCTCT | 900 |
| Qy | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
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| Qy | 321 | GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln | 340 |
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QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
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QY 372 AenGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
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QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
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RESULT 5
RAD27192
ID AAD27192 standard; cDNA; 2694 BP.
XX
AC AAD27192;
DT
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5 cDNA.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antitense therapy;
KW synaptic transmission; electrical excitability; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..2694
XX /*tag= a
XX /product= "Human KCNQ5 protein"
XX
XX MO200192526-Al.
XX
XX 06-DEC-2001.
XX
XX 24-MAY-2001; 2001WO-US017314.
XX
XX 26-MAY-2000; 2000US-0207389P.
XX
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XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Doretzky SI, Ramanathan CS, Trojnecki JT, Boisard CG;
 PI Griboff VK;
 XX WPI: 2002-122069/16.
 DR P-PSDB; ABE16S99.
 XX Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding
 PT it, for diagnosing, treating and identifying modulators useful in
 PT treating neurological, neuropsychological and neuropsychological
 PT diseases.
 XX Claim 3; Fig 1; 128pp; English.
 XX The invention relates to potassium channel polypeptides referred to as
 CC KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5
 CC polypeptides are useful for identifying compounds that modulate their
 CC biological activity. The compounds identified and KCNQ5 polynucleotides
 CC are useful for treating acute and chronic pain, migraine, acute stroke,
 CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),
 CC multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,
 CC depression, bipolar disorders, sleep disorders, eating disorders,
 CC addiction, myokymia, Alzheimer's disease, age-associated memory loss,
 CC learning deficiencies, cognitive disorders and motor neuron diseases. The
 CC nucleic acid molecules of the invention are further useful for treating
 CC neuropsychological, neuropsychological disorders, asthma, neuron cell
 CC death and brain tumours. They are also used in gene therapy and antisense
 CC therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical
 CC excitability in the brain and are useful for generating antibodies. They
 CC are also useful to affinity purify biological effectors from biological
 CC materials e.g. disease tissues or cells. The present sequence is human
 CC KCNQ5 cDNA
 XX Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 0 Length: 2694
 Score: 4527.50 Matches: 887
 Percent Similarity: 99.00% Conservative: 1
 Best Local Similarity: 98.89% Mismatches: 0
 Query Match: 99.57% Indels: 9
 DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x AAD27192 (1-2694)

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 DB 61 GACGCGCTACTCTGGGACCCCGCGGGCCACGCTTGGTGGCGGGCGGTGGCTG 120
 QY 41 ArgGluSerArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
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Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 811
Db 2401 ATCAGTCCGACGAGAACTGAATATACAACCTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2460
Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2461 GCGACCCCAAGATTTTTACCCCAATGGAGGGAATCCAAATTTGTTATTAACATGATGAAGAG 2520
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2521 GTGGTCCGGAAGACAGACAGACACACTTTTGATGCCGACCCGACCTGCCAGGGA 2580

Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
Db 2581 GCTGCCCTTTGCATCAGACTCTCTAAGGACTCGAAGTCAAGATCATCTCAGAGCATTTGT 2640
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACGTGAAA 2691
RESULT 6
AAC85414
ID AAC85414 standard; cDNA; 3137 BP.
XX
AC AAC85414;
XX
DT 20-APR-2001 (first entry)
XX
DE Human KCNQ5 potassium channel subunit coding sequence.
XX
KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;
central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;
CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;
compulsive behaviour; dementia; depression; Huntington's disease; mania;
memory impairment; memory dysfunction; spinal cord damage; phobia;
pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;
ds.
KW
XX
OS Homo sapiens.
XX
FH
FT Key Location/Qualifiers
FT CDS 1..2694
FT /*tag= a
FT /product= "KCNQ5 subunit"
XX
XX WO200077035-A2.
XX
XX 21-DEC-2000.
XX
XX 29-MAY-2000; 2000WO-DK000289.
XX
XX 11-JUN-1999; 99DK-00000828.
XX
XX (NEUR-) NEUROSEARCH AS.
XX
XX Jentsch TJ;
XX
XX WPI; 2001-080678/09.
XX P-PSDB; AAB47046.
XX
XX Novel genes encoding KCNQ5 potassium channel subunits, useful for
treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,
depression, Huntington's disease, schizophrenia and Parkinson's disease.
XX
XX Claim 2; Page 44-48; 50pp; English.
XX
XX This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms
heteromeric channels with other KCNQ channel subunits, in particular
KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of
chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5
are useful for diagnosis, treatment, prevention or alleviation of
diseases related to diseases or adverse conditions of the central nervous
system (CNS), including affective disorders, Alzheimer's disease,
anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative
illness, cognitive deficits, compulsive behavior, dementia, depression,
Huntington's disease, mania, memory impairment, memory disorders, memory
dysfunction, motion disorders, motor disorders, neurodegenerative
diseases, Parkinson's disease and Parkinson-like motor disorders,
phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,
stroke, tremor, seizures, convulsions and epilepsy
XX
XX Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 U; 0 Other;
Alignment Scores: 0 Length: 3137
Pred. No.: 0

Score: 4527.50 Matches: 887
 Percent Similarity: 99.00% Conservative: 1
 Best Local Similarity: 98.89% Mismatches: 0
 Query Match: 99.57% Indels: 9
 DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x AAC85414 (1-3137)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAargGly 20
 Db 1 ATGAAGAGATGTGGAGTCGGCGCGGAGGTGCTGCTGAACCTCGGACGCGCGAGGGGC 60

Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
 Db 61 GACGCGCTGCTACTGCTGGGACCGCGCGGCCACGCTCGTGGCGCGGGTGGCGCTG 120

Qy 41 ArgGluSerArgGlyGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 Db 121 AGGGAGACCGCGGGGGACGAGGGGGCCCGGATGAGCCTGCTGGGGAAAGCCGCTCTCT 180

Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
 Db 181 TACACGAGTAGCAGAGCTGCGCGCGCAACGTCAGTACCGCGCGGTGCAGAACTACCTG 240

Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
 Db 241 TACACGCTGCTGGAGAGACCGCGCGCTGGCGCTTCATCTACCAACGCTTCGTTTTCTC 300

Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
 Db 301 CTGTGCTTTGGTGTGCTGATTTGTGCTGTTTCTACCATCCCTGACACACAAATG 360

Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
 Db 361 GCCTCAAGTGCCTCTCTGATCTCGAGTTCGTGATGATGTCGCTCTTTGGAGTTC 420

Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
 Db 421 ATCATTCGAATCTGCTCGCGGTTGCTGTTGTCGATATAGAGGATGCAAGGAGACTG 480

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180
 Db 481 AGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATTCGCTTCATAGCA 540

Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
 Db 541 GTTGTCTCGCAAAACTCAGGTAATATTTTGGCCAGTCTGCACTCAGAACTCTCGT 600

Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
 Db 601 TTCTTACAGATCCTCCGATGTCGCGCATGGACCGAAGGGGAGGCACCTTGGAAATTA 660

Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
 Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTATAGGATTTTG 720

Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
 Db 721 GTTCTTATTTTCT 780

Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
 Db 781 TCTACATATGAGATGCTCTCTGTTGGGGCACAAATTAATGACAACTATTGGCTATGGA 840

Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
 Db 841 GACAAACTCCCTTAACTTGGTGGGAGATGCTTCTCTGCAAGGCTTTCACCTCTCTGGC 900

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
 Db 901 ATTTCTTTCTTTCATCTCTGCGGATCTTCTGCTCAGGTTTTCATTAAGATACAA 960

Qy 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340

Db 961 GAACAACACCGCCAGAAACACCTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTTG 1020

Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360

Db 1021 TGTGTTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371

Db 1081 CACTTGAAGGCTTTGCACACCTGCAGCCCTACCAAGAAAGAACCAAGGGAAGCATCAAGC 1140

Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391

Db 1141 AGTCAGAAGCTTAAGTCTTAAAGACGAGTGGCGCATGCTAGCCCGAGGGGCGCAGATATT 1200

Qy 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411

Db 1201 AAGAGCGCACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1260

Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431

Db 1261 GGCAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGGCC 1320

Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451

Db 1321 TCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTAGATGCTGACACAGCCCTTGGC 1380

Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471

Db 1381 ACTGATGATGATATGATGATAAAGAGTCCAGCTGATGATGATGATGATGATGATGATGAT 1440

Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491

Db 1441 CCACCACTTAAACTGTCTTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1500

Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511

Db 1501 AAGTTTAAAGGAAACATTCAGTCCATATGATGATAAAGATGTCATTGAAACAATTTCTGCT 1560

Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531

Db 1561 GGTCACTCGACATGTTGTGTAGAAATTAAGAGCTTCAACACAGCTGTTGATCAAAATCTCT 1620

Qy 532 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 551

Db 1621 GGAAAAGGGCAATACATCAGATAGAAAGAGCGCAGAGAAATAACACAGACAGACATGAG 1680

Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571

Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAACAGGTACAGTCC 1740

Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591

Db 1741 ATAGAACTCAAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1800

Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611

Db 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCCCTTTTGAATGTGAACAGACATCT 1860

Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631

Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGACAAACAGTGGCTGTC 1920

Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651

Db 1921 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGGCTGCAGTTCATTTGACGCGCAAT 1980

Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671

Db 1981 GAGTTCACTGCGCCAGACTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2040

Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGln 691

Db 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCAATTCGCAACCAA 2100
 Qy 692 IleAenThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
 Db 2101 ATAAATACGGACCCACAGCCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
 Qy 712 AlalLeLysHisLeuProArgProGluThrLeuHisProAenProAlaGlyLeuGlnGlu 731
 Db 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCTCTGCAGGCTTACAGGAA 2220
 Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAenValGlnValAlaGln 751
 Db 2221 AGCATTTCTGACGTCAACACTGCTCTGCTTCCCAAGGAAATGTTTCAGGTTGCACAG 2280
 Qy 752 SerAenLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
 Db 2281 TCNAATCTCACCAAGGACCGTTCTATGAGGAAGCTTTTGACATGGGAGGAGAACTCTG 2340
 Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAenLeu 791
 Db 2341 TTGTCTGTCTGCCATGTCGCGAAGGACTTGGCAAAATCTTTGTCTGTGCAAAACCTG 2400
 Qy 792 IleArgSerThrGluGluLeuAenIleGlnLeuSerGlySerGluSerSerGlySerArg 811
 Db 2401 ATCAGGTCGACCGAGGAACCTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
 Qy 812 GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu 831
 Db 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGAATCCAAATGTTTATTAACGTATGAGAG 2520
 Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
 Db 2521 GTGGTCCCGAAGACAGACAGACACTTTTGTATGCCCGCACCGCAGCTGCCAGGAA 2580
 Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
 Db 2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCCAGATCATCTCAGAGCATTTGT 2640
 Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 Db 2641 AAGCAGAGGAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2691

RESULT 7
 AAS14651
 ID AAS14651 standard; cDNA; 3071 BP.
 XX
 AC AAS14651;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human cDNA for voltage gated potassium channel hKCNQ5.
 XX
 KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;
 KW cerebroprotective; neurotropic; analgesic; vision disorder;
 KW central nervous system disorder; epilepsy; migraine; hearing disorder;
 KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;
 KW pain; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO200170759-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 20-MAR-2001; 2001WO-US009328.
 XX
 PR 21-MAR-2000; 2000US-0190954P.
 XX
 PA (ICAG-) ICAGEN INC.
 XX
 PI Jegla TJ;
 XX
 PI WPI; 2001-611467/70.
 XX
 DR

XX
 PT Polypeptides and polynucleotides of potassium channel KCNQ5 for
 PT identifying a compound modulating ion flux in eukaryotic cell or cell
 PT membrane expressing the protein, comprises KCNQ approximately a- subunits.
 PS Claim 5; Page 61-62; 78pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an alpha-
 CC subunit of a KCNQ potassium channel, with a subsequence having 65%
 CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence
 CC and forms a KCNQ potassium channel having the characteristic of voltage-
 CC gating with at least an additional KCNQ alpha-subunit. Also included in
 CC the scope of the invention are the nucleic acids encoding hKCNQ5
 CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression
 CC vectors encoding them, antibodies against them, the use of 3-dimensional
 CC computer modelling to identify molecules that bind to a KCNQ containing
 CC potassium channel and modulate ion flux through the channel. The KCNQ
 CC polypeptide is useful for identifying a compound that increases or
 CC decreases ion flux through a potassium channel expressed in an eukaryotic
 CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when
 CC used in gene therapy) is useful as a pharmaceutical agent for treating
 CC diseases involving abnormal ion flux, such as disorders of the central
 CC nervous system, such as epilepsy, migraines, hearing and vision problems,
 CC psychotic disorders, seizures, learning and memory disorders, stroke and
 CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a
 CC human tissue and the use of a nucleotide sequence of KCNQ5 to search
 CC computer databases to find variants of the sequence which are associated
 CC with disease states, is useful for screening mutations of KCNQ5. The
 CC present sequence is a representative cDNA for hKCNQ5

SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 0 Length: 3071
 Score: 4523.50 Matches: 886
 Percent Similarity: 98.89% Conservative: 1
 Best Local Similarity: 98.77% Mismatches: 1
 Query Match: 99.48% Indels: 9
 DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x AAS14651 (1-3071)

Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAenSerAlaAlaArgGly 20
 Db 10 ATGAAGGATGTGGAGTCGGCCGGGCGAGGCTGTCTGAACCTCGCAGCGCCGAGGCG 69
 Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGly 40
 Db 70 GACGGCTGTCTACTGTGGGACCCCGCGGCCACGCTTGTGGCGGGGCTGGCTG 129
 Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
 Db 130 AGGAGAGCCCGCGGCGCAGAGGCGCCGGATGAGCTGTGGGAGCCCTCTCT 189
 Qy 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAenTyrLeu 80
 Db 190 TACACGAGTAGCCAGAGCTGCCGCGCAAGCTCAAGTACCGCGGGTGCAGAACTACCTG 249
 Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
 Db 250 TACAACTGTGTGGAGAGACCCCGCGCTGCGGTTCATCTACCAACGCTTTCGTTTTCTC 309
 Qy 101 LeuValPheGlyCysLeuLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
 Db 310 CTGTCTTTGGTTGCTTGAATTTTGTCAAGTGTCTTACCATCCCTGAGCAGCACAATG 369
 Qy 121 AlaSerSerCysLeuLeuLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140
 Db 370 GCCTCAAGTTGCCTCTTGAATCTCGAGTTCGTGTATGATTCGTCTTTGGTTGGAGTTC 429
 Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
 Db 430 ATCAATTCGAATCTGGTCTGCGGGTGTCTGTGTTCATATAGAGATGAGGAGGAGACTG 489

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 490 AGGTTTGTCTCGAAGCCCTTCTGTATTATAGATACCAATTGTTCTTATCGCTTCAATAGCA 549
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 550 GTTGTTTCTCGAANAACCTCAGGGTAATATTTTTCACGCTCTGCACCTCAGAACTCTCCGT 609
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 610 TTCTTACAGATCCTCCGCGATGTCGCGATGGACCGAAGGGAGGCACCTTGGAAATTAATCTG 669
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 670 GGTTCAGTGGTTTATGCTTCACAGCAAGGAATTAATCACAGCTTGGTATAGGATTTTGT 729
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 730 GTTCTTATTTTTCGTCTTTCTCTGCTATCTGGTGGAAAGAGATGCCAATAAAGAGTTT 789
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 790 TCTACATATGAGATGCTCTCTGTGGGGGCACAAATTACATTGACAACTATTGGCTATGGA 849
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 850 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCGAGGCTTTGACACTCCTTGGC 909
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 910 ATTCTTTCTTGGCACTTCTCGCCGGCATTTCTTGGCTCAGGTTTTCGATTAAAGATACAA 969
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 970 GAACAAACCCGCCAGAAACACTTTGAGAAAGAGGAACCCAGCTGCCAACTCATTCAG 1029
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1030 TGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1089
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1090 CACTTGAAGGCCCTGCACACCTGCGCCCTACCAAGAAAGAACAGGGGAAGCATCAAGC 1149
Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1150 AGTCAGAGCTAAGTTTTAAGAGCGAGTGGCGATGGCTAGCCCGCAGGGGCCAGAGTATT 1209
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 1210 AAGAGCCGACAAGCCCTCAGTAGTGCACAGGAGGTCCCCAAGCACCGACATCACAGCCGAG 1269
Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1270 GGCAGTCCCAACAAAGTCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGCCC 1329
Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1330 TCGCTCGCCCTCAAAAGTTCTCAGCCCAAAACAGTGATAGATGCTGCACAGCCCTTGGC 1389
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1390 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGATCATCAGTGGAAAGACCTCACC 1449
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1450 CCACCACCTAAACCTGTCTATTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1509
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1510 AAGTTTAAAGAAACCTTACGTCATATGATGTAAAGATGTCATTGAACATATTTCTGCT 1569

Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1570 GGTCACTGGACATGTTGTGTAGAAATTAAGAGCCCTCAAAACACGCTGTTGATCAAAATCTT 1629
Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1630 GGAANAAGGCAATCATCATAGATAGAGAGCGAGAGAAATTAACAGCAGACATCAG 1689
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1690 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1749
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1750 ATAGAAATCCAGCTGGGACTGCTTACTAGACATCTATCAACAGGTCCTTCGAAAAGGCTCT 1809
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 1810 GCCTCAGCCCTCGCTTGGCTTCATTCCAGTTCACCTTTTGAATGTGAACACATCT 1869
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1870 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGACACAAAACAGTGGCTGC 1929
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1930 TTATCCAGATCACTAGTGGCAACATCTCGAGAGGCTTCGAGTTCATTCTCAGCGCAAT 1989
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1990 GAGTTCAGTCCCGAGACTTCTACGCGTTAGCCCTACTATGCACAGTCAGACACACAG 2049
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2050 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2109
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2110 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2169
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2170 GCCATCAAGCATCTGCCCGCAGCCAGAAACTCTGCACCTTAACCTTCGAGGCTTACAGGA 2229
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2230 AGCATTTCTGACGTCACCCACCTGCTTGTTCCTCCAAAGGAAATGTTTCAGGTTGCACAG 2289
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 771
Db 2290 TCAATCTCAAGGACCGGTTCTATAGGAAAAGCTTTTGACATGGGAGGAGAACTCTG 2349
Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2350 TTGTCGTCTGTCCTCATGGTGGCCAGGACTTGGGCAAACTCTTGTCTGTGCAAAACCTG 2409
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2410 ATCAGGTCGACCGAGGAACTGAATATACACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2469
Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG 2529
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2530 GTGGGTCCGGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCTTCGCCAGGAA 2589
Qy 852 AlalaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2590 GCTGCCTTTGCACTCTCTAAGGACTCGAAGGTCACGATCATCTCAGAGCAATTTGT 2649
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888

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Db      2650 AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACACTGAAA 2700
|||||
RESULT 8
AAH49499
ID   AAH49499 standard; DNA; 3074 BP.
XX   AC
XX   AAH49499;
DT   11-DEC-2001 (first entry)
XX   DE
XX   Human KCNQ5 DNA.
KW   KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW   anticonvulsant; excitability modulator; membrane potential; neuron;
KW   voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW   screening; central nervous system disease; cardiovascular disease; ds.
XX
OS   Homo sapiens.
XX
PH   Key Location/Qualifiers
FT   CDS 110..2908
FT   /*tag= a
FT   /product= "KCNQ5"
XX
PN   DE10013732-A1.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2000; 2000DE-01013732.
XX
PR   21-MAR-2000; 2000DE-01013732.
XX
PA   (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
XX   Steinmeyer K, Lerche C, Scherer C, Seebohm G, Busch AE;
PI   P-PSDB; AAB86979.
DR   WPI; 2001-571700/65.
XX
XX   New DNA sequence encoding potassium channel KCNQ5, useful in screening
XX   for specific modulators, potential agents for treating central nervous
XX   system and cardiovascular diseases.
XX
PS   Claim 2a; Page 9-10; 20pp; German.
XX
CC   This invention describes a novel DNA sequence (I) encoding: (i) a
CC   polypeptide (ii) with potassium channel KCNQ5 activity; (ii) a
CC   polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
CC   the invention have neurological, cardiovascular and anticonvulsant
CC   activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC   channel, a key regulator of membrane potential and modulator of
CC   excitability of electrically activated cells such as neurons and
CC   cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC   are used to screen for compounds that modulate the activity of KCNQ5,
CC   potentially useful for treating central nervous system (e.g. epilepsy)
CC   and cardiovascular diseases. This sequence encodes the human potassium
CC   channel KCNQ5 protein described in the invention
XX
SQ   Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 4 Gaps: 1
US-09-810-796-5 (1-888) x AAH49499 (1-3074)
Qy      1 MetIlyAspValGluSerGlyArgGlyValLeuLeuAanSerAlaAlaAargGly 20
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Db      215 ATGAAGGATGTGGAGTCGGGCGGCGGCGAGGTGCTGCTGAACCTCGGCGAGCGCGAGGGGC 274
Qy      21  AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeu 40
Db      275 GACGGCTGTCTACTGTCTGGGCAACCCGCGCGGCCACGCTTGGTGGCGGCGGCGGTGGGCTG 334
Qy      41  ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuLeuGlyLysProLeuSer 60
Db      335 AGGAGAGAGCCCGGCGGCGAGAGCGGCGCGGATGAGCCCTGCTGGAGAGCCGCTCTCT 394
Qy      61  TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAanTyrLeu 80
Db      395 TACACGAGTAGCAGAGCTCGCGCGCAACGCTCAAGTACCGCGGCGGTGCAGAACTACTCTG 454
Qy      81  TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db      455 TACAACGTGTGGAGAGACCCCGCGCTGGCGGTTCATCTACCACGCTTTCGTTTTCTCTC 514
Qy      101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db      515 CTTGTCTTTGGTTGCTTGATTTTGTCACTGTCTTCTACCATCCCTGAGCACACAAAATTG 574
Qy      121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db      575 GCCTCAAGTTGCCTCTTGATCTCGTAGTTCGTGATGATTCGTCTCTTTGGTTTGGAGTTC 634
Qy      141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db      635 ATCATTCGAATCTGGTCTCGGGTGTCTGTGTGATATAGATACCATTTCTTATCGCTTCAATAGCA 754
Qy      161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db      695 AGGTTTGTCTGAAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 754
Qy      181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db      755 GTTGTCTTCTGAAAACCTCAGGGTAATATATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT 814
Qy      201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLeuLeuLeu 220
Db      815 TTCTACAGATCTCCCGCATGGTGGCGATGGACCGAAGGGGAGGACCTTGGAAATTTACTG 874
Qy      221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db      875 GGTTCACTGGTTTATGCTACAGACAGGAATTAATCACAGCTTGGTACATAGGATTTTG 934
Qy      241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAanLysGluPhe 260
Db      935 GTTCTTTATTTTTCGTTCTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 994
Qy      261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db      995 TCTACATATGAGATGCTCTCTGTGGGGGCAAAATTAATTAATTAATTAATTAATTAATTAATTA 1054
Qy      281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db      1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTTCTCAGGCTTTTGCACCTCTCTTGGC 1114
Qy      301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db      1115 ATTTCTTTCTTTCGACTTCTCGCGGCAATTTCTTGGCTCAGGTTTTCATTAATAAGTACAA 1174
Qy      321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAanLeuIleGln 340
Db      1175 GAACAACCGCCGCAAAACACTTTTGAGAAAAGAGAACCCAGCTGCAACCTCATTTTTCAG 1234
Qy      341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
Db      1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA 1294
Qy      361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db      1295 CACTTGAAGGCTTGCACACTCGAGCCCTTACCAGAAAGAACAGAGGGGAGAGCATCAAGC 1354

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QY 372 AenGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db : : : : :
1355 AGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGAGGGGCCAGAGTATT 1414
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db : : : : :
1415 AAGACCCGACAGACCTCAGTAGGTGACAGAGGTCCTCCAGACCCGACATCACAGCCGAG 1474
QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db : : : : :
1475 GGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCGCTTCGGGCC 1534
QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db : : : : :
1535 TCGCTGCCCTCAAAAGTTCTCAGCCAAACCCAGGTAGATGCTGTGACACAGCCCTTGGC 1594
QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db : : : : :
1595 ACTGATGATGATATGATGAAGAGATGCCAGTGTGATGATCATCATGAGTGAAGACCTCAC 1654
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db : : : : :
1655 CCACCACCTAAACCTGCTATTCGAGCTATCAGAAATTATGAATTTTCATGTTGCAAAACGG 1714
QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db : : : : :
1715 AAGTTTAAAGGAACATTAACGTCATATGATGATAAAGATGTCATTTGAACAATATTCTGCT 1774
QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
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1775 GGTCACTCGGACATCTGTGTAGAAATTAAGAGCTTCAACACGCGTTGATCAAAATCTT 1834
QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db : : : : :
1835 GGAAAGGCGCAATCACATCAGATAAGAGAGCGAGAGAAATAAACAGCAGACATCAG 1894
QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
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1895 ACCACAGACGATCTCAGTAGTCTCGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1954
QY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
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1955 ATAGAAATCCAGCTGGATGCTCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 2014
QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db : : : : :
2015 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db : : : : :
2075 GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTCGGGTTCGACACAAAACAGTGGCTGC 2134
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QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
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2255 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2314
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QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db : : : : :
2375 GCCATCAGCATCTGCCCGAGCCAGAAACTCTGCACCCCTAACCTTCGAGGCTTACAGAA 2434
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Db : : : : :
2435 AGCAATTTCTGACGTCACACCTGCCTTGTTCCTCCCAAGGAAAATGTTTCAGGTTGCACAG 2494
QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
Db : : : : :
2495 TCAAAATCTCACAAGGACCGTTCATATGAGGAAAAGCTTTTGACATGGGAGGAGAACTCTG 2554
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db : : : : :
2555 TTGTCTGTCTGTCCATGGTGGCCGAAGGACTTGGGCAAACTCTTTGTCTGTGCAAAACCTG 2614
QY 792 IleArgSerThrGluGluLeuAsnIleGlnIleuSerGlySerGluSerSerGlySerArg 811
Db : : : : :
2615 ATCAGGTCCGACCGAGGAATGAATATACAACTTTTCAGGAGTGAAGTGGCTCCAGA 2674
QY 812 GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu 831
Db : : : : :
2675 GGCAGCCAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTATTAACATGATGAAGAG 2734
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db : : : : :
2735 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCGCACCGCAGCCTGCCAGGAA 2794
QY 852 AlaIlePheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
Db : : : : :
2795 GCTCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAGAGCATTTGT 2854
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db : : : : :
2855 AAGCAGAGGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2905

RESULT 9
ADB78684
ID ADB78684 standard; cDNA; 3074 BP.
XX
AC ADB78684;
DT 04-DEC-2003 (first entry)
XX
DE Human potassium channel subunit mutant cDNA SEQ ID NO:55.
KW ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU0000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
PI
PI Mulvey JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
DR WPI; 2003-239332/23.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
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XX Claim 6; SEQ ID NO 55; 106pp; English.

XX The invention relates to a novel method for identifying a subject predisposed to a disorder associated with ion channel dysfunction. The method comprises ascertaining if at least one of the genes encoding ion channel subunits (IGS) has undergone a mutation event so that a cDNA derived from the subject has any of 134 nucleotide sequences. The method of the invention has nootropic, neuroprotective, inotropic, antipyretic, antiarrhythmic, antimigraine, antidepressant, antiparkinsonian, neuroleptic, tranquilizer, analgesic, nephroretropic, antidiabetic, and ophthalmological activity. A polynucleotide of the invention acts as an ion channel agonist, or ion channel antagonist. The methods, isolated nucleic acids, polypeptides, antibody, selective agonist, antagonist or modulator of an ion channel, cells and genetically modified non-human animal, are useful for the diagnosis and treatment of epilepsy and/or a disorder associated with ion channel dysfunction, such as hyper- or hypokalemic periodic paralysis, myotonias, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety, depression, phobic obsessive symptoms, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, dent's disease, hyperinsulinemic hypoglycaemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour blindness. The present sequence represents a mutant cDNA of the invention. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservative: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 10 Gaps: 1

US-09-810-796-5 (1-888) x ADB78684 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAArgGly 20
DB 215 ATGAAGGATGTGGAGTCGGCGCGGCGAGGTGCTGTGTAACCTCGGACGCCCGCGGCG 274
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 275 GACGCCCTGCTACTCTCTGGCACCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCTG 334
QY 41 ArgGluSerArgArgGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 335 AGGGAGAGCCCGCGGCGCAAGCAGCGGCGCGGCGGATGAGCCTGCTGGGAAGCGCGCTCT 394
QY 61 TyrThrSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
DB 395 TACACGAGTAGCAGAGCTGCGGCGCAACGTCAGTACCGCGCGGTCGCAACCTACCTG 454
QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
DB 455 TACAACGTCGTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCGCTTTGTTTTCTC 514
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrIysLeu 120
DB 515 CTTGTCTTTGGTGTCTGATTTGTCTAGTGTCTTCTACCATCCCTGAGCACACAAAATTG 574
QY 121 AlaSerSerCysLeuLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140
DB 575 GCCTCAAGTGCCTCTGATCCTGGAGTTCGGATGATGTGCTTTGGTTGGAGTTC 634
QY 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrPglnglyArgLeu 160
DB 635 ATCATTCGAACTGTCTGGGGTGTCTGTCTCGATATAGAGGATGCGAAGAGACTG 694

QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 695 AGGTGTGCTCGAAAGCCCTTCTGTATTATAGATACCATTTCTTATCGCTTCAATAGCA 754
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 755 GTTGTCTTCTCAAAAACCTCAGGGTAATATATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT 814
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrPlyLeuLeu 220
DB 815 TTCTACAGATCTCCCGCATGGTGGCATGGACGAAAGGAGGACCTTGGAAATTAATCTG 874
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrPlyIleGlyPheLeu 240
DB 875 GGTTCACTGGTTTATGCTCACAGCAGGAATTAATCACAGCTTGGTACATAGGATTTTG 934
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 935 GTTCTTATTTTTCGTCTTCTTCTGTCTATCTGGTGGAAAGGATGCGCAATAAGAGTTT 994
QY 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
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QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLeuValGln 320
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QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1175 GAACAACACCGCCGCAAGAACACTTTTGAGAAAAGAGAACCCAGCTGCAACCTCATTCAG 1234
QY 341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrPlyPro 360
DB 1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1294
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1295 CACTTGAAGGCTTTCACACTCTGCAGCCCTACCAAGAAAGAACAGGGAGCATCAAGC 1354
QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
DB 1355 AGTCAGAAGCTAAGTTTTAAGGAGCGAGTGCGCATGCTAGCCCGAGGGCGCAGATATT 1414
QY 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
DB 1415 AAGAGCCGCAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCAGCCGACATCACAGCCGAG 1474
QY 412 GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro 431
DB 1475 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCGCTTCGGGCC 1534
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DB 1535 TCGTCTGCGCTCAAAAGTTCTCAGCCAAAACCAAGTGTATGCTGTGACACAGCCCTTGGC 1594
QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
DB 1595 ACTGATGATGATATGATGATAAAGAGTGCAGTGTGATGTATCAGTGGGAAGACCTCACC 1654
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
DB 1655 CCACACTTAAACCTGCTCATTCGAGCTATCAGATTTATGAAATTCATGTTGCAACAGCG 1714
QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
DB 1715 AAGTTTAAAGGAAACATTACGTCATATGATGATAAAGATGTCAATTAACCAATATTCGCT 1774
QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531

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Db 1775 GGTCACTGGACATCTGTGTAGAAATTAAGCCCTTCAACACAGGTGTGATCAAAATCTT 1834
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Db 1835 GGAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACACAGACATCAG 1894
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1895 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGTACAGTCC 1954
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1955 ATAGAAATCAAGCTGAGCTGCTTCTAGACATCTATCAACAGGCTCTTCGGAAGGCTCT 2014
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCACTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 2075 GACTATCAAGGCCCTGTGTAGTACGAAGATCTTTCGGGTTCGGCAAAAACAGTGGCTGC 2134
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCCAGATCACTAGTGGCCAACTCTCGAGAGGCTTCGAGTTCTTCTGACGCCAAT 2194
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTCAAGTCCAGACCTTCTACGGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTAGTCAAAAGGATGGCTTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACAA 2314
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
Db 2315 ATAAATACGGACCCCAAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2374
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2375 GCCATCAAGCATCTGCCAGCCGAGAACTCTGCACCCCTAACCTTCAGGCTTACAGGA 2434
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
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Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
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Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2555 TTGCTGTCTGTCCCATGTCGCGAAGGACTTGGGCAAAATCTTCTCTGTGCAAAACCTG 2614
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
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Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2675 GGCACCCCAAGATTTTATCCCCAAATGGAGGGAAATCCAAATGTTTATTAACATGATGAAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 851
Db 2735 GTGGTCCCGAAGACAGACAGACACACTTTTGTATGCCGACCCGACCTCCAGCGGAA 2794
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
Db 2795 GCTGCTTTTGCATCAGATCTCTAAGGACTGGAAGGTACGATCATCTCAGAGCAATTTGT 2854
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValIleLys 888
```

```
Db 2855 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2905
RESULT 10
AAC64371
ID AAC64371 standard; cDNA; 3718 BP.
XX
AC AAC64371;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
Stargardt-like macular dystrophy; cone-rod macular dystrophy;
Salla disease; ophthalmological; auditory; central nervous system;
cardioactive; anticonvulsant; gastrointestinal; muscular active;
age-related macular degeneration; macular degeneration; deafness;
epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
gastrointestinal disorder; 88.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009587.
XX
PR 14-APR-1999; 99US-0129274P.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
XX
DR WPI; 2000-647417/62.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
inhibitors and activators which can treat e.g. Stargardt-like macular
dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS Claim 3; Fig 2; 99pp; English.
XX
CC The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
which is a voltage-gated potassium channel protein. Human KCNQ5 has
ophthalmological, auditory, central nervous system (CNS), cardioactive,
anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
identifying activators or inhibitors of KCNQ5 protein. These activators
and inhibitors are useful for treating Stargardt-like macular dystrophy,
cone-rod dystrophy, Salla disease, age-related macular degeneration,
other forms of macular degeneration, deafness, epilepsy, and different
forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
chromosome 6q
XX
SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3718
Score: 4346.50 Matches: 850
Percent Similarity: 98.84% Conservativeness: 1
Best Local Similarity: 98.72% Mismatches: 1
Query Match: 95.59% Indels: 9
DB: 3 Gaps: 1

US-09-810-796-5 (1-888) x AAC64371 (1-3718)
Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 93 GGCGTGGCTGAGGAGAGAGCCGCGGCAAGCAGGCGGCGCGGATGAGCTGCTGGGG 152
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
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Db ||||| 153 AAGCGCTCTCTTACAGAGTAGCAGAGCTGCGCGCAACGTCAGTACCGCGGGTG 212
Qy ||||| 77 GlnAsnTyrLeuTyrAsnValLeuGluuArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db ||||| 213 CAGAACTACCTGTACAGCTGCTGAGAGACCCCGCGCTGCGCGTTTCATCTACACGCT 272
Qy ||||| 97 PheValPheLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db ||||| 273 TTCGTTTTCTCTGTGCTTGTGTTGCTGATTTGTTCAGTGTTCATCCATCCCTGAG 332
Qy ||||| 117 HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValPhe 136
Db ||||| 333 CACAAAAATGGCCCTCAAGTTGCTTGTGATCTCTGAGGTTCTGATGATGCTGCTCTT 392
Qy ||||| 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysCysArgTyrArgGlyTyr 156
Db ||||| 393 GGTITGGAGTTTCATCATTCGAATCTGGTCTGCGGTTGCTGTGTCGATATAGAGATGG 452
Qy ||||| 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
Db ||||| 453 CAAGGAAGACTGAGGTTTGCTCGAAGCCCTTCTGTGTATAGATACCATTTGTTTATC 512
Qy ||||| 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db ||||| 513 GCTTCAATAGCAGTTGTTTCTGCAAAAACTCAGGGTAATATTTTGGCCACGCTCTGCATC 572
Qy ||||| 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThr 216
Db ||||| 573 AGAAGTCTCCGTTTCTCTACAGATCTCCGATGGTGGCATGGACCGAAGGGAGGCACT 632
Qy ||||| 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyr 236
Db ||||| 633 TGGAAATTTACTGGGTTTCAAGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTAC 692
Qy ||||| 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db ||||| 693 ATAGATTTTGGTTCTTATTTTTCGTTCTTCTCTGTTCTATCTGCTGGTGGAAAGGATGCC 752
Qy ||||| 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThr 276
Db ||||| 753 AATAAAGAGTTTTCTACATATGAGATGCTCTCTGCTGGGCGACAAATTACATTTGACAACT 812
Qy ||||| 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db ||||| 813 ATTGGCTATGAGACAAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCGAGCTTT 872
Qy ||||| 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db ||||| 873 GCACCTCTTGGCATTTCTTCTTGTGACTTCTGCGGCAATTTCTGGCTCAGGTTTGTGA 932
Qy ||||| 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
Db ||||| 933 TTAAAGTACAAAGAACAACCGCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCC 992
Qy ||||| 337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAla 356
Db ||||| 993 AACCTCATTCAGTGTGTTTGGGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCA 1052
Qy ||||| 357 ThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db ||||| 1053 ACCTGGAAGCCACACTTGAAGCCCTTGACACCTTGACACCTTGACGCGCTTACCAAGAAAGAAAGG 1112
Qy ||||| 372 -----AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArg 387
Db ||||| 1113 GAAGCATCAAGCAGTCAGAGCTAAGTTTTAAGAGCGAGTGGCATGGCTAGCCCCAGG 1172
Qy ||||| 388 GlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAsp 407
Db ||||| 1173 GGCCAGAGTATTAAGAGCCGCAAGCCCTCAGTAGGTGACAGAGGTCCTCCCAAGCACCGAC 1232
Qy ||||| 408 IleThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThr 427

Db ||||| 1233 ATCAAGCCGAGGCGAGTCCCAACAAAGTGCAGAAAGAGCTGGAGCTTCAACAGCCGACCC 1292
Qy ||||| 428 ArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAsp 447
Db ||||| 1293 CGCTTCGGGCCCTCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTGATAGATGCTGAC 1352
Qy ||||| 448 ThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerVal 467
Db ||||| 1353 ACAGCCCTTGGCACTGATGATGATATATGATGAAAGAGTGCAGTAGTGATGTATCAGTG 1412
Qy ||||| 468 GluAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHis 487
Db ||||| 1413 GAAGACCTCAACCCACACCTTAAACCTGTATTCGAGCTATCAGAAATATGAAATTCAT 1472
Qy ||||| 488 ValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGlu 507
Db ||||| 1473 GTTCCAAAACGGAAGTTTAAAGAAACATTAAGTCCATATGATGTAAGAAGATGTCATTGAA 1532
Qy ||||| 508 GlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgVal 527
Db ||||| 1533 CAATATTTCTGCTGCTCATCTGGACATGTGTGTAGAAATTAAGAGCCCTTCAACACAGTGTT 1592
Qy ||||| 528 AspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThr 547
Db ||||| 1593 GATCAAAATTTCTGAAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACA 1652
Qy ||||| 548 AlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLys 567
Db ||||| 1653 GCAGAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGTTGAAANA 1712
Qy ||||| 568 GlnValGlnSerIleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeu 587
Db ||||| 1713 CAGGTACAGTCCATAGAAATCCAAGCTGAGCTGCCTACTAGACATCTATCAACAGGTCCTT 1772
Qy ||||| 588 ArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys 607
Db ||||| 1773 CGGAAAGGCTCTGCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCAACCTTTTGAATGT 1832
Qy ||||| 608 GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln 627
Db ||||| 1833 GAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGCACAA 1892
Qy ||||| 628 AsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIle 647
Db ||||| 1893 AACAGTGGCTGCTTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTCGAGTTCATT 1952
Qy ||||| 648 LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSer 667
Db ||||| 1953 CTGACGCCAAATGAGTTTCAGTGCCAGACTTTCTACGCGCTTAGCCCTACTATGACAGT 2012
Qy ||||| 668 GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThr 687
Db ||||| 2013 CAAGCAACACAGTGGCCATTTAGTCAAAAGCATGGCTCAGCAGTGGCAGCCACCAACACC 2072
Qy ||||| 688 IleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro 707
Db ||||| 2073 ATTGCAAAACCAATAAATACGGCACCCCAAGCAGCAGCCCAACCAACTTACAGATCCCA 2132
Qy ||||| 708 ProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAla 727
Db ||||| 2133 CCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCCCTAACCCCTGCA 2192
Qy ||||| 728 GlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaLeuSerLysGluAsnVal 747
Db ||||| 2193 GGCTTACAGAAAGCATTTCTGAGCTCACCCCTGCTGCTTGTGCTCCAGGAAAATGTT 2252
Qy ||||| 748 GlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGly 767
Db ||||| 2253 CAGTTGCAAGTCAAAATCTCACCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGA 2312
Qy ||||| 768 GlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSer 787
Db ||||| 2313 GGAGAAACTCTGTTGCTGTCTGTCTGTCCTGTCGCGAGGACTTGGGCAATCTTTGTCT 2372

QY 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333
 Db 1042 CGGCTTTGCCCTGAAGTCCAGGAGCAGCAGCGGAGAGCACITTCGAGAAGCGGAGAT 1101
 QY 333 nProAlaAlaLeuLeuGlnCysValTrpArgSerTyrAlaAlaAsp----GluLysSe 352
 Db 1102 GCCGCGACCAACCTCATCCAGGCTGCCTGGCGCTGTACTCCACCGATATGAGCGCGGC 1161
 QY 352 rValSerileAlaThrTrp----- 358
 Db 1162 CTACCTGACGACCACTGGTACTACTATGACAGATATCTCCATCTTCAGAGAGCTGGC 1221
 QY 358 ----- 358
 Db 1222 CCTCTTGTGTGAGCAGTGCACAGCGGCCGCAATGGGGGCTTACGGCCCTTGGAGGTGCG 1281
 QY 359 -----LysProHisLeuLysAlaLeuHisTh 367
 Db 1282 GGGGGCGCGGTACCCGAGGAGCACCTCCCGTTACCCGCGGTGCCACCTGCCACCG 1341
 QY 367 r-----CysSerProThrAsnGlnLysLeuSerPheLysGluArgVa 381
 Db 1342 GCCGGGACGACCTCTCTGCGCTGGGGAAGAGCGCGATGGCATCAAGACCGCAT 1401
 QY 381 lArgMetAlaSerProArgGlyGlnSerileLysSerArgGln-----AlaSerValGl 399
 Db 1402 CCGCATGGGCGAGTCCCGAGCGCGAGCGGTCTTCCAAAGCAGCAGCTGGCACCTCCAAC 1461
 QY 399 yAspArgArgSerProSerThrAspIleThAlaGluGly---SerProThrLysValGl 418
 Db 1462 AATGCCCACTCCCAAGCAGCAGCGAGTGGGTGGAGGCCACCGCCCAAGAGGTGCA 1521
 QY 418 nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSe 438
 Db 1522 AAAGAGCTGGAGCTTCATGACCGCACCGCTTCGGGCATCTCTGAGACTC----- 1573
 QY 438 rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGl 458
 Db 1574 -----AAAGCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGGAAGTAGCAGAGA 1623
 QY 458 uLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIl 478
 Db 1624 GAAGAGCTACAGGTGTGAGCTCAGCGTGGAGCAGCATCATGCTGCTGTGAAGAGAGATCAT 1683
 QY 478 eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuAr 498
 Db 1684 CGCTCCATCAGGATCTCAAGTTCCTGCTGGCCAAAGAAATTCAGGAGAGACACTGCG 1743
 QY 498 gProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCy 518
 Db 1744 ACCGTACGACGTGAAGGACGTCATTGAGCAGTACTCTCAGCAGGCCACCTGGACATGCTGG 1803
 QY 518 sArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSe 538
 Db 1804 CCGGATCAAGAGCTTGCAAACTCGGGTGGACCAATGTGGGTGGGGG-----CCCGG 1857
 QY 538 rAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluThrThrAspAs 555
 Db 1858 GGACAGGAAGCCCGGAGAGAGCGACAGGGGCCCTCCAGCGGAGGTGGTGATGA 1917
 QY 555 pLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLy 575
 Db 1918 AATCAGCATGATGGGACGCGTGGTCAAGGTGGAGAGCAGGTGAGTGCATCGAGACAA 1977
 QY 575 sLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLe 595
 Db 1978 GCTGACCTGCTGTGGGCTCTATTCGCGTCCCTGCGCTGCGACCTCGGCC----- 2032
 QY 595 uAlaLeuAlaSerPheGlnIleProProPheGluCysGlnGlnThrSerAspTyrGlnSe 615
 Db 2033 -AGCCTGGCGCGCGTGAAGTGGCGCTGTTCGACCCGACATCATCTCCGACTACCACAG 2091
 QY 615 rProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSe 635

Db 2092 CCCTGTGGACACGAGGACATCTCGTCTCGCACAGACGCTCAGC---ATCTCCCGCTC 2148
 QY 635 rThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAl 655
 Db 2149 GGTCAAGCACCACATGAGCTGAGG----- 2173
 QY 655 aGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSe 675
 Db 2174 -----ACTTC 2178
 QY 675 rGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAl 695
 Db 2179 TCAGAGGCGGCGAGCACA-----CGGCCAGC 2205
 QY 695 aProLysProAlaAlaProThrThrLeu-GlnIleProProProLeuProAlaIleLysH 715
 Db 2206 CCGCGCGCTGGCGCTCCGACTGCCCTCGGAGCTCCGACTCTCTCGTACTTGAAC 2265
 QY 715 isLeuProArgProGluThrLeuHis 723
 Db 2266 CACTCCCTCAGCGGAGAGAGACCAC 2291
 RESULT 13
 ADS17851
 ID ADS17851 standard; cdna; 5595 BP.
 XX
 AC ADS17851;
 DT 02-DEC-2004 (first entry)
 XX
 DE Rattus norvegicus KCNQ cdna #2.
 XX
 KW KCNQ; potassium channel; anxiety; insomnia; hyper-excitability disorder;
 KW Alzheimer's disease; peripheral neuropathy; neurodegenerative disease;
 KW neuroprotective; anticonvulsant; nootropic; tranquiliser; sedative;
 XX norway rat; gene; ss.
 XX
 OS Rattus norvegicus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1553..4111
 FT /*tag= a
 FT /product= "KCNQ protein"
 XX
 PN US2004175691-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 08-APR-2004; 2004US-00820307.
 XX
 PR 03-DEC-1998; 98US-0110804P.
 PR 03-DEC-1999; 99US-00454868.
 XX
 PA (BROW)/ BROWN B S.
 PA (MCKI)/ MCKINNON D.
 XX
 PI Brown BS, McKinnon D;
 DR WPI; 2004-642119/62.
 DR P-PSDB; ADS17852.
 XX
 PT Evaluating compound for utility in treating neurological disease such as
 PT epilepsy and anxiety, involves contacting compound with cell co-
 PT expressing KCNQ2 and KCNQ3 that form potassium channel, and measuring
 PT activity of potassium channel.
 XX
 PS Disclosure; SEQ ID NO 8; 38pp; English.
 XX
 CC The present invention relates to a method of evaluating a compound for
 CC utility in treating neurological disease. The method involves contacting
 CC a compound with a cell that co-expresses KCNQ2 and KCNQ3, where the KCNQ2
 CC and KCNQ3 form a potassium channel and measuring the activity of the

CC potassium channel. The invention is useful for treating anxiety, insomnia
 CC or other hyper-excitability disorders and Alzheimer's disease, peripheral
 CC neuropathy or other neurodegenerative diseases. The present sequence is
 CC the Rattus norvegicus KCNQ cDNA. This sequence is used to illustrate the
 CC method of invention.

SQ Sequence 5595 BP; 1272 A; 1536 C; 1563 G; 1224 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,42e-143 Length: 5595
 Score: 1810.00 Matches: 416
 Percent Similarity: 59.84% Conservative: 92
 Best Local Similarity: 49.00% Mismatches: 189
 Query Match: 39.81% Indels: 153
 DB: 13 Gaps: 22

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Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
 Db 1652 TCCACTCGCGAGCGCGCTACTCATCGCGGCTCCGAGGCCCCCAAG-----CGC 1702
 Qy 37 GlyGlyGlyLeuArgGlySerArgGlyGlyLeuGlyGlyGlyAlaArgMetSerLeuGly 56
 Db 1703 GGCAGCGTTTGGACGACCGCGGAGCGCGCGCGCGGAGCC-----GGG 1747
 Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
 Db 1748 AAGCCC-----CCAAAGCGCAACGCGCTTCTACCGCAAGCTG 1783
 Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
 Db 1784 CAGAAATTTCCATACAACTGTAGAGCGCGCGCGGTTGGCGGTTTCATCTACCAACGCC 1843
 Qy 97 PheValPheLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlu 116
 Db 1844 TACGTGTTCTTTAGTCTTCTCTGCTTTCCTGCTTTCCTGTTTCCGTTTCCACCATCAAGGAG 1903
 Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValPhe 136
 Db 1904 TATGAGAAGAGTTCGGAAGGGGCCCTTACATCTTTGGAATCGTGACCATCGTGTATTTC 1963
 Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
 Db 1964 GGTGTGTAGTACTTGTGAGAATCTGGGCTGCAGGCTGCTGCGGTATTCGAGGCTGG 2023
 Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
 Db 2024 AGGGGCGCGCTCAAGTTTCCAGGAAGCCATTCGTGTGATCGACATCATGTGCTGATT 2083
 Qy 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
 Db 2084 GCCTCCATTGCTGCTGGCTGCTGGCTCCAGGGCAATGTCTTTGCTACGCTGCACTT 2143
 Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216
 Db 2144 CGGAGCTTGGGTTCTTCAAAATCTTACGGATGATCCGTTATGGACCGGAGGGCGGCACC 2203
 Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
 Db 2204 TGGAGCTCTCGGATCGGTGCTGTACCTTCACAGCAAGGAGCTGTGACTGCTGGTGTAC 2263
 Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
 Db 2264 ATTGGCTTCTCTGCTCATCTGCGCTTCTGCTGTTCTGTTGTTACTTGGCAGAAAAGGTGAG 2323
 Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276
 Db 2324 AATGACCACTTCGACACCTTACCGGATGCACTCTGGTGGGTCTGTATCACCTCGACAACC 2383
 Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlyValArgLeuLeuSerAlaGlyPhe 296
 Db 2384 ATTGGCTACGGGGAAGAAGTACCTCAGACCTGGAACGGGAGGCTGTGTAGCGGACGCTT 2443

Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
 Db 2444 ACCCTCATTTGGTGTCTCATTTCTCGCTTCTCTGCTGGCATTTTGGGATCGGCTTTGCC 2503
 Qy 317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAla 336
 Db 2504 CTGAAGTCCAAGAGCAGCATCGCAAAACACCTTTGAGAAACGCGCGGATCTCTGCGGCA 2563
 Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIle--- 355
 Db 2564 GGTCTGATCCAGTCTGCTGAGATTCTATGCTACTAACTCTCACGACCGACCTGCAC 2623
 Qy 356 AlaThrTrpLys----- 359
 Db 2624 TCCACGTGGCAGTACTACGAGCGGACAGTCACGTGTCCTCCCATGATCAGCTCACAACCTCAA 2683
 Qy 360 -----ProHisLeuLysAlaLeuHisThrCys----- 368
 Db 2684 ACCTATGGGCTCCAGACTCATTCGCTCTGACAGCTGGAGATGCTCAGGAAATCTC 2743
 Qy 369 -----SerProThrAsn 372
 Db 2744 AAGAGCAAACTCGSACTCACCTTCAGGAAGGAGCCACAGCCAGAGCCATCACCA---AGT 2800
 Qy 373 GlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLys 392
 Db 2801 CAGAAGTTCAGTTTGAAGATCGTGTCT---TTCCTCCAGCCCCGAGGCGTGTGCCCAAG 2857
 Qy 393 SerArgGlnAlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAla 410
 Db 2858 GGGHAGGGGTCTCCAGGCGCCAGACCGTCCGCGGTCTCCCGAGTGGGATCAGAGTCTC 2917
 Qy 411 GluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArg 430
 Db 2918 GATGACAGCCCAAGCAAGGTGCCCCAGAGCTGGAGCTTTGGTGACCGCAGCGTGCACGC 2977
 Qy 431 ProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeu 450
 Db 2978 CAGGCTTTCGTATCAAGGCGCTGCATCCCGGAGCAACTCAGAAAGCAAGGCTCCCT 3037
 Qy 451 GlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeu 470
 Db 3038 GGGGAGGATATCTGTGGAGGACACAGAGCTGTAACTCGGAGTTGTGACTGAAGATCTT 3097
 Qy 471 ThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLys 490
 Db 3098 ACCCTCGGCTCAAAGTCAGCATCAGAGCTGTGTGTGTATGCGGTTCTTGTATCTAAG 3157
 Qy 491 ArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSer 510
 Db 3158 CGAAAGTTCAAAGAGAGTCTCGGCCCATATGACGTGATGGATGTCTCGAACAGTACTCG 3217
 Qy 511 AlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIle 530
 Db 3218 GCCGACACTTGGATATGTTGTCCCGATCAAGAGCTGCTGAGTCCAGAGTGGACAGATT 3277
 Qy 531 LeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHis 550
 Db 3278 GTGGGGCGGGCCCGCAACAATAACGGAC---AAGGACCGCACCAAGGCCCCGAGGAGCG 3334
 Qy 551 GluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGln 570
 Db 3335 GAATCGCCGAAGAGCCCGACATGATGGAGCGCTTGGGAAGGTTGGAAAAACAGGCTCTTG 3394
 Qy 571 SerIleGluSerLysLeuAspCysLeuAspIleTyrGlnGlnValLeuArgLysGly 590
 Db 3395 TCCATGGAAGAGAGCTAGACTTCTGTGTAGCATCTACACAGC-----AGATGGGC 3448
 Qy 591 SerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys----- 607
 Db 3449 -----ATCCCAACGAGCAGACAGAGGCGCTAT 3475

Db 2301 GCGGACGACGACAGCTCCATCTCCATCCCGTCCGCTG-----GACCACGAGGAGCTGGA 2354
 Qy 799 nileGlnLeuSerGlySerGlnSerGlySerGlySerGlnAsp----- 815
 Db 2355 GGGTCTTTCAGCGGCTTCAGCATCTCCAGTCCCAAGAGAACCTGGATGCTTCAACAG 2414
 Qy 816 -PheTyrPro-LysTyrArg-----GlnSerLysLeuPheIleThrAspGluGluV 832
 Db 2415 CTGCTACCGCGCGTGGCGCTTGTGCCAAGTCAAGCCCTACATGCGGAGGAGATC 2474
 Qy 832 alGlyProGluGluThrGluThrAspThrPheAsp----- 843
 Db 2475 AGACACCGACTCCGACCTCTGTACCCCGTGTGCGGCGCCCGCCACGCTCGGCCACCGCGGA 2534
 Qy 844 -----AlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerA 857
 Db 2535 GGGTCCCTTGTGTAGTGGCTGGCGCGGCCAGGAAGTGAAGCGCGCTGGGC----- 2590
 Qy 857 spSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGly 874
 Db 2591 -----CAGTGGACCGCGCGCGCTCTCTCAGCACGGTGTCTCCGAGGT 2635

RESULT 15

ADB78685
 ID ADB78685 standard; cDNA; 7407 BP.

AC ADB78685;

DT 04-DEC-2003 (first entry)

XX Human potassium channel subunit mutant cDNA SEQ ID NO:56.

XX ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipruritic; antiarrhythmic; antimigraine;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.

OS Synthetic.

OS Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

PA (WALL/) WALLACE R. W.

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.

XX Claim 6; SEQ ID NO 56; 106pp; English.

XX The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipruritic,
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,

CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant cDNA of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 7407 BP; 1353 A; 2329 C; 2355 G; 1370 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.: 4.73e-142 Length: 7407
 Score: 1797.00 Matches: 411
 Percent Similarity: 60.66% Conservative: 101
 Best Local Similarity: 48.70% Mismatches: 182
 Query Match: 39.52% Indels: 151
 DB: 10 Gaps: 22

US-09-810-796-5 (1-888) x ADB78685 (1-7407)

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 Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuGly 56
 Db 193 GGCAGCATCTCTCAGCAAACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
 Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
 Db 238 AAGCCC-----CCCCAGCGCAACGCCCTTCTACCGCAAGCTG 273
 Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
 Db 274 CAGAAATTCCTTACACAGTGTGGAGCGCGCGCGCTGGGGGTTCATCTACACGCC 333
 Qy 97 PheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlu 116
 Db 334 TACGTGTTCCTCTGTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393
 Qy 117 HistHrLysLeuAlaSerSerCysLeuLeuLeuLeuPheValMetIleValValPhe 136
 Db 394 TATGAGAAGAGCTCGGAGGGGGGCTCTACATCTGGAAATCGTGACTATCGTGGTGT 453
 Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
 Db 454 GCGTGGAGTACTTCGTGCGGATCTGGCGCGAGGCTGCTGCTGCTGCTGCTGCTG 513
 Qy 157 GlnGlyArgLeuArgPheAlaArgLysPropheCysValIleLeuSerThrIleValLeu 176
 Db 514 AGGGCGCGCGCTCAAGTTTGGCCGAAACCGTCTCTGTGTGATTGACATCATGTGCTCATC 573
 Qy 177 AlaserIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
 Db 574 GCCTCCATTCGGTGTGCGCGCGCTCCAGGGCAACGCTCTTGGCACATCTGCCCTC 633
 Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216
 Db 634 CGGAGCGTGGCTTCTCTGCGAGATTCGCGGATGATCGCATGATCGCGCGGGGAGGCC 693
 Qy 217 TrpLysLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyr 236

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 06:46:36 ; Search time 1190.47 Seconds
(without alignments)
4514.709 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547

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Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 4547 | 100.0 | 2667 | 9 | US-09-810-796-3 |
| 2 | 4547 | 100.0 | 2772 | 9 | US-09-825-147-1 |
| 3 | 4547 | 100.0 | 2772 | 18 | US-10-803-268-1 |
| 4 | 4547 | 100.0 | 3111 | 9 | US-09-825-147-3 |
| 5 | 4547 | 100.0 | 3111 | 18 | US-10-803-268-3 |
| 6 | 4527.5 | 99.6 | 2694 | 9 | US-09-866-020-1 |
| 7 | 4527.5 | 99.6 | 2694 | 9 | US-09-810-796-2 |
| 8 | 4527.5 | 99.6 | 2694 | 9 | US-10-948-493-1 |
| 9 | 4527.5 | 99.6 | 3137 | 18 | US-10-661-629-1 |
| 10 | 4523.5 | 99.5 | 3071 | 9 | US-09-810-796-1 |
| 11 | 4513.5 | 99.3 | 3074 | 9 | US-09-813-148-1 |
| 12 | 2007.5 | 44.1 | 2335 | 17 | US-10-353-690-55 |
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| 14 | 1810 | 39.8 | 5595 | 18 | US-10-820-307-8 |
| 15 | 1797 | 39.5 | 7411 | 18 | US-10-335-053-6 |
| 16 | 1797 | 39.5 | 7420 | 17 | US-10-295-027-281 |
| 17 | 1797 | 39.5 | 7420 | 18 | US-10-843-795A-75 |
| 18 | 1797 | 39.5 | 7420 | 19 | US-10-948-518-75 |
| 19 | 1797 | 39.5 | 7863 | 15 | US-10-084-817-335 |
| 20 | 1794 | 39.5 | 3237 | 16 | US-10-096-578-95 |
| 21 | 1792.5 | 39.4 | 3287 | 13 | US-10-128-870-19 |
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| 26 | 1788 | 39.3 | 3232 | 15 | US-10-345-680-16 |
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| 31 | 1611 | 35.4 | 1848 | 18 | US-10-744-796-5 |
| 32 | 1604 | 35.3 | 1878 | 18 | US-10-744-796-3 |
| 33 | 1602 | 35.2 | 1932 | 18 | US-10-744-796-1 |
| 34 | 1587.5 | 34.9 | 2565 | 13 | US-10-131-685-26 |
| 35 | 1587.5 | 34.9 | 2565 | 14 | US-10-131-685-26 |
| 36 | 1587.5 | 34.9 | 2755 | 18 | US-10-820-307-4 |
| 37 | 1587.5 | 34.9 | 2914 | 16 | US-10-096-578-6 |
| 38 | 1550.5 | 34.1 | 2814 | 16 | US-10-096-578-90 |
| 39 | 1547.5 | 34.0 | 2766 | 18 | US-10-820-307-6 |
| 40 | 1495.5 | 32.9 | 4596 | 18 | US-10-723-860-7636 |
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| 43 | 1226.5 | 27.0 | 1425 | 10 | US-09-873-319-313 |
| 44 | 1226.5 | 27.0 | 1425 | 16 | US-10-116-712-662 |
| 45 | 1207.5 | 26.6 | 900 | 13 | US-10-128-870-5 |

ALIGNMENTS

RESULT 1

US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; OTHER INFORMATION: human outwardly rectifying, voltage-gated
;
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
;
; NAME/KEY: CDS
;
; LOCATION: (1)..(2667)
;
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

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Alignment Scores:

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| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-810-796-5 (1-888) x US-09-810-796-3 (1-2667)

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| Qy | 21 | AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu | 40 |
| Db | 61 | GAAGGCTCTACTGCTGGCACCCGCGCGGCCACGCTGTGTGGCGGGCGGTGACCTG | 120 |
| Qy | 41 | ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 |
| Db | 121 | AGGGAGAGCGCGGGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGGAGACCGCTCTCT | 180 |
| Qy | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu | 80 |
| Db | 181 | TACACGAGTAGCACAGAGCTGGCGGGCAACGCTCAAGTACCGGGGGTGCAGAACTACCTG | 240 |
| Qy | 81 | TyrAsnValLeuGluArgProArgGlyTrrAlaPheIleTyrHisAlaPheValPheLeu | 100 |
| Db | 241 | TACACGCTGTGGAGAGACCCCGGGCTGGCGCTTCATCTACACGCTTTCGTTTTCTTC | 300 |
| Qy | 101 | LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu | 120 |
| Db | 301 | CTTGTCTTTGGTGTCTGATTGTGTCAAGTGTTCACCATCCTGAGCACACAAATTTG | 360 |
| Qy | 121 | AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 |
| Db | 361 | GCCTCAAGTGTGCTCTTATCTGGAGTTCGTGAAGATTGTGCTTTTGGTTTGGAGTTCT | 420 |
| Qy | 141 | IleIleArgIleTrrSerAlaGlyCysCysArgTyrArgGlyTrrGlnGlyArgLeu | 160 |
| Db | 421 | ATCATTCGAATCTGTGCTCGGGTTGCTGTTCGATATAGAGATGGCAAGGAAGACTG | 480 |
| Qy | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 |
| Db | 481 | AGGTTTGTCTGAAAGCCCTCTGTGTATATAGATACCATTTCTTATCGCTTCAATAGCA | 540 |
| Qy | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 |
| Db | 541 | GTTGTTCTGCAAAAACCTCAGGGTAATATTTTTGCCAGCTCTGCATCAGAGCTCCCGT | 600 |
| Qy | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu | 220 |
| Db | 601 | TTTCTACAGATCCTCCGCATGTGTCGATGACCGAAGGGGAGGCACCTTGAAATTTTACTG | 660 |
| Qy | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu | 240 |
| Db | 661 | GGTTTCAGTGGTTATGTCTCACAGCAAGAAATTAAATCAAGCTTGGTACATAGAGATTGTTG | 720 |
| Qy | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| Db | 721 | GTTCTTAATTTTTTCGCTTCTCTGTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT | 780 |
| Qy | 261 | SerThrTyrAlaAspAlaLeuTrrPtdGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 |
| Db | 781 | TCTACATATGAGATGCTCTCTGGTGGGGCAATTACATTGACAACTATTTGGCTATGGA | 840 |

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Qy 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProAspProGlu 720
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Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrCysLeu 740
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Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2221 GTTGCTCCAAAGGAAATGTTTCAGGTTGCACAGTCAAAATCTCACCAAGGACCGTTCTATG 2280
Qy 761 ArgLysSerPheAspMetGlyGlyGlnThrLeuLeuSerValCysProMetValProLys 780
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RESULT 2

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US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIORITY FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIORITY FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; ORGANISM: homo sapiens
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Score: 4547.00 Matches: 888
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Best Local Similarity: 100.00% Mismatches: 0
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US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)

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Db 166 GACGGCTGTCTACTGCTGGGCACCCGGCGGCCACGCTCGGTGGCGCGGGTGGCGCTG 225
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGAGAGCCCGCGGGCAAGCAGGGGGCCGGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTAGCAGAGCTGCCGGCGGACGTCAGGTACCGCGGGTGCAGAACTACCTG 345
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACAACCTGTGTGAGAGACACCCCGGCTGGGGCTTCTATACACACGCTTTCGTTTTCTC 405
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTTGCTCTTGGTCTCTGATTTTGTCAAGTGTCTGATGATGTCGTCTTTGGTGGAGTTC 465
Qy 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTTGCCCTTGTATCTCGAGTTCGTGATGATGTCGTCTTTGGTGGAGTTC 525
Qy 141 IleIleArgLefTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 526 ATCATTGCAATCTGCTCTGGGGTGTGTTGTTCGATATAGAGGATGCAAGGAAGACTG 585
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTTGTGCGAAAGCCCTTCTGTATTATAGATACCATTTGTTTATCGCTTCAATAGCA 645
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTGTTCTGCAAAACCTCAGGGTAAATATTTTCCAGCTCTGCACCTCAGAACTCCGT 705
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220
Db 706 TTCTACAGATCTCTCCGTCATGTCGCGATGACGACGAGGGGAGGCACCTTGAAATTA 765
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 766 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATACAGCTTGGTACATAGGATTTT 825
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGAGATGCTCTCTGTTGGGGCACAATTAACATTGACAACTATTGGCTATGGA 945
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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Db 946 GACAAACTCCCTAACTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACATCTCTTGGC 1005
Qy 301 lIeSerPhePheAlaLeuProAlaGlyLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCCTTTTGGCACTTCTCCCGCGCATCTTGGCTCAGGTTTGGCAATTAAGATACAA 1065
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAACAACACCGCCAGAAACACTTTGAGAAAGAGAACCCAGCTGCCAACCCTCATTCAG 1125
Qy 341 CysValTrpArgSerTyAlaAlaAspGluLysSerValSerIleAlaLathTrpLysPro 360
Db 1126 TGTGTTTGGCGTAGTTACGCACTTGCACCTTGCAGCTTACCAATCAGAAGCTAAGTTTAAAGAGCGA 1245
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1186 CACTTGAAGGCTTTCACACCTTGCAGCTTGCAGCTTACCAATCAGAAGCTAAGTTTAAAGAGCGA 1245
Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1246 GTGGCATGGCTAGCCCCAGGGCCAGAGATTAAGAGCCGACCAAGCCTCAGTAGGTGAC 1305
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1306 AGGAGGTCCCCAAGCAGCCGACATCACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGC 1365
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1366 TGGAGCTTCAAGCAGCAACCGCTTCCGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCGCA 1425
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyAspGluLysGly 460
Db 1426 AAACCAAGTATAGATGCTGACACAGCCCTTGGCACTGATGATGATATATATGATGATAAAGGA 1485
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
Db 1486 TGCCAGTGTGATGATCATGTAGTGGAGACCTACCCACCACCTTAAACACTGTCTATTCGAGCT 1545
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1546 ATCAGATATATGAATTTTCATGTTGCAAAACGGAAGTTTAAGAAACATTAACGTCCATAT 1605
Qy 501 AspValLysAspValIleGluGlnTySerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1606 GATGTAAAGATGTCATTGAACAATATCTGCTGCTCATCTGGACATGTTGTGTAGAAAT 1665
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1666 AAAAGCCCTTCAACACACGTTGATCAAAATCTTGGAAAAGGGCAAAATCACATCAGATAAG 1725
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCCGAGAGAAATTAACAGCAGACATGAGACCAACAGATCTCAGTATGCTCGT 1785
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1786 CGGGTGGTCAAGGTGAAACACAGTACAGTCCATAGAAATCAAAGTGGACTGCTACTA 1845
Qy 581 AspIleTyArgGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuSerPhe 600
Db 1846 GACATCATATCAACAGGCTCTTCGGAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCATTC 1905
Qy 601 GlnIleProPheGluCysGluGlnThrSerAspTyArgGlnSerProValAspSerLys 620
Db 1906 CAGATCCACCTTTGATGTGACAGACATCTGACTATCAAGCCCTGTGGATAGCAAA 1965
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 1966 GATCTTTCGGGTTCCGACAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACCAATC 2025
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyAla 660
Db 2026 TCGAGAGCCCTGCAGTTTCATCTGACGCCAAATGAGTTTCAGTGGCCAGACTTTCTACGGC 2085

Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2086 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAGAGTGGCTCA 2145
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2146 GCAGTGGCAGCCACCAACACCATTTGCAACCAATTAATACGGCACCCACAGCAGGCC 2205
Qy 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2206 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2265
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
Db 2266 ACTCTGCACCTTAACCTGAGGCTTACAGAAAGCAATTTCTGACGTACCACTGCTCTT 2325
Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2326 GTTGCCTTCCAAGGAAATGTTTCAGTTTGCAGTCAAAATCTCACCAAGGACCGTTCTATG 2385
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2386 AGGAAAGCTTTGACATGGGAGGAGAACTCTGTGTCTGTCTGTCTGCCATGTCGCGAAG 2445
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2446 GACTTGGGCAATCTTTGTCTGTGCAAACTGATCAGGTGCGACCGAGAACTGAATATA 2505
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyProLysTrp 820
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Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2566 AGGGAATCCAATTTGTTTATACTGATGAAGAGTGGTCCCGAAGAGACAGACAGAC 2625
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2626 ACTTTGATGCGCAGCCAGCTGCGCAGGAGAGTGCCTTTGCATCAGACTCTCTAAGG 2685
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2686 ACTGGAAGTCCAGATCATCTCAGAGCATTTGTAAGGAGGAGAAAGTACAGATGCCCTC 2745
Qy 881 SerLeuProHisValLysLeuLys 888
Db 2746 AGCTTGCTCATGTCAAACTGAAA 2769

RESULT 3

US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

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; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-1 (1-2772)

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Db 106 ATGAAGGATGTGGAGTCGGCGCGGCAAGGTGCTGCTGAACTCGGAGCGCGCAGGGGC 165
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 166 GACGGCTCTGCTACTGCTGGGACCCGCGCGCCACGCTCGGTGGCGCGGGTGGCGCTG 225
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGGAGAGCCCGCGGGCAAGCAGCGCGCGCCACGCTCGGTGGGGAAGCCGCTCTCT 285
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTACGACAGCTGCGCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 345
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACACGCTGCTGGAGACCCCGCGCTGGCGGCTTCATCTACCAACGCTTCGTTTTCTC 405
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTGTGCTTTGGTGTGATTTGTGAGTGTTCAGTGTTTTCTACCATCCCTGAGCACACAAAATTG 465
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTGTCTTCATCTCGAGTTCGTGATGATGTCGTCCTTTGGTTGGAGTTC 525
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 526 ATCATTCGAATCTGCTCTGCGGGTGTGCTGATATAGAGGATGCAAGGAAGACTG 585
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTTGTCTGAAAGCCCTTCGTGTTATAGATACCATTTGTTTCCTTCATAGCA 645
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTTCCTGCAAAACCTCAGGGTAATATTTTGGCAGCTGCTGCACTCAGAACTCCGT 705
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 706 TTCCTACAGATCTCCGCGATGTCGCGCATGAGCCGAGGGGAGGCACATTGAAATTAATCTG 765
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 766 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTCATAGGATTTTGT 825
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTTATTTTTCTCTTCCTCTCTCTATCTGGTGGAAAGGATGCCAATAAGAGTTT 885
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGCAGATGCTCTCTGCTGGTGGGCAATTAATTACATTGACAACTATTGGCTATGGA 945
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300

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Db 946 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACACTCCTTGGC 1005
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTTCTTTTGCACTTCTCGCGGCATTTCTTGGCTCAGGTTTGTGATTAAGATGACA 1065
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAACACACCGCCAGAAACACTTTTGAGAAAAGAAAGAACCCAGCTGCCAACCCTCATTCAG 1125
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1126 TGTGTTTGGCTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1185
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1186 CACTTGAAGGCTTTGCACACCTGCAGCCCTACCAATCAGAAGCTTAAGTTTTTAAGAGAGCA 1245
Qy 381 ValArgMetAlaSerProArgGlyGlnSerLysSerArgGlnAlaSerValGlyAsp 400
Db 1246 GTGGCATGGCTAGCCCGGCGCCAGAGTATTNAGAGCCGCAAGCCTCAGTAGGTGAC 1305
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1306 AGGAGTCCCCAGACCGACATCACAGCCGAGGCGAGTCCCAACAAAGTCGAGAAGAGC 1365
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1366 TGGAGCTTCAACGACCGAAACCGCTTCGGGCCCTCGCTGGCGCTCAAAAGTTCTCAGCCA 1425
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1426 AAACAGTGTAGATGTCACAGCCCTTGGCACTGATGATGATATGATGATGATAAAGAGA 1485
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
Db 1486 TGCCAGTGTGATGTATCAGTGGAGACCTCACCCACCACCTTAAACACTGTTCATTCGAGCT 1545
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1546 ATCAGAATTATGAAATTTCTATGTTGCAAAACGGAAGTTTAAAGAAACATTAACGTCATAT 1605
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1606 GATGTAAAGATGTCATTGAACAAATTTCTGCTGTCATCTGGACATGTTGTGTAGAAAT 1665
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1666 AAAGACCTTCAACACACGCTGTTGATCAATTTCTGGAAAAGGGCAATCACATCAGATAAG 1725
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCCGAGAGAAAATAACAGCAGAGACATGAGACCACAGACGATCTCAGTATGCTCGGT 1785
Qy 561 ArgValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1786 CGGTGTGTCAAGTTGAAAACACAGTACAGTCCATAGATAATCCAAGCTGGAATGCTGCTACTA 1845
Qy 581 AspileTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1846 GACATCTATCAACAGGTCCTTCGGAAGGCTCTGCCTCAGCCCTCGCTTGTGCTTCATTC 1905
Qy 601 GlnIleProPhePheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1906 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGTGATAGCAAA 1965
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 1966 GATCTTTGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTAGCCCAATC 2025
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2026 TCGAGAGCCCTGCGATTCATTTCTGACGCCAAATGAGTTCACTGCGCCAGACTTTCTACGG 2085

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QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
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QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
DB 2146 GCAGTGGCAGCCACCAACACCATTCGAAACCAATAAATACGGCACCCCAAGCCAGCAGCC 2205
QY 701 ProThrThrLeuGlnIleProProProProProProAlaIleLysHisLeuProArgProGlu 720
DB 2206 CCAACAACCTTACAGATCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2265
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
DB 2266 ACTCTGACCCCTTAACCTTCGAGCTTACAGGAAGCAATTCGTGAGTCCACCATCTGCCCT 2325
QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
DB 2326 GTTGCTCCAAAGAAATGTTTCAGGTTGCACAGTCAAAATCTCACCAAGGACCGTTCTATG 2385
QY 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
DB 2386 AGGAAAGCTTGTACATCGGAGGAGAAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 2445
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
DB 2446 GACTTGGGCAAACTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2505
QY 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
DB 2506 CAACCTTCAGGGAGTGAGTCAAGTGGCTCCAGAGGCGAGCAAGATTTTATCCCAATGG 2565
QY 821 ArgGluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAsp 840
DB 2566 AGGGAATCCAAATGTTTATTAACATGATGAAGAGTGGGTCCCGAAGACAGACAGACAGAC 2625
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
DB 2626 ACTTTGATGCGCACCCGAGCTGCCAGGAGTGGCTTGTGATCAGATCTCTTAAG 2685
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
DB 2686 ACTGGAAGGTCAACGATCATCTCAGAGCATTTGTAAGGCGAGGAGAAAGTACAGATGCCCTC 2745
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RESULT 4

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US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
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; ORGANISM: homo sapiens

US-09-825-147-3

Alignment Scores:

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Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-810-796-5 (1-888) x US-09-825-147-3 (1-3111)

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QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 225 GACGGCTGTCTACTGTGGGCACCCGCGGCCACGCTCGGTGGCGGCGGTGGCTG 284
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 285 AGGAGAGCCCGCGGGCAAGCAGGGGGCCGGATGAGCCTGTGCTGGGGAGGCCGCTCTCT 344
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 345 TACACAGAGTGGCAGACTGCGCGCGCAACGTCAAGTACCGCGGGGTGCAGAACTACCTG 404
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 405 TACAACGTGTGGAGAGACCCCGCGCTGGCGGTTCATCTACCAACGCTTTCGTTTTCTC 464
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 465 CTTGTCTTTGGTGTGATTTTGTACAGTGTCTTCTACCATCCCTGAGCAGCAAAAATTG 524
QY 121 AlaSerSerCysLeuLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 525 GCCTCAAGTGGCTTCTGTGATCTGGAGTTGTGTGATGATGTGTCTTTGGTTGGAGTTC 584
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 585 ATCATTGCAATCTGGTCTGGGGTGTGTGTGTGATATAGAGGATGCAAGGAAAGACTG 644
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
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QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
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Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTriPlysPro 360
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Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrIleGlnLysLeuSerPheLysGluArg 380
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Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1305 GTGGCATGGCTAGCCCCAGGGGCCAGAGTATTAAAGCCGACCAAGCCTCAGTAGGTGAC 1364
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
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Qy 421 TrpSerPheAenAspArgThrArgPheArgProSerIleuArgLeuLysSerSerGlnPro 440
Db 1425 TGGAGCTTCAACGACCGAACCCGCTTCGCGCCCTCGCTGCGCCCTCAAAAGTTCTCAGCCA 1484
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1485 AAACAGTGATAGATCTGACACAGCCCTTGGCACTGATGATGATATATGATGATAAGAAAGGA 1544
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
Db 1545 TGCCAGTGTGATGATCAGTGGAGACCTCACCCACCACCTTAAACATGTCATTCGAGCT 1604
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1605 ATCAGAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAACATTAACGTCCATAT 1664
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1665 GATGTAAAGATGTCATTGAAACATATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAAT 1724
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1725 AAAAGCCTTCAACACACGTTGATCAAAATTTCTGGAAAAGGGCAATCAACATCAGATAAG 1784
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACACACAGACGATCTCAGTATGCTCGGT 1844
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1845 CGGTGGTCAAGTTGAAAAACAGGTACAGTCCATAGAAATCAAGCTGGAGTGGCTACTA 1904
Qy 581 AsplIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1905 GACATCTATCAACAGGTCTCTCGGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCATTC 1964
Qy 601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCCAACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAA 2024
Qy 621 AspLeuSerGlySerAlaGlnAAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTTTGGGTTCGGCAAAACAGTGGCTCTTATCCAGATCAACTAGTGGCCAAATC 2084
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAenGluPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGGCTGCAGTTCTATCTGACGCCAAATGATGTTTCAGTGGCCAGACTTTCTACGG 2144
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680

Db 2145 CTTAGCCCTACTATGCAAGTCAAGCAACACAGGTGCCAATAGTCAAAAGCGATGGCTCA 2204
Qy 681 AlaValAlaAlaThrAenThrIleAlaAAsnGlnIleAenThrAlaProLysProAlaAla 700
Db 2205 GCACTGGCAGCCACCAACCATTTGCAAAACCAATATAATACGGCACCCCAAGCAGCACC 2264
Qy 701 ProThrThrLeuGlnIleProProLeuProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2265 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCGCAGAA 2324
Qy 721 ThrLeuHisProAenProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
Db 2325 ACTCTGACCCCTAACCTTGCAGGCTTACAGAAAGCATTTCTGACGTCACCACTGCTCTT 2384
Qy 741 ValAlaSerLysGluAAsnValGlnValAlaGlnSerAAsnLeuThrLysAspArgSerMet 760
Db 2385 GTTCCCTCCAAGGAAATGTTACAGTTCAGTTCGACAGTCAAACTCTCACCAAGGACCGTTCTATG 2444
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2445 AGGAAAAAGCTTTGACATGGGAGGAGAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 2504
Qy 781 AspLeuGlyLysSerLeuSerValGlnAAsnLeuIleArgSerThrGluGluLeuAAsnIle 800
Db 2505 GACTTGGGCAATCTTTGCTGTGCAAAACCTGATCAGTCCAGCGAGAACTGTAATATA 2564
Qy 801 GlnLeuSerGlySerGlySerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
Db 2565 CAACCTTTCAGGAGTGTGATCAAGTGGTCCAGAGGCGAGCAAGATTTTATCCCAAAATGG 2624
Qy 821 ArgGluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAsp 840
Db 2625 AGGGAATCCAAATTTGTTTATAACTGATCAAGAGTGGTCCCGAAGACAGACAGACAGAC 2684
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2685 ACTTTGATGCGCAGCCGAGCTGCCAGGAGTGCCTTTGTCATCAGACTCTCTAAGG 2744
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2745 ACTGGAAGGTCAACGATCATCTCAGAGCATTTGTAAGCGAGGAGAAAGTACAGATGCCCTC 2804
Qy 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGCCTCATGTCAAACTGAAA 2828

RESULT 5
US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA

i ORGANISM: homo sapiens
US-10-803-268-3

Alignment Scores:

Pred. No.: 0 Length: 3111
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-3 (1-3111)

Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAasnSerAlaAlaalaArgGly 20
Db 165 ATGAGGATGTGAGTCCGGCCGGGCGAGGTCGTGTAACCTCGGAGCCGCCAGGGGC 224
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGCTACTGCTGGCACCCCGCGCCACGCTCGGTGGCGCGGGTGGCTG 284
Qy 41 ArgGluSerArgArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 285 AGGAGAGCCGCGGGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGAAGCCGCTCTCT 344
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 345 TACAGAGTACCCAGAGCTGCGGCGCAACGTCAAGTACCGGGGTGCAGACTACCTG 404
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheileTyrHisAlaPheValPheLeu 100
Db 405 TACACGTGCTGGAGAGACCCCGCGCTGGCGCTTCACTACACGCTTTCGTTTTCTC 464
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTGTGCTTGGTGTGATTTGTCAGTGTTCACCATCCCTGAGCACACAAAATTG 524
Qy 121 AlaSerSerCysLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTGTCTCTGATCCTGGAGTTCGTGATGATGTCGCTTGTGGAGTTC 584
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 585 ATCAATGAAATCTGCTGCGGGTGTGTTGTGATATAGAGGATGCAAGGAGACTG 644
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 645 AGTTTGTCTGAAAGCCCTTCGTGTTATAGATACCATGTTCTATCGCTTCAATAGCA 704
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 705 GTTGTCTTCCAAAACCTCAGGTAATATTTTTCACAGTCTGCACTCAGAACTCCGT 764
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 765 TTCTACAGATCTCCCGATGCTGGCATGACCCGAGGGGAGGCACCTTGGAAATTAATG 824
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu 240
Db 825 GGTTCAGTGGTTATGCTCACAGCAGGAATTAATCAAGCTTGTGATAGGATTTTTG 884
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTATATTTTCTGCTCTTCTGCTATCTGTTGGAAAGGATGCCAATAAAGAGTTT 944
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGAGATGCTCTCTGCTGGGGCAATTAATCAATTAATGATGCTATGGA 1004
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuGly 300
Db 1005 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTCTGACGCTTTCGACTCTCTGGC 1064

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTCTTTGACATTCCTGCGGCATTCCTGGCTCAGGTTTTTGGCTTTAAAGTACA 1124
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCCCGCAGAAACACTTTTGAGAAAAGAGAACCCAGCTGCCCACTCATTCAG 1184
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTTGGCGTAGCTAGCGAGCTGATGAGAAATCTGTTCATTTGCAACCTGGAAGCCA 1244
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1245 CACTTGAAGGCTTGGCACCTCGACCTTACCAATCAGAACTTAAGTTTTTAAGAGGCGA 1304
Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1305 GTGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAAGAGCCGACAAAGCTCAGTAGGTGAC 1364
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1365 AGGAGGTCCCCAACACCCGACATCACAGCCGAGGGCAGTCCCACCAAAGTGCAGAAGAGC 1424
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1425 TGGAGCTTCAAGACCCGACCCGCTTCGGGCCCTCGCTGCGCTCAAAAGTTCTCAGGCA 1484
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1485 AAACCACTGATAGTGTGACACAGCCCTTGGCACTGATGATGATATATGATGATAAAGGA 1544
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
Db 1545 TGCAGTGTGATGATGATCAGTGAAGAGCTCACCCACCACTTAAACCTGATTCGAGCT 1604
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1605 ATCAGATTATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAAAATATTACGTCATAT 1664
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1665 GATGTAAAGATGTTCATTGAACAAATATTCGTGCTCATCTGGACATGTTGTGTAGAATT 1724
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1725 AAAAGCCCTTCAACACAGCTGTGATCAATTTCTTGGAAAAGGCAATCACATCAGATAAG 1784
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1785 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACACACAGCATCTCAGTATCTCGGT 1844
Qy 561 ArgValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1845 CGGTGTGTCAAGTTGAAAACACAGGTACAGTCCATAGATCCAGAGCTGCGCTACTA 1904
Qy 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLysPhe 600
Db 1905 GACATCTATCAACAGGTCCTTGGAAAAGGCTCTGCTCCTCAGCCCTCGCTTGGCTTCATC 1964
Qy 601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCACCTTTTGAATGTGAACACAGCATCTGACTATCAAAAGCCCTGTGGATAGCAA 2024
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTTTGGGTTCGCGACAAAACAGTGGCTGCTTATCCAGATCACTAGTGGCAACATC 2084
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGGCTTGAGTTTCATCTTCAGCCCAAAAGAGTTTCAGTCCCAAGACTTTCTACGG 2144
Qy 661 LeuSerProThrMetHisSerGlnAlaThrValProIleSerGlnSerAspGlySer 680

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Db      2145 CTTAGCCCTACTATGTCACAGTCACAGCAGAGTGGCCCAATTAGTCAAGCGATGGCTCA 2204
Qy      681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db      2205 GCAGTGGCAGCCACCACACCATTCGAAACCAATAAATACGGCACCCCAAGCCAGCAGCC 2264
Qy      701 ProThrThrLeuGlnIleProProLeuProLeuProAlaIleLysHisLeuProArgProGlu 720
Db      2265 CCAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGCCAGAA 2324
Qy      721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrCysLeu 740
Db      2325 ACTCTGACCTTAACCTTGAGGCTTACAGAAAGCAATTTCTGAGTCCACCATCGCCTT 2384
Qy      741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db      2385 GTTGCTCCAAAGGAAATGTTTCAGGTTGCACAGTCAAAATCTCACCAGGACCGTTCATG 2444
Qy      761 ArgLysSerPheAspMetGlyGlyThrLeuLeuSerValCysProMetValProLys 780
Db      2445 AGGAAAGCTTTGACATGGGAGGAGAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 2504
Qy      781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db      2505 GACTTGGGCAATCTTTGTCTGTGCAAACTGATCAGTCCAGCGAAGAACTGAAATATA 2564
Qy      801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheThrProLysTrp 820
Db      2565 CAATCTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGCGAGCAAGATTTTATCCCAATGG 2624
Qy      821 ArgGluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAsp 840
Db      2625 AGGAAATCCAAATTTGTTTATAACTGATGAAGAGTGGTCCCGAAGACAGACAGAC 2684
Qy      841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db      2685 ACTTTGNTGCGCAGCCAGCCTGCCAGGAGAGCTGCTTTGATCAGATCTCTAAGG 2744
Qy      861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db      2745 ACTGGAAGTCCAGCATCATCTCAGAGCATTTGTAAGCGAGGAGAAAGTACAGATGCCCTC 2804
Qy      881 SerLeuProHisValLysLeuLys 888
Db      2805 AGCTTGCCCTCATGTCAAACTGAAA 2828

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RESULT 6

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US-09-866-020-1
; Sequence 1, Application US/09866020
; Publication No. US20020040000A1
; GENERAL INFORMATION:
; APPLICANT: DWORETZKY, STEVEN I
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: TROJNACKI, JOANNE T
; APPLICANT: BOISSARD, CHRISTOPHER G
; APPLICANT: GRIKOFF, VALENTIN K
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 3053-4091US1
; CURRENT APPLICATION NUMBER: US/09/866,020
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/207,389
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-020-1
Alignment Scores:

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Pred. No.: 0
Score: 4527.50
Percent Similarity: 99.00%
Best Local Similarity: 98.89%
Query Match: 99.57%
DB: 9
Length: 2694
Matches: 887
Conservative: 1
Mismatches: 0
Indels: 9
Gaps: 1

US-09-810-796-5 (1-888) x US-09-866-020-1 (1-2694)

Qy      1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAaArgGly 20
Db      1 ATGAAGGATGTGGAGTCCGGCCGGGCGAGGTGCTGTGAATCTGGCAGCCGCCAGGGGC 60
Qy      21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db      61 GACGGCTGTCTACTGTCTGGGCACCCCGCGCCACGCTTGTGTGGCGCGCGGTGGCGCTG 120
Qy      41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db      121 AGGAGAGCCCGCGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Qy      61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db      181 TACACGAGTAGCCAGAGCTGCCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 240
Qy      81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db      241 TACAACGTGTGGAGAGACCCCGCGGTGGCGGTTCATCTACCAACGCTTTCGTTTTCTC 300
Qy      101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db      301 CTTGTCTTTGGTGTCTGTGATTTTGTTCAGTGTTCCTACCATCTCCCTGAGCACACAAAATG 360
Qy      121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db      361 GCCTCAAGTTGCCTCTTGTGATCTCGAGCTTCGTGATGATGTCGCTTTGGTTGAGTTC 420
Qy      141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db      421 ATCATTCGAATCTGTCTGGCGGTGCTGTGTTCGATATAGAGGATGCAAGGAAGACTG 480
Qy      161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db      481 AGTTTGTCTGAAGAGCCCTTCTGTGTATAGATACCAATGTTCTTATCGCTTCAATAGCA 540
Qy      181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db      541 GTTGTCTTCGAAAACTCAGGGTAATATTTTCCACGCTCGCACTCAGAAAGTCTCGGT 600
Qy      201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db      601 TTCTTACAGATCTCTCCGATGTCGATGACCCGAGGGGAGGACACTTGGAAATTAATCTG 660
Qy      221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db      661 GGTTTCAGTGGTTTATGCTACAGCAAGAAATTAATACAGCTTGGTACATAGGATTTTTG 720
Qy      241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db      721 GTTCTTATTTTTCGTTCTCTCTCTATCTATCTGTGTGAAAGGATGCAATAAAGAGTTT 780
Qy      261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db      781 TCTACATATGCAGATGCTCTCTGCTGGGCGCACAAATTACATTGACAACATTAATGGCTATG 840
Qy      281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db      841 GACAAAACCTCCCTTAACCTTGGCTGGGAGGATTTGCTTTTCGAGGCTTTTGCACCTCTTGGC 900
Qy      301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db      901 ATTTCTTTCTTTCGACTTCTCTCGCGGCAATCTTGGCTCAGGTTTTCGATTAAGAATACAA 960

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QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GAAACAACCCGCGCAGAAACACTTTTCAGAAAAGAGAACCCAGCTGCCAACTCATTTGAG 1020
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1080
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1081 CACTTGAAGGCTTCACACCTTGCAGCCCTACCAAGAAAGAACAGGGAAGCATCAAGC 1140
QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAGCTAAGTTTAAAGGAGCGAGTGGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200
QY 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGAGCCGACAAAGCCTCAGTAGTGCACAGGAGTCCCAAGCACCAGCATCACAGCCGAG 1260
QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1261 GCGAGTCCCAACAAAGTCAGAGAGCTGGAGCTTCAACGACCGGACCCGCTTCGGGCC 1320
QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACCCAGTGATAGATGCTGCACAGCCCTTGGC 1380
QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1381 ACTGATGATGATATGATGATAAAGAGATGCCAGTGTGATGTATCAGTGGAAAGACTCACC 1440
QY 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1441 CCACCACTTAACACTGTCATTGCGACTATCAGAAATTTCAATTTTCATGTGCAAAACGG 1500
QY 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1501 AAGTTTAAAGGAAACGTTACGTCATATGATGATAAAGATGTCATTTGAACATATTTCTGT 1560
QY 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1561 GGTCACTCGGACATGTTGTTGTAGAAATTAAGAGCCTTCAAAACACGCTGTTGATCAAAATCTT 1620
QY 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1621 GGAAAGGCGCAATCACATCAGATAAGAGAGCCGAGAGAAATAACACGACAGACATGAG 1680
QY 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTCGGTGGTCAAGGTTGAAACACAGGTACAGTCC 1740
QY 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1741 ATAGAGTCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800
QY 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACACACATCT 1860
QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCGACAAAACAGTGGCTGC 1920
QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1921 TTATCCAGTCAACTAGTGGCAACATCTCGAGAGCCCTGCGAGTTTCATTTGACGCCAAAT 1980
QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1981 CAGTTCACTGCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040
QY 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
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Db 2041 GTGCCAATTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACACCATTTGCCAACCA 2100
QY 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2101 ATAAATACGGCACCCAAAGCCAGCAGCCCAACAACTTTACAGATCCCACCTCTCTCCA 2160
QY 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2161 GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCTTAACCTCGAGGCTTACAGAA 2220
QY 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2221 AGCATTTCTGACGTCACCACTGCTTGTGGCTCCAAAGGAATGTTTTCAGTTGACAG 2280
QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
Db 2281 TCAAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2341 TTGTCTGTCTGTCTCCATGGTGGCAGAGACTTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2400
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 811
Db 2401 ATCAGGTCGACCGAGGAACATGAAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460
QY 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2461 GCGAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTATTAACATGATGAAGAG 2520
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2521 GTGGTCCCGAGAGACAGACAGACACACTTTTGTATGCCGACCGCAGCCCTGCCAGGGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2581 GCTGCTTTGCATCAGACTCTCTAAGGACTGGAAGGTGCAAGTCACTCATCTCAGAGCATTTGT 2640
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACACTGAAA 2691

RESULT 7
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCN05, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCN05-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCN05-1
US-09-810-796-2

Alignment Scores: 0 Length: 2694
Pred. No.: 4527.50 Matches: 887
Score:
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 Db 1081 CACTTGAAGGCGCTTGACACCTGCGAGCCCTACCAAGAAAGAAACAAGGGAAGCATCAAGC 1140
 Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
 Db 1141 AGTCAGAAGCTAAAGTTTAAAGAGCGAGTGCGCATAGCTAGCCCGAGGGGCGCAGATATT 1200
 Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
 Db 1201 AAGAGCCGACCAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCAGCAGCATCACAGCCGAG 1260
 Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
 Db 1261 GCGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCGCTTCGGGCC 1320
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 Db 1321 TCGCTGGCGCCTCAAAAGTCTCAGCCAAAACAGTGATAGATGCTGACAGCCCTTGGC 1380
 Qy 452 ThrAspAspValTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
 Db 1381 ACTGATGATGTATATGATGAANAAGGATGCCAGTGTGATGATCAGTGGAGAGACTCAC 1440
 Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
 Db 1441 CCACCACTTAAACCTGTCATTGCGAGCTATCAGATTATGAAATTTGATGTTGCAAAACGG 1500
 Qy 492 LysPheLysGluThrLeuArgProTyAspValLysAspValIleGluGlnTySerAla 511
 Db 1501 AAGTTTAAAGGAACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
 Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
 Db 1561 GGTATCTGGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
 Db 1621 GGAAAGGCGCAATCACATCAGATGAAGAAGAGCGAGAGAAATAACAGCAGACATCAG 1680
 Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
 Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCAAGGTGAAAGAACAGGTACAGTCC 1740
 Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyGlnGlnValLeuArgLysGlySer 591
 Db 1741 ATAGAGTCCAGCTGGACTGCTACTACATCTATCAACAGGTCTTCGGAAGGCTCT 1800
 Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
 Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCCAGATCCCACTTTTGAATGTGAACAGACATCT 1860
 Qy 612 AspTyGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
 Db 1861 GACTATCAAGCCCTGTGGATGACAAAGATCTTTCGGGTTCGCAACAAACAGTGGCTGC 1920
 Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
 Db 1921 TTAITCCAGATCACTAGTGCCACATCTCGAGAGCCCTGAGTTCATTCTCAGCCCAAT 1980
 Qy 652 GluPheSerAlaGlnThrPheTyAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
 Db 1981 GAGTTTCAGTCCGACACTTCTACGCGCTTAGCCCTTACTATGACAGTCAAGCAACACAG 2040
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 Db 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2100
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 Db 2101 ATAAATACGGCACCCCAAGCCAGCAGCCCAACACTTTTACAGATCCCACTCTCTCCCA 2160

Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
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 Db 2281 TCAATCTCAACCAAGGACCGTCTATGAGGAAAGCTTTCATCATGCGGAGGAGAACTCTG 2340
 Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
 Db 2341 TTGTCTCTCTGCTCCATGGTGGCGAAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2400
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 Db 2521 GTGGGTCCCAAGAGACAGACAGACACTTTTGATCCGCCAGCCCTGCCAGGGAA 2580
 Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
 Db 2581 GCTGCCCTTGCATCAGACTCTCTAAGGACTTGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
 Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
 Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAAA 2691

RESULT 9

US-10-661-629-1

; Sequence 1, Application US/10661629

; Publication No. US20040180405A1

; GENERAL INFORMATION:

; APPLICANT: JENTSCH, Thomas

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS

; FILE REFERENCE: 2815-0236P

; CURRENT APPLICATION NUMBER: US/10/661,629

; CURRENT FILING DATE: 2003-09-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3137

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(2691)

; US-10-661-629-1

Alignment Scores:

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|------------------------|---------|---------------|------|
| Pred. No.: | 0 | Length: | 3137 |
| Score: | 4527.50 | Matches: | 887 |
| Percent Similarity: | 99.00% | Conservative: | 1 |
| Best Local Similarity: | 98.89% | Mismatches: | 0 |
| Query Match: | 99.57% | Indels: | 9 |
| DB: | 18 | Gaps: | 1 |

US-09-810-796-5 (1-888) x US-10-661-629-1 (1-3137)

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Db 1 ATGAAGATGTGAGTGGGCGGCGAGGTGTGTGTAACCTCGGACGCCAGCGGCG 60

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Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGAGAGCGCGCGGGGAGCAGGGGGCCGGATGAGCCTGCTGGGGAAGCGCTCTCT 180
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCCAGAGCTGCCGCGCGCAACGTCAGATACCGCGGGTGCAGACTACCTG 240
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
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Db 301 CTGTGCTTTGGTGTCTGATTTGTGTCAGTGTTCCTACCATCCCTGGAGCACACAAATTG 360
Qy 121 AlaSerSerCysLeuLeuIleLeuPheValMetIleValValPheGlyLeuGluPhe 140
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Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGGTTTGTCTGNAAGCCCTTCGTGTTTATAGAACCATTTGTTCTATCGCTTCATATGCA 540
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Qy 281 AsplysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
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Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
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Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
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Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
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Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
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Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
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Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
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Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2101 ATAAATACGCAACCCAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCTCCCA 2160
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
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Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2221 AGCATTTCTGACGTCACCACTGCTTTGTTGCTTCCAGGAAATGTTTCAGGTTGACAG 2280

QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
DB 2281 TCAATCTCACCAGGACCGTTCTATAGAGAAAGCTTTGACATGGGAGGAGAACTCTG 2340
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
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DB 2401 ATCAGGTCCGACGAGGAACTGAATATACAACTTTTCAGGAGTGAGCTCAAGTGGCTCCAGA 2460
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DB 2521 GTGGTCCCGAAGAGACAGACACACTTTTGTATGCCGACCGACCTGCCAGGGAA 2580
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
DB 2581 GCTGCTTTGCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
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RESULT 10

US-09-810-796-1
; Sequence 1, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, INC.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1
; NAME/KEY: CDS
; LOCATION: (10)..(2703)
; OTHER INFORMATION: KCNQ5-1

US-09-810-796-1

Alignment Scores:
Pred. No.: 0 Length: 3071
Score: 4523.50 Matches: 886
Percent Similarity: 98.89% Conservative: 1
Best Local Similarity: 98.77% Mismatches: 1
Query Match: 99.48% Indels: 9
DB: 9 Gaps: 1

US-09-810-796-5 (1-888) x US-09-810-796-1 (1-3071)

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QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
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QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysPheLeuSer 60
DB 130 AGGAGAGACCCCGCGGCAAGCAGGGGCCCGGATAGCCTGCTGGGGAAGCCGCTCTCT 189
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 190 TACACGAGTACCCAGAGCTGCCGCGCAACGTCAAGTACCGCGGGGTGCAGACTACCTG 249
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 250 TACAACGTGTGGAGAGACCCCGCGCTGGCGTTTCATCTACCAAGCTTTTCGTTTTCTC 309
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 310 CTTCTCTTTGGTTGCTTGAATTTGTCAGTGTGTTTCTACCATCCCTGAGCACACAAATG 369
QY 121 AlaSerSerCysLeuLeuIleLeuGlnPheValMetIleValValPheGlyLeuGluPhe 140
DB 370 GCCTCAAGTTCCTTCATCTCGAGTTCTGTGATGATTCGTCCTTTGGTTTGGAGTTC 429
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 430 ATCATTCGAATCTGTCGTGCGGTTGCTGTTGTCGATATAGAGATGCAAGGAAGACTG 489
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 490 AGGTTGTCGAAAGCCCTTCTGTGTTATATAGATACCATTTGTTCTTATCGCTTCAATAGCA 549
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DB 850 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGCTTTGCACTCTCTGCGC 909
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QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
DB 1090 CACTTGAAGGCTTTCACACCTGCAAGGCTTACCAAGAAAGAACCAAGGGAAGCATCAAGC 1149
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DB 1150 AGTCAGAGACTAAGTTTTTAAGAGCGAGTGGCATGGCTAGCCCCCAGGGGCCAGATATT 1209

Qy 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
Db 1210 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCAGCATCACAGCCGAG 1269
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Db 1270 GGCAAGTCCCAAGTGCAGAAAGAGCTGGAGCTTCAACGACCGAACCCTCGGGCCC 1329
Qy 432 SerLeuArgLeuLysSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1330 TCGTGGCCCTCAAAAGTTCTCAGCCAAACAGTAGATAGTGTGACACAGCCCTTGGC 1389
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1390 ACTGATGATGATATGATGATAAAGAGTGCAGTGTGATGATCAGTGGAAAGACTCAC 1449
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1450 CCACCACTTAAACCTGCTCAGAGCTATCAGAAATTATGAAATTTCATGTTGCAAAACGG 1509
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1510 AAGTTTAAGGAAACRTTACGTCCATATGATGATAAAGATGTCATTTGAACAATATCTGCT 1569
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1570 GGTATCTGGACATGTTGTGTAGAAATTAAGAGCCTTCAACACAGCTGTTGATCAAAATCTT 1629
Qy 532 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1630 GGAAAGAGGCAAAATCACATCAGTAAGAAGAGCCGAGAGAAATAAACAACGACATGAG 1689
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValLysGlnValGlnSer 571
Db 1690 ACCACAGCATCTCAGTATGCTCGGTGGGTGTCAAGTTTGAATAACAGATGACAGTCC 1749
Qy 572 IleGluSerLysLeuAspCysLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1750 ATAGAATCCAAGCTGGAGCTACTACATCATCATCAACAGGTCTTCGGAAAGGCTCT 1809
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 1810 GCCTCAGCCCTCGCTTGGCTTCATTCAGTTCCTCCACCTTTTGAATGGAACACATCT 1869
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1870 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGACACAAACAGTGGCTGC 1929
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 1930 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGCCCTGCAGTTTCATTTGACGCCAAAT 1989
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1990 GAGTTCAAGTCCAGACTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2049
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
Db 2050 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2109
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2110 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2169
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2170 GCCATCAGCATCTGCCAGCCAGCAAACTCTGCACCCCTAACCTCTGCAGGCTTTACAGAA 2229
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
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Qy 812 GlySerGlnAspPheTyrProLysTrpArgGlnSerLysLeuPheIleThrAspGluGlu 831
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Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2530 GTGGGTCCCAAGAGAGACAGACAGACACTTTTGTATGCCGACCCGACGCTTGCACGGGAA 2589
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2590 GCTGCTTTGCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2649
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700

RESULT 11

US-09-813-148-1

; Sequence 1, Application US/09813148

; Patent No. US20020076809A1

; GENERAL INFORMATION:

; APPLICANT: STEINMEYER, Klaus

; APPLICANT: LERCHE, Christian

; APPLICANT: SCHERER, Constanze

; APPLICANT: SEEBOHM, Guiscard

; APPLICANT: BUSCH, Andreas E.

; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN

; FILE REFERENCE: 38005-119

; CURRENT APPLICATION NUMBER: US/09/813,148

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: DE 100 13 732.6

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/194,041

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3074

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-813-148-1

Alignment Scores:

Pred. No.: 0 Length: 3074

Score: 4513.50 Matches: 885

Percent Similarity: 98.77% Conservative: 1

Best Local Similarity: 98.66% Mismatches: 2

Query Match: 99.26% Indels: 9

DB: 9 Gaps: 1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

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Db 215 ATGAAGATGTGGAGTCGGCCGGGGGAGGTGCTGTGAACTCGGACGCCCGCAGGGGC 274
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 275 GACGGCTGTACTGTCTGGGACCCCGCGCCACGCTTGGTGGCGCGGGTGGCTG 334
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60

Db 335 AGGAGAGCCCGCGGCAAGCGGGCCCGGATGAGCTGCTGGGAAGCCGCTCTCT 394
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValIysTyrArgArgValGlnAsnTyrLeu 80
Db 395 TACACGAGTAGCCAGAGCTGCGCGGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 454
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
Db 455 TACAACGTGCTGGAGAGACCCCGGGCTGGCGGTTTCATCTACACGCTTTCGTTTCCTC 514
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 515 CTGTGCTTTGGTGTGATTTGTCAAGTGTTCACCATCCCTGAGCACACAAAATTG 574
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValPheGlyLeuGluPhe 140
Db 575 GCCTCAAGTTCGCTTCGATCCTGGAGTTCGTGATGATGTCGTCCTTTGGTGGAGTTC 634
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 635 ATCATTCGAATCTGCTCGCGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAAGACTG 694
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 695 AGGTTTGTCTCGAAAGCCCTCTGTGTTATAGATACCATTTGTTCTATCGCTTCAATAGCA 754
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 755 GTTGTTCGTCGAAAACTCAGGGTAATATTTTGGCCAGCTCTGCACCTCAGAACTCCGT 814
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
Db 815 TTCCTACAGATCTCCGATGTCGCGATGACGACGAGGGGAGGCACCTTGGAAATTAAGT 874
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
Db 875 GGTTCAGTGGTTATGCTCAGCAAGGAATTAATACAGCTTGTGTACATAGGAATTTTG 934
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 935 GTTCTTATTTTCGCTCTTCCTGCTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT 994
Qy 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrIleGlyTyrGly 280
Db 995 TCTACATATGAGATGCTCTCTGTTGGGGCAACAATTACATTTGACAACCTATTGGCTATGGA 1054
Qy 281 AspLysThrProLeuThrTrpLeuGlyValArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1055 GACAAATCTCCCTAACTTTGGCTGGGAAGATGCTTTCTGCAGGCTTTTGCACCTCCTTGGC 1114
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1115 AFTTCTTTCTTGCATCTCTCGCGGCATCTTGGCTCAGGTTTGCATTAAGAAGTACAA 1174
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1175 GAACAACACCCGCAAGAAACATTTGAGAAAAGAGGAACCCAGCTGCGCAACTCATTCAG 1234
Qy 341 CysValTyrArgSerTyrAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1235 TGTGTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1294
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1295 CACTTGAAGGCTTGCACACCTGACGCTTACCAAGAAAGAACAGGGAAGCATCAAGC 1354
Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1355 AGTCAGAAGCTAAAGTTTTAAGAGCGAGTGGCGCATGGCTAGCCCCAGGGGCGAGATTT 1414
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411

Db 1415 AAGAGCCGACAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1474
Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1475 GGCAGTCCCACCAAGTGCAGAGAGAGCTGGAGCTTCAACGACCGAAACCGCTTCGGGCC 1534
Qy 432 SerLeuArgLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1535 TCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTGTATGCTGACACAGCCCTTGGC 1594
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1595 ACTGATGATGTATGATGAAGAAGATGCGAGTGTGATGTATCAGTGGGAAGACTCAC 1654
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491
Db 1655 CCACCACTTAAACCTGTCAATTCGAGCTATCAGAATTATGAATTTCAATGTGCAAAACGG 1714
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511
Db 1715 AAGTTTAAGGAAACATTACGTCCATATGATGTAAGAAGATGTCATTGAACCAATATTCGT 1774
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531
Db 1775 GGTCACTCGGCACATGTTGTGTAGNAATTAAGAAGCTTCAACACCGTGTGTGATCAATCTT 1834
Qy 532 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1835 GGAAGAAGGCAATCACATCAGATAAGAAGCCGAGAGAAAATAACAGCAGAAACATGAG 1894
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 571
Db 1895 ACCACAGACATCTCAGTATGCTCGGTGGGTGTCGAGGTGTAANAACAGGTACAGTCC 1954
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1955 ATAGATCCAGCTGGACTGCTACTAGACATCTATCAACAGTCTCTTCGGAAGGCTCT 2014
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 2074
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGCGACAAAACAGTGGCTGC 2134
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCCAGATCACTAGTGCACATCTCGAGAGGCTCGCAGTTCATTCTGACGCCAAT 2194
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTCAGTCCCAAGACTTCTACGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2254
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2314
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711
Db 2315 ATAAATACGCAACCAAGCCAGCCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2374
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2375 GCCATCAAGCATCTGCCCGCCAGCAAACTCTGCACCTTAACCTCGAGGCTTACAGGA 2434
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2435 AGCATTTCTGACGTCACCACTGCTGTTGTTCCTCCCAAGGAAATGTTTCAGTTGACAG 2494
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyThrLeu 771
Db 2495 TCAAAATCTCAACAGGACCGTTCTATGAGGNAAGCTTTGACATGGGAGGAACCTCTG 2554


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Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2555 TTGTCTGTCTGCCATGTCGCGAGAGACTTGGCAATCTTTGTCTGTGCAAAACCTG 2614
Qy 792 IleArgSerThrGluLeuAsnLeuGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2615 ATCAGTTCGACCGAGAACTGAATATACAACTTTCCAGGAGTGAGTCAAGTGGCTCCAGA 2674
Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGlu 831
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Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2735 GTGGGTCCGAGAGACAGACACACTTTTGATGCGGACCCAGCCCTGCCAGGAA 2794
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2795 GCTGCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2854
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RESULT 12

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US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: Cardiovascular disease using 1882, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26696, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 of 6585 molecules
; FILE REFERENCE: MPI02-018PIRNMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55
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Score: 2007.50 Matches: 434
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Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
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US-09-810-796-5 (1-888) x US-10-353-690-55 (1-2335)
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Db 166 ---CGTGCAGAGCGAACAGGGCGGAGCGGG-----CGGGGCGG 201
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Qy 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnVallyTy 73
Db 262 GCGGGGCTCCGGCTCGGGCTCCGCTCGCGCGCAGCGCTCTCGCGCGCGCAAGCGCTA 321
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Qy 133 eValValPheGlyLeuGluPheIleArlleTrpSerAlaGlyCysCysArgGly 153
Db 502 CGTGGTTCGCGCTTGGAGTACATCGTCCGGGTCTGTGTCCGGGAGTGTGTGTGTGTGTGT 561
Qy 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI 173
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Qy 173 eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193
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Qy 213 gGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleTh 233
Db 742 CGCGCGCACCTGGAAGCTGTGGGCTCAGTGGTCTACGCGCATAGCAAGAGGTGTATCAC 801
Qy 233 rAlaTrpTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGl 253
Db 802 CGCTGTGTATCATCGGTTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861
Qy 253 uLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleTh 273
Db 862 GAAGGAGCGCACTCCGACTTCTCTCTACGCGGACTCGCTGTGTGTGTGTGTGTGTGTGTGT 921
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Db 166 ---CGTGAGAGCAAGAGCGAGCGGG-----CGGGCGG 201
Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyIlyPProLeu----- 59
Db 202 CTCGCCGCGCGCTCTGGCCCTCTGGGAGAGCCCTCGCGCGCGCGCGCTCCCTCG 261
Qy 60 -----SerTy-Thr-Ser-SerGlnSerCysArgArgAsnValIlyeTy 73
Db 262 GCCGGCTCCGGCTCGGCTCGGCTCGGCGAGCGCTCTCGGCGCGCGCAAGCGCTA 321
Qy 73 rArgArgValGlnAsnTyLeuTyAsnValLeuGluArgProArgGlyTrpAlaPheII 93
Db 322 CGCGCGCTCGAGAACTGGGTCTCAACGCTGTGGAGCGCGCGCGCTGGGCTTGGT 381
Qy 93 eTyRHisAlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113
Db 382 CTACACGCTCTTCAATATTTTGGTGTCTTCTCAGCTGCGCTGGTGTCTGTGCTGCAC 441
Qy 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetII 133
Db 442 TATCCAGAGCACAGGAACTTGCCACAGAGTGTCTCTCATCTTGGAAATTCGTGATGAT 501
Qy 133 eValValPheGlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTy 153
Db 502 CGTGGTTTTCGGCTTGGAGTATCATCGTCCGGTCTGGTCCGCGGATGCTGCTGCGCTA 561
Qy 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgIlyProPheCysValIleIleAspThrII 173
Db 562 CCGAGATGGCAGGCTCGCTTCGCTTTGCGAGAAAGCCCTTCTGTGTCATCGACTTCAT 621
Qy 173 eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193
Db 622 CGTGTTCGGCTCGGTGGCGGTATCGCGCGGGTATCCAGGGCAACATCTTCGCCAC 681
Qy 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr 213
Db 682 GTCCGCGCTGGCGAGCATCGCTTCTGCAGATCTTGGCATCTGTGCGCATGAGCGCG 741
Qy 213 gGlyGlyThrTrpLysLeuLeuGlySerValValTyAlaHisSerLysGluLeuIleTh 233
Db 742 CGCGCGCACTCGGAAGCTGTGGGCTCAGTGGTCTACGCGCATGACGAGGAGCTGATCAC 801
Qy 233 rAlaTrpTyIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyLeuValGI 253
Db 802 CGCTGTGTATCATCGGTTCTGTGTCTCATCTTCGCTTCTTCTGTGTCTACTTGGCGGA 861
Qy 253 uIysAspAlaAsnLysGluPheSerThrTyAlaAspAlaLeuTrpTrpGlyThrIleTh 273
Db 862 GAAGGACGCCAACTCCGAACTTCTCTCTACGCGGACTCGCTCTGTGGGGGAGCATATAC 921
Qy 273 rLeuThrThrIleGlyTyArgLysPheLeuThrProLeuThrTrpLeuGlyArgLeuLeuSe 293
Db 922 ATTGACACCACTCGGTATGTGTGACAGACACCGACACATGGCTGGGCGGGTCTGGG 981
Qy 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313
Db 982 TGCTGGCTTCGCTTACTGGGCATCTCTTCTTGGCTGTGCTGGCGGCATCTTAGGCTC 1041
Qy 313 rGlyPheAlaLeuLysValGlnGluHisArgGlnLysHisPheGluLysArgArgAs 333
Db 1042 CGGCTTTTGGCTGAAGGTTCAGGAGCAGCAGCGGAGAGCACTTCGAGAGAGCGAGGAT 1101
Qy 333 nProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyAlaAlaAsp---GluLysSe 352
Db 1102 GCCGGCAGCCAACTCATCCAGGCTGCTGGGCTGTACTTCCACCGATATGAGCCGGGC 1161
Qy 352 rValSerIleAlaThrTrp----- 358
Db 1162 CTACTGACAGCCACTGGTACTACTATGACAGTATCTCCCATCTTCAGAGAGCTGGC 1221
Qy 358 ----- 358

Db 1222 CCTCTTGTTTGAGCACGTGCAACGGGCGCGCAATGGGGGCTACTGGGCGCTCGAGGTGCG 1281
Qy 359 -----LysProHisLeuLysAlaLeuHisTh 367
Db 1282 GCGGGCGCGGTACCCGACGAGACACCTCCGTACCCGCGCTTCCACCTCCACCG 1341
Qy 367 r-----CysSerProThrAsnGlnLysLeuSerPheLysGluArgVa 381
Db 1342 GCCGGGAGCACCTCTCTTCTGCGCTGGGAAAGCAGCGGATGGGCATCAAGACCGCAT 1401
Qy 381 lArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValGI 399
Db 1402 CGCATGGGAGCTCCAGCGCGGAGCGGTCTTCAAGCAGCAGCTGGCAGCTCCCAAC 1461
Qy 399 yAspArgSerProSerThrAspIleThrAlaGluGly---SerProThrLysValGI 418
Db 1462 AATGCCACCTCCCAAGCAGCAGCGAGGTGGGTGAGGCCACCCAGCCCAAGAGGTGCA 1521
Qy 418 nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLysSerSe 438
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Qy 438 rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyAspGI 458
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Qy 458 uLysGlyCysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValII 478
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Qy 555 pLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLy 575
Db 1918 AATCAGCATGAGGAGCGCTGTGTCAAGGTGGAGAACAGCAGTGCAGTCCATCGAGCAAA 1977
Qy 575 sLeuAspCysLeuLeuAspIleTyGlnGlnValLeuArgLysSerAlaSerAlaLe 595
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Qy 595 uAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSerAspTyGlnSe 615
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Qy 635 rThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAl 655
Db 2149 GGTGAGCACCAATGACTGAGG----- 2173
Qy 655 aGlnThrPheTyAlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSe 675
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Job time : 1261.47 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 02:34:27 ; Search time 6829.39 Seconds
(without alignments)
4949.353 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547
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Ygapop 10.0 , Ygapext 0.5
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Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 3099 | 68.2 | 2014 | 9 AY407014 | AY407014 Pan trogl |
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ALIGNMENTS

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DEFINITION Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence, 2733 bp DNA linear GSS 15-DEC-2003
ACCESSION AY407013
VERSION AY407013.1 GI:39762984
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2733)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2733)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
Location/Qualifiers
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ORIGIN

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| Best Local Similarity: | 99.66% | Mismatches: | 3 |
| Query Match: | 99.60% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-810-796-5 (1-888) x AY407013 (1-2733)

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| Qy | 21 | AspGlyLeuLeuLeuLeuGlyThrAlaAlaThrLeuGlyGlyGlyGlyLeu | 40 |
| Db | 127 | GACGGCTGCTACTGCTGGGACCGCGCGCGCACGCTCGGTGGCGGGGGTGGCGCTG | 186 |
| Qy | 41 | ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer | 60 |
| Db | 187 | AGGGAGACCGCGCGGCGAGCAGGGGCGCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT | 246 |
| Qy | 61 | TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu | 80 |
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| Db | 367 | CTTGCTTTGGTTGCTGATTTGTCAGTGTTTCTACCATCCCTGAGCACACAAATG | 426 |
| Qy | 121 | AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe | 140 |
| Db | 427 | GCCTCAAGTGTCTTGCATCTGGAGTTCGTGATGATGTCGTTTGGAGTTC | 486 |
| Qy | 141 | IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu | 160 |
| Db | 487 | ATCATTCGAATCTGGTCTGCGGGTGTGTTGTGATATAGGATGGCAAGGAGACTG | 546 |
| Qy | 161 | ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla | 180 |
| Db | 547 | AGGTTTGTCTGAAAGCCCTCTGTGTTATAGATACCATTTGTTCTATCGTTCATAGCA | 606 |
| Qy | 181 | ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg | 200 |
| Db | 607 | GTTGTTTCTGCAAAACTCAGGGTAATATTTTGCACGCTCGCACTCAGAACTCCGT | 666 |
| Qy | 201 | PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrLysLeuLeu | 220 |
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| Qy | 221 | GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu | 240 |
| Db | 727 | GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGATAGGATTTTG | 786 |
| Qy | 241 | ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe | 260 |
| Db | 787 | GTTCTTAATTTTTCGCTCTCTATCTGCTATCTGGTGGAAAGGATGCAATAAAGATT | 846 |
| Qy | 261 | SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly | 280 |
| Db | 847 | TCTACATATGAGATGCTCTCTGGTGGGGGCAATTAATTCATTGCAACTATTGGCTATGGA | 906 |

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| Qy | 281 | AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly | 300 |
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| Qy | 301 | IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln | 320 |
| Db | 967 | ATTTCTTTCTTTCACCTTCTGCGGCAATCTTGCTCAGGTTTTCATTTAAAGTAGCAA | 1026 |
| Qy | 321 | GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln | 340 |
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| Qy | 341 | CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro | 360 |
| Db | 1087 | TGTCTTTGGCGTAGTTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA | 1146 |
| Qy | 361 | HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg | 380 |
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| Db | 1687 | AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACACACAGCATCTCAGTATGTCGT | 1746 |
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| Qy | 601 | GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys | 620 |
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| Qy | 621 | AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle | 640 |
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RESULT 2
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 genomic survey sequence.
 AY407015
 ACCESSION AY407015.1 GI:39762986
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2729)
 REFERENCE
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302

REFERENCE 2 (bases 1 to 2729)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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 Query Match: 92.84% Indels: 16
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US-09-810-796-5 (1-888) x AY407015 (1-2729)
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 Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
 Db 169 GACGGCTGTGTGTCTGCGACCCCGCGCGCGCTCGCGGAGCGCGCGGCTTG 228
 Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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 Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
 Db 289 TACACACAGCAGCAGAGCTGTGCGCGCAACGTCAAGTACCGCGGGTGCGAACTATCTG 348
 Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
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 Qy 101 LeuValPheGlyCysLeuLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
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 Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
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 Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
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QY 531 LeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHis 550
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 LOCUS
 DEFINITION
 Mus musculus adult male cortex cDNA, RIKEN full-length enriched library, clone:7730402H11 product:potassium voltage-gated channel, subfamily Q, member 5, full insert sequence.
 AK033079
 VERSION
 AK033079.1 GI:26328812
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 TITLE
 High-efficiency full-length cDNA cloning
 JOURNAL
 Mech. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99279253
 PUBMED
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE
 20499374
 PUBMED
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 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL
 Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE
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 PUBMED
 11076861
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 TITLE
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 JOURNAL
 Nature 409, 685-690 (2001)
 MEDLINE
 11076861
 PUBMED
 11076861

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 2276)

Adachi, J., Aizawa, K., Akimura, T., Azakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saigo, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 2,9e-248 Length: 2276
 Score: 2655.50 Matches: 524
 Percent Similarity: 94.05% Conservative: 13
 Best Local Similarity: 91.77% Mismatches: 25
 Query Match: 58.40% Indels: 9
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US-09-810-796-5 (1-888) x AK033079 (1-2276)

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 QY 346 TyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuLysAlaLeu 365
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 QY 366 HisThrCysSerProThr-----AsnGlnLysLeuSer 376
 DB 123 CACACCTGCAGCCCTTACCAGAAAGAACAGGGGAGGATCAAGCAGTCAGAAAGCTGAGC 182
 QY 377 PheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAla 396
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 QY 417 ValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLys 436
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 QY 697 LysProAlaAlaProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeu 716
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 LOCUS Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430075J21 product:potassium voltage-gated channel, subfamily Q, member 4, full insert sequence.
 DEFINITION
 ACCESSION AK040190
 VERSION AK040190.1 GI:26333632
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system - 384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1571)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome.res@sc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel.81-45-503-9222,
Fax:81-45-503-9216)

Score: 1258.50 Matches: 237
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US-09-810-796-5 (1-888) x BB609854 (1-997)

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RESULT 7

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DEFINITION 55049367J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629762
VERSION CD629762.1 GI:40278028
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 797)
AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com

FEATURES
source
1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:
Pred. No.: 1.15e-103 Length: 797
Score: 1171.50 Matches: 238
Percent Similarity: 94.90% Conservative: 4
Best Local Similarity: 93.33% Mismatches: 3
Query Match: 25.76% Indels: 11
DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x CD629762 (1-797)

QY 330 LysArgArgAsnProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp 349
Db 764 GAAAGAAAGAGCCAGCTGCCAATCTCATCTCAGTGTGTTTG-CGTAGTTACGCGATTGAT 706

QY 350 GluLysSerValSerIleAlaThrTrpLysProHisLeuLysAlaLeuHisThrCysSer 369
Db 705 GAGAAATCTGTTTCCATTGCAACTGGAGGCCACACTTGAAGCCCTTGCACACTGCGACG 646

QY 370 -ProThr-----AsnGlnLysLeuSerPheLysGluAr 380
Db 645 CCCTACCAAGAAAGGACAGGGGGAAGCATCAAGCAGCTCAGAAGCTAAGTTTAAAGGAGCG 586

QY 380 gValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAs 400
Db 585 AGTGGCGATGGCTTAGCCCCAGGGGCGAGAGTATTAAAGAGCCGACAGCCCTCAGTAGTGA 526

QY 400 pArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSe 420
Db 525 CAGAGGTCCCCAAGCAGCCGACATCACGCCGAGGGCAGTCCACCACCAAGTGCAGAGAG 466

QY 420 rTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPr 440
Db 465 CTGGAGCTTCAACGACGGAACCCGCTTCGCGCCCTCGCTGCGCTCCTCAAAAGTTCTCAGCC 406

QY 440 oLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGI 460
Db 405 AAAACAGATGATAGATGCTGACACAGCCCTTGGCATCTGATGATGATATATGATGATAAAGG 346

QY 460 YCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAl 480
Db 345 ATGCCAGTGTGATGATATCAGTGGAGACCTCACCCACCCACTTAAACCTGTCATTGCGAGC 286

QY 480 alIeArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTy 500

Db 285 TATCGAATTATGAATTTTCATGTTGCAAAACGGAGTTTAAAGGAAACATTACGTCCATA 226

Qy 500 rAspVallysAspValIleGluInTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520

Db 225 TGATGTAAGAGATGTCAATTGAACAATAATTCGTGTCTATCTGGACATGTTGTGTAGAA 166

Qy 520 elysSerLeuGlnThrArgValAspGlnIleLeuGlyHisLeuGlyGlnIleThrSerAspIly 540

Db 165 TAAAGCCCTTCAACACGTGTGTATCAAAATTCCTTGGAAAAGGCGCAATACATCAGATAA 106

Qy 540 sLysSerArgGluLysIleThrAlaGluHisGlnThrThrAspAspLeuSerMetLeuG1 560

Db 105 GAAGAGCCGAGAGAAATAACAGCAGACATGAGACACAGCATCTCAGTAGTGTCTCGG 46

Qy 560 YArgValLysValGluLysGlnValGlnSerIleGluSer 574

Db 45 TCGGTGTCTCAAGGTTGAAAACAGGTACAGTCCATAGATCC 3

RESULT 8

CK772601 864 bp mRNA linear EST 20-FEB-2004

LOCUS 961159 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.

DEFINITION CK772601

ACCESSION CK772601

VERSION CK772601.1 GI:42726744

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE

1 (bases 1 to 864)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pettea, G., Holt, I., Katamychewa, S., Liang, F., Ouackenbush, J. and Keelie, J.W.

AUTHORS

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

11282978

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

TITLE

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.

Plate: 40 row: C column: 8

Seq primer: GTAATACGACTCACTATAGG.

FEATURES

source

1..864

Location/Qualifiers

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 2BOV"

/note="Vector: pCMV SPORT6; Site1: NotI; Site2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

ORIGIN

Alignment Scores:

Pred. No.: 1.04e-98 Length: 864

Score: 1121.50 Matches: 209

Percent Similarity: 86.03% Conservative: 25

Best Local Similarity: 76.84% Mismatches: 37

Query Match: 24.66% Indels: 1

DB: 7 Gaps: 1

US-09-810-796-5 (1-888) x CK772601 (1-864)

Qy 89 GlyTrpAlaPheIleTyrHisAlaPheValPheLeuLeuValPheGlyCysLeuIleLeu 108

Db 3 GCGTGGGGTTCATCTACCAAGCTTACGTCTCTGCTGCTCTCTCTGCTGCTGCTGCTG 62

Qy 109 SerValPheSerThrIleProGluHisThrLysLeuAlaSerSerCysLeuLeuIleLeu 128

Db 63 TCCGTGTTCTCCACCATCAAGGAGTATCAGAGAGCTCTGAGGGCGCGCTCTACATCCTG 122

Qy 129 GluPheValMetIleValValPheGlyLeuGluPheIleIleArgIleTyrSerAlaGly 148

Db 123 GAAATCGTGACCATCGGTGTTTCGGTGTGAGTACTTCGTGCGGATCTGGCTCGGGT 182

Qy 149 CysCysCysArgTyrArgGlyTyrGlnGlyArgLeuArgPheAlaArgLysProPheCys 168

Db 183 TGTCTGTTGTGGTACCGGGCTGGAGAGGGGGCTCAAGTTTGGCCGGAAGCCCTTCTGT 242

Qy 169 ValIleAspThrIleValLeuIleAlaSerIleAlaValValSerAlaLysThrGlnGly 188

Db 243 GTGATTGCATCATGTTGCTCATCGCTCCATCGGTGCTGCTGCTGCTGCTGCTGCTG 302

Qy 189 AsnIlePheAlaThrSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetVal 208

Db 303 AATGTGTTCGCCACATCGGGCTCCGGAGCTCGGCTTCCTGCGAGATCTCGCGATGATC 362

Qy 209 ArgMetAspArgArgGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSer 228

Db 363 CGAATGACCGCTCGGGGGCGCACCTGGAAGCTGCTGGCTCCGTGGTCTATGCGGACAGC 422

Qy 229 LysGluLeuIleThrAlaTyrTyrIleGlyPheLeuValLeuIlePheSerSerPheLeu 248

Db 423 AAGGAGTTGGTCACTGCTTGTGTACATCGGCTTCCTCTGCTCATCTGCGCTCATTTCTG 482

Qy 249 ValTyrIleValGluLysAspAlaAsnLysGluPheSerThrTyrTyrAlaAspAlaLeuTrp 268

Db 483 GTGTACTTGGCAGAGAGGGGAGAGCATCATTGTATACCTACGCGGAGCGACTCTGG 542

Qy 269 TrpGlyThrIleThrLeuThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeu 288

Db 543 TGGGGCTGTATCACCCTGACACCATTTGGTACGGGACAGTACCTCAGACCTGGAGAC 602

Qy 289 GlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAla 308

Db 603 GGGAGGCTCTGGCAGCGACCTTCACCTCATCGGTGTCTCTCTCTCTCTCTCTCTCTCT 662

Qy 309 GlyIleLeuGlySerGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPhe 328

Db 663 GGCATTTTGGGGTCTGGCTTTGCCCTGAAAGTTCAAGAGCAGCACCGCTGAGAGCACTTT 722

Qy 329 GluLysArgArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAla 348

Db 723 GAGAAGAGCGGAACCCCGCAGCAGGCTGATCAGTCCGCTCGGCTGGAGGTTCTATGCCACC 782

Qy 349 AspGluLysSerValSerIle---AlaThrTrpLys 359

Db 783 AACTGTTCGGCAGCGGACCTGCATCCACGTGGCGAG 818

RESULT 9

CD629756/c 732 bp mRNA linear EST 12-JAN-2004

LOCUS 55049343J1 FLP Homo sapiens cDNA, mRNA sequence.

DEFINITION CD629756

ACCESSION CD629756

VERSION CD629756.1 GI:40278022

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 732)

Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

Circular rapid amplification of cDNA ends for high-throughput

JOURNAL
COMMENT

extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

FEATURES

source
1. .732
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/notes="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:
Pred. No.: 2,91e-97 Length: 732
Score: 1105.50 Matches: 230
Percent Similarity: 93.88% Conservativity: 0
Best Local Similarity: 93.88% Mismatches: 4
Query Match: 24.31% Indels: 13
DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x CD629756 (1-732)

QY 339 ileGlnCysValTrpArgSer-TyrAlaAlaAspGluLysSerValSerIleAlaThrTr 358
Db 731 ATTCACTGTGTTGGCGTAGTTAACCGACGCTGATGAGAATCTGTTTCATTCGCACTG 672
QY 358 pLysProHisLeuLysAlaLeuHisThrCysSerProThrAsn----- 372
Db 671 GAAGCCACACTTGAAGGCGCTTCACACCTGCAGCCCTACCCA-AGAAAGAACACAGGGGA 613
QY 373 -----GlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgG1 388
Db 612 AGCATCAACGACGTCAGAGCTAAGTTTAAAGAGCGAGTGCATGGCTAGCCCGAGGG 553
QY 388 yGlnSerIleLysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspI1 408
Db 552 CCAGAGTATTAAAGCCGACAGCCCTCAGTAGGTGACAGGAGGTCCTCCCAACGCGACAT 493
QY 408 eThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrAr 428
Db 492 CACAGCCGAGGCGAGTCCACCAAGTGCAGAGAGCTGAGGCTTCAACGCCCGAACCCG 433
QY 428 gPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspTh 448
Db 432 CTTCCGGCCCTCGCTCGCCTCAAAAGTTCTCAGCCCAAAACCACTGATGATGCTGACAC 373
QY 448 tAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValG1 468
Db 372 AGCCCTTGCCACTGATGATGATATATGATGATAAAGGAGTCCAGTGTGATGATCAGTGA 313
QY 468 uAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisVa 488
Db 312 AGACCTCACCCACCACCTTAAACTGTCATTCGAGCTATCAGAAATATGAATTTCAATG 253
QY 488 lAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluG1 508
Db 252 TGCAAAACGGAAGTTTAAAGAAACATTACGTCCATATGATGATAAAGATGTCATTGAACA 193
QY 508 nTyrSerAlaGlyHisLeuAspMetLeuCysAtqIleLysSerLeuGlnThrArgValAs 528
Db 192 ATATTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAAAACAGCTGTGA 133
QY 528 pGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAl 548
Db 132 TCAAAATCTTGAAAAGGCGCAATACATCAGATAAGACGCGAGAGAAATATACAGC 73
QY 548 aGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysG1 568
Db 72 AGAATGAGACACACGACGATCTCAGTATGCTCGGTGCGTGTGCTCAG-GTTGAAAACA 14

QY 568 nValGlnSerIle 572
Db 13 GGTACAGTCCATA 1

RESULT 10

BE158938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BE158938 658 bp mRNA linear EST 21-JUN-2000
MRO-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.
BE158938
BE158938.1 GI:8621659
EST
Homo sapiens (human)

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

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ORIGIN

Alignment Scores:

Pred. No.: 1,06e-96 Length: 658
Score: 1099.00 Matches: 211
Percent Similarity: 99.53% Conservativity: 1
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 24.17% Indels: 0
DB: 2 Gaps: 0

US-09-810-796-5 (1-888) x BE158938 (1-658)

QY 278 GlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAla 297

Db 18 GGCTATGGAGACAAACCTCCCTTAACCTTGGCTGGGAGATTGCTTCTGCAGGCTTTCGA 77

QY 298 LeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeu 317

```

Db      78 CTCTTGGCAATTTCTTTTGGCACTTCTCTCCGCGCATCTTGGCTCAGGTTTGGCAATTA 137
Qy      318 LysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsn 337
Db      138 AAAGTACAAGAACACACCGCCAGAACACATTTTGAGAAAGAGAACCCAGCTGCCAAC 197
Qy      338 LeuLeuGlnCysValTrpArgSerTyrAlaAlaLysGluLysSerValSerIleAlaThr 357
Db      198 CTCAATTCAGTGTGTGTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTCGAACC 257
Qy      358 TrpLysProHisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPhe 377
Db      258 TGGAAAGCCACACTTGAAGGCGCTTGACACACCTGCGAGCCCTACCAATCAGAAAGCTAAGTTTT 317
Qy      378 LysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSer 397
Db      318 AAGGAGCGAGTGGCGATGGCTAGCTAGCCAGGCGCCAGAGTATTAAAGAGCCGACAGCCCTCA 377
Qy      398 ValGlyAspArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysVal 417
Db      378 GTAGGTGACAGAGGTCCCGAAGCAGCCAGCTCAGCCGAGGCGAGTCCCGACCAAGTGTG 437
Qy      418 GlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer 437
Db      438 CAGAAGAGCTGGAGCTTCAAGACCGAAGCCGCTTCCGCGCCCTCGCTCGGCTCAGAAAGT 497
Qy      438 SerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspValTyrAsp 457
Db      498 TCTCAGCCAAACAGTGTATAGCTGACACAGCCCTTGGCACTGATGATGATATGAT 557
Qy      458 GluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrVal 477
Db      558 GAAAAGAGTATGCCAGTGTGTATCAGTGTGAAGACCTCACCCACCACTTAAAGTGTG 617
Qy      478 IleArgAlaIleArgIleMetLysPheHisValAlaLys 490
Db      618 ATTCAGCTATCAGAAATATGAAATTTCTTGTGTCAAA 656

```

```

RESULT 11
CD629754/c
LOCUS      CD629754      742 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 55049327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD629754
VERSION    CD629754.1  GI:40278020
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE  1 (bases 1 to 742)
AUTHORS   Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE     Circular rapid amplification of cDNA ends for high-throughput
            extension cloning of partial genes
JOURNAL   Genomics 84 (1), 205-210 (2004)
COMMENT   Contact: Fu GK
            Incyte Genomics, Inc.
            3160 Porter Dr., Palo Alto, CA 94304, USA
            Tel: 6508454102
            Email: gfu@incyte.com.

```

```

FEATURES             source
            1..742
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone_lib="FLP"
            /note="Vector: pDrive Cloning Vector"
ORIGIN

```

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Alignment Scores:
Pred. No.:      1,39e-95      Length:      742
Score:          1088.50      Matches:      229
Percent Similarity: 93.12%      Conservative: 1

```

```

Best Local Similarity: 92.71%      Mismatches: 5
Query Match:          23.94%      Indels: 13
DB:                   6          Gaps: 1

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```
US-09-810-796-5 (1-888) x CD629754 (1-742)
```

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Qy      340 GlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLys 359
Db      740 CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 682
Qy      360 ProHisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db      681 CCACACTTGAAGCGCTTGACACACCTGCGAGCGCGCATGGCTAGCCAGGCGGCCAGA 622
Qy      372 ----AsnGlnLysLeuSerPheLysGlu-ArgValArgMetAlaSerProArgGlyGlns 390
Db      621 AAGCAGTCAGAAAGCTAAGTTTAAAGGAGCGCGAGTGGCTAGCTAGCCAGGCGGCCAGA 562
Qy      390 erlleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrA 410
Db      561 GTATTAAAGAGCCGACAAAGCCTCAGTAGGTGACAGAGGTCCCCAAAGCACCCACATCACAG 502
Qy      410 laGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheA 430
Db      501 CCAGGCGCAGTCCCGACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 442
Qy      430 rgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaL 450
Db      441 GGCCCTCGTGGCGCTCAAAAGTTCTCAGCCAAACCCAGTGTATGATGATGATGATGATGAT 382
Qy      450 euGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspL 470
Db      381 TTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 322
Qy      470 euThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaL 490
Db      321 TCACCCCAACCACTTAAAGCTGTGCTTTCAGCTATCAGAAATATGAAATTTTCAATTTGCA 262
Qy      490 ysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrS 510
Db      261 AACGGAAGTTTAAAGTAAACATTTACGTCATATGATGATGATGATGATGATGATGATGATGAT 202
Qy      510 erAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnI 530
Db      201 CTGCTGTGTCATCTGGACATGTGTGTAGAAATTAAGAGCCCTTCAACACAGCTGTGATCAAA 142
Qy      530 leLeuGlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluH 550
Db      141 TTCTTGGAAAGGCAATCACATCAGATAGAGAGCGCCGAGAGAAATAACAGCAGAAC 82
Qy      550 isGluThrThrAspAspLeuSerMetLeuGlyArgVal-VallysValGluLysGlnVal 569
Db      81 ATGAGACACACAGACGATCTCAGTATGCTCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGA 22
Qy      570 GlnSerIleGluSer 574
Db      21 CAGTCCATAGATCC 7

```

```
RESULT 12
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```
CD6244389
```

```
LOCUS
```

```
DEFINITION
```

```
UI-M-PY0-cdq-c-03-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
```

```
IMAGE:6832924 5', mRNA sequence.
```

```
ACCESSION  CB244389
```

```
VERSION    CB244389.1  GI:28366033
```

```
KEYWORDS   EST.
```

```
SOURCE     Mus musculus (house mouse)
```

```
ORGANISM   Mus musculus
```

```
REFERENCE  1 (bases 1 to 744)
```

```
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
```

```
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
```

```

CB244389      744 bp      mRNA      linear      EST 09-JUL-2003
UI-M-PY0-cdq-c-03-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6832924 5', mRNA sequence.

```

```
ACCESSION  CB244389
```

```
VERSION    CB244389.1  GI:28366033
```

```
KEYWORDS   EST.
```

```
SOURCE     Mus musculus (house mouse)
```

```
ORGANISM   Mus musculus
```

```
REFERENCE  1 (bases 1 to 744)
```

```
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
```

```
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
```

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1..744

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6832924"

/tissue_type="whole brain"

/dev_stage="embryo 13.5, 14.5, 15.5, 16.5, 17.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH-BMAP_Fy0"

/note="Organ: Brain; Vector: pYX-Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 9,396-95 | Length: | 744 |
| Score: | 1080.00 | Matches: | 216 |
| Percent Similarity: | 91.46% | Conservative: | 9 |
| Best Local Similarity: | 87.80% | Mismatches: | 21 |
| Query Match: | 23.75% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-810-796-5 (1-888) x CB244389 (1-744)

| | | | |
|----|-----|--|-----|
| QY | 622 | LeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSer | 641 |
| DB | 7 | CTGTCGGCTCAGCACAAACAGCGGCTGTTTAAACAGAGTCAGCAGTCGCCACATCTCA | 66 |
| QY | 642 | ArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyAlaLeu | 661 |
| DB | 67 | AGAGCCCTGCAGTTCATCCTAACCAACCAATGAGTTCAGTGTCTCAGACTTTCTATGCGCTT | 126 |
| QY | 662 | SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAla | 681 |
| DB | 127 | AGCCCTACTATGCACAGCCAGACTACCAGGTACCCATGAGTCAAAATGACGGCTCTCC | 186 |
| QY | 692 | VallalaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaPro | 701 |
| DB | 187 | GTGTAGCCACCAATAACATTGCAAAACCAATAAGCGCGCACCCAGCAGCCCA | 246 |
| QY | 702 | ThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGluThr | 721 |
| DB | 247 | ACAATTACAGATCCCTCTCTCTCGGCCATCAGACATGTCTCAGGCCAGAACCT | 306 |
| QY | 722 | LeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuVal | 741 |

| | | | |
|----|-----|--|-----|
| DB | 307 | CTGCTCTCAAAACCCACCGCTTACAGAGAGTATTCTTGATGTACACACCTGCTGTGT | 366 |
| QY | 742 | AlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArg | 761 |
| DB | 367 | GCCTCCAAAGGAAGTGTTCAGTTTTCAGTCAACCTGACCAAGGACCGTTCCTGAGG | 426 |
| QY | 762 | LysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLysAsp | 781 |
| DB | 427 | AAAAGTTTCGACATGGGAGGAGAACTCTGTGTCTGTCGCGCCCATGGTGCCCAAGAT | 486 |
| QY | 782 | LeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGln | 801 |
| DB | 487 | TTGGGCAAAATCTCTGTCTGTACAAACCTGATCAGTTCGACAGAGAACTGAACTTACAG | 546 |
| QY | 802 | LeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyProLysThrArg | 821 |
| DB | 547 | TTTTTCAGGCGAGCGAGTCAAGCGCTCTCGAGGCGAGTCAAGATTTTATCCCAAGTGGA | 606 |
| QY | 822 | GluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAspThr | 841 |
| DB | 607 | GAATCCANATTGTTTATTAATGATGAGAGAGTCTGTCGAGAGAGACAGAAACAGACT | 666 |
| QY | 842 | PheAspAlaProGlnProAlaArgGluAlaPheAlaSerAspSerLeuArgThr | 861 |
| DB | 667 | TTTGACGCGCACCCACCGCTCTGCGGGGAGGCTGCTTCTCATCAGACTCTCTAGGACT | 726 |
| QY | 862 | GlyArgSerArgSerSer 867 | |
| DB | 727 | GGAAGGTACCGGTCACT 744 | |

RESULT 13

BX917798/c

LOCUS

DEFINITION

BX917798 Sus Scrofa library (scan) Sus scrofa cDNA clone

scan0033d.1.06 5prim, mRNA sequence.

ACCSSION

BX917798

VERSION

BX917798.1

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Tosser-Klopp G

Genetique Animale

Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan

cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@oulouse.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us

at sigenasupport@jouy.inra.fr to obtain the chromatogram of this

sequence.

Plate: 0033 row: 1 column: 6.

Location/Qualifiers

1..628

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scan0033d.1.06"

/tissue_type="mixed"

/dev_stage="from embryos to adults"

/clone_lib="Sus Scrofa library (scan)"

/note="tissues: adipose tissue, brain, kidney, liver,

muscle, ovary, testis, heart, hypothalamus, pancreas,

skin, spleen, thymus, placenta, pituitary gland, seminal

vesicle, small intestine, uterus, adrenals, bulbo uretral

gland, cerebral trunk, epididymis, female gonad,

gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN

Alignment Scores:
Pred. No.: 3,44e-94 Length: 628
Score: 1073.00 Matches: 207
Percent Similarity: 99.52% Conservative: 1
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 23.60% Indels: 0
DB: 5 Gaps: 0

US-09-810-796-5 (1-888) x BX917798 (1-628)

Qy 195 AlaLeuArgSerLeuAArgPheLeuGlnLeuArgMetValArgMetAspArgGly 214
Db 628 GCACCTGCGAAGTCTCGCTTCTTGACAGATCTCCGATGCTGGCATGGACCGCGAGGG 569
Qy 215 GlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuThrAla 234
Db 568 GGCACCTGGAAGTTACTGGGCTCCGTGTTATGCTCACAGCAAGGAATTAATCACAGCG 509
Qy 235 TrpTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLys 254
Db 508 TGGTACATAGAGATTTTGGTCTTATTTTTCATCTTCTTCTTATCTGGTGAAGAAG 449
Qy 255 AspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeu 274
Db 448 GATGCAATATAGGAGTTTCTACATATGACATGCTCTCTGGTGGGCGACAAATACATTG 389
Qy 275 ThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuSerAla 294
Db 388 ACAACGATTGGCTATGGAGACAAAACCCCTGACTTGGCTGGGAAGCTGCTCTGTCA 329
Qy 295 GlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGly 314
Db 328 GGCCTTGACATCTCTGGCATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 269
Qy 315 PheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAsnPro 334
Db 268 TTTGCAATATAAGTCAAGAACAGCACCGCCAGAAACACTTTGAGAAAGAAAGAACCG 209
Qy 335 AlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSer 354
Db 208 GCTGCCAACCTTATTCAGTGGCTTTGGCGAGTTATGACGCGCGAGAAATCTGTCTCC 149
Qy 355 IleAlaThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLys 374
Db 148 ATTGCAACTGGAAGCCACACTGAAGGCTTGACACCTGACGCCCCCACCACCAATCAGAAG 89
Qy 375 LeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArg 394
Db 88 CTCAGCTTTAAGGAGCGGTGGCATGCCAGCCCGGCGGCGAGCATTAAGAGCAGA 29
Qy 395 GlnAlaSerValGlyAspArgSer 403
Db 28 CAAGCTTAAGTGGGTGACAGGAGGTCC 2

RESULT 14
CD629766/c
LOCUS CD629766 717 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049391J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629766
VERSION CD629766.1 GI:40278032
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 717)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)
COMMENT Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
source
1. .717
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:
Pred. No.: 5.47e-92 Length: 717
Score: 1051.50 Matches: 218
Percent Similarity: 92.95% Conservative: 6
Best Local Similarity: 90.46% Mismatches: 4
Query Match: 23.13% Indels: 13
DB: 6 Gaps: 1
US-09-810-796-5 (1-888) x CD629766 (1-717)
Qy 345 SerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuLysAla 364
Db 715 AGTTACGACGCTGATGAGAAATCTGTGCCATTTGCACCTGGAGGCCACACTTGAAGGT 656
Qy 365 LeuHisThrCysSerProThr-----AsnGlnLysLeu 375
Db 655 TTGCACACTCGAGCCCTTACCAGAAAGAACAGAGGGAAGCATCAAGCAGTCAGAGCTA 596
Qy 376 SerPhe-LysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArg-G 395
Db 595 AGTTATTAAAGAGCGAGTCCGATGGCTAGCCCGAGGGCGGAGTATTAAAGACCGGAC 536
Qy 395 InAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGluGlySerProT 415
Db 535 AAGCTCTAGTAGTGACAGAGAGTCCCAAGCAGCCGACATCACAGCCGAGGCGAGTCCCA 476
Qy 415 hrLysValGlnLysSerTrpSerPheAsnAspArgTrpArgPheArgProSerLeuArgL 435
Db 475 CCAAGTGCAAGAGCTGGAGCTTCAACGACCCGCTTCCGCGCTTCCGCTCGCC 416
Qy 435 euLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspV 455
Db 415 TCAAAAGTTCTCAGCCAAACCCAGTGATGATGCTGACACAGCCCTTGGCACTGATGATG 356
Qy 455 alTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuL 475
Db 355 TATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGAAAGACCTACCCACCACCTTA 296
Qy 475 ysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysG 495
Db 295 AAATGTCATTCGAGCTATCAGAAATTTGAAATTTTCATGTTGCAAAACGGAAGTTAAGT 236
Qy 495 luThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuA 515
Db 235 AAACATTACGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 176
Qy 515 spMetLeuCysArgIleLysSerLeuGln-ThrArgValAspGlnInIleLeuGlyLysGly 534
Db 175 ACATGTTGTGTAGAAATTAAGAACCTTCAATAACACGCTGTGTGATCAAAATTTCTTGG 116
Qy 535 GlnIleThrSerAspLysLys-SerArgGluLysIleThrAlaGluHisGluThrAs 554
Db 115 CAATCATCATCAGATAGAAGACGAGCCGAGAGAAATAATACAGCAGAACATGAGACACCA 56
Qy 554 pAspLeuSerMetLeuGlyArgValValLysValLysGlnValGlnSerIle 572
Db 55 CGATCTCACTATGCTCGGTGGTCAAGGTTGTTAAACAGGTACAGTCCATA 1

RESULT 15

CD629755 691 bp mRNA linear EST 12-JAN-2004
 LOCUS 55049343H1 FLP Homo sapiens cDNA, mRNA sequence.
 DEFINITION CD629755
 ACCESSION CD629755.1 GI:40278021
 VERSION EST.
 KEYWORDS

SOURCE

Homosapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 691)
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.I.
 TITLE Circular rapid amplification of cDNA ends for high-throughput
 extension cloning of partial genes

JOURNAL

Genomics 84 (1), 205-210 (2004)

COMMENT

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 3160 Porter Dr., Palo Alto, CA 94304, USA
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FEATURES

Location/Qualifiers

1..691
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="FLP"
 /note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:

Pred. No.: 6.44e-92 Length: 691
 Score: 1050.50 Matches: 215
 Percent Similarity: 93.94% Conservative: 2
 Best Local Similarity: 93.07% Mismatches: 4
 Query Match: 23.10% Indels: 12
 DB: Gaps: 1

US-09-810-796-5 (1-888) x CD629755 (1-691)

QY 266 AlaLeuTTPTrpGlyThrIleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeu 285
 Db 1 GCTCTCTGTGGGGGACAAATACATGACACTATTGGCTATGGAGACAAACCTCCCTA 60
 QY 286 ThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPheAla 305
 Db 61 ACTTGGCTGGGAAGATTGCTTTCTGCAGCTTTGCACCTCTTGGCAATTTCTTTTGA 120
 QY 306 LeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGlnGlnHisArgGln 325
 Db 121 CTTCCTGCGGCAATCTTGGCTCAGGTTTGCATTAAGATACAAAGAACACACCGCCAG 180
 QY 326 LysHisPheGluLysArgArgAsnProAlaAlaLeuIleGlnCysValTrpArgSer 345
 Db 181 AAACACTTTGAGAAAGAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGTAGT 240
 QY 346 TyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuLysAlaLeu 365
 Db 241 TACGCACTGATGAGAAATCTGTTTCCATTGCACTGGAAGCCACACTTGAAGGCTTG 300
 QY 366 HisThrCysSerProThr-----AsnGlnLysLeuSer 376
 Db 301 CACACCTCGACCCCTACCAGAAAGAACAGGGGAAGCATCAAGCAGTCAGAACTAAGT 360
 QY 377 PheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAla 396
 Db 361 TTTAAGGAGCGAGTGGCGATGGCTAGCCCCAG-GGCCAGAGTATTAGAGCCGACAAAGCC 419
 QY 397 SerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu-GlySerProThrLy 416
 Db 420 TCAGTAGGTGACGAGAGTCCCAAGCACCACATCACGCCGAGGGGCGAGTCCCAACAA 479
 QY 416 sValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLy 436

Db 480 AGTCAGAAAGAGCTGGAGCTTCAACGGCCGAAACCGCTTCCGGCCCTCGCTGCGCCTCAA 539
 QY 436 sSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTy 456
 Db 540 AAGTTCTCAGCCAAACCCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGATA 599
 QY 456 rAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysTh 476
 Db 600 TGATCAAAAGAGATGCCAGTGTGATGATCATCATGGAAGAACTCACCCCCACACTTAA-AC 658
 QY 476 rValIleArgAlaIleArgIleMetLysPhe 486
 Db 659 TGTCAATTCGAGCTATCAGAAATTAATAATTC 689

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